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 ACCESSION AR062838  
 VERSION AR062838.1 GI:5990529  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 1713)  
 Russell, R. Joyce., Newcomb, R. David., Robin, G. Charlesde, Quetleville.,  
 Boyce, T. Mark., Campbell, P. Malcolm., Parker, A. Gerard.,  
 Oakeshot, J. Graham. and Smyth, K. -A.  
 TITLE Enzyme based bioremediation  
 JOURNAL Patent: US 5843758-A 2 01-DEC-1998;  
 FEATURES Location/Qualifiers  
 source 1..1713  
 BASE COUNT 506 a 299 c 363 g 515 t 30 others  
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 Best Local Similarity 72.5%; Pred. No. 7.5e-269;  
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ACCESSION	ARI53440
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SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified. 1 (bases 1 to 1713)
AUTHORS	Russell, R. Joyce., Newcomb, R. David., Campbell, P. Malcolm., Robin, G. Charlesde, Queteville., Claudianos, C., Smyth, K. -A., Boyer, T. Mark., Oakeshott, J. Graham, and Brownlie, J. Colin. Malathion carboxylesterase Patent: US 6235515-A 5 22-May-2001;
TITLE	Journal
JOURNAL	Patent: US 6235515-A 5 22-May-2001;
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 ORGANISM Drosophila melanogaster.  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT

Neoptera: Endopterygota; Diptera; Brachycera: Muscomorpha: Ephydroidea: Drosophilidae; Drosophila.  
 1 (bases 1 to 2017)  
 Stapleton, M., Broksstein, P., Hong, L., Abghayani, A., Carlson, J., Champe, M., Chavez, C., Dorset, V., Farrant, D., Frise, E., George, R., Gonzalez, M., Gharin, H., Li, P., Liao, G., Miranda, A., Mungall, C. J., Nunoo, J., Paclib, J., Paragas, V., Park, S., Phouanavong, S., Wan, K., Yu, C., Lewis, S. E., Rubin, G. M. and Celniker, S.  
 Direct Submission  
 Submitted (10-AUG-2001) Berkeley Drosophila Genome Project, Lawrence Berkeley National Laboratory, One Cyclotron Road, Berkeley, CA 94720, USA  
 Sequence submitted by:  
 Lawrence Berkeley National Laboratory  
 Berkeley Drosophila Genome Project  
 Lawrence Berkeley National Laboratory  
 Berkeley, CA 94720  
 This clone was sequenced as part of a high-throughput process to sequence clones from Drosophila gene collection 1 (Rubin et al., Science 2000). The sequence has been subjected to integrity checks for sequence accuracy, presence of a polyA tail and contiguity within 100 kb in the genome. Thus we believe the sequence to reflect accurately this particular cDNA clone. However, there are artifacts associated with the generation of cDNA clones that may have not been detected in our initial analyses such as internal priming, priming from contaminating genomic DNA, retained introns due to reverse transcriptase errors that result in single base changes, reverse transcriptase errors that result in single base changes. For further information about this sequence, including its location and relationship to other sequences, please visit our web site (<http://fruitfly.berkeley.edu>) or send email to [cdna@fruitfly.berkeley.edu](mailto:cdna@fruitfly.berkeley.edu).

FEATURES

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 QY 1525 ACCACCGCAACATATACAGCATATGATGCGGATGGAACCACTCACCTGGATGCC 1584  
 Db 1618 GCGAGGCTATTCCTACAGCAGAGATATGACGATGGAACACTCTGACCATTTGATTC 1677  
 QY 1585 ATAAAAAATTCGATGATGCTATTAATGTTTAAATGCGGATGATGAAAGTATG 1644  
 Db 1678 GTTCCCAATTCGACAGAGTATATGATGCTTCACTCACTAGTATGACCTGAAATTCATC 1737  
 QY 1645 GATTTGCCAGAAATGATTAATTAATTAATGAGGCAAGTATTTGATTAAGAAAGAGAA 1704  
 Db 1738 GATTCGCTGATGTTGCCCAATTAAGTCTGGAGAGCTCTATACGACCAAAAGAT 1797  
 QY 1705 TTGTT 1709  
 Db 1798 TTATTT 1802

RESULT 13  
 LOCUS AY058637  
 DEFINITION Drosophila melanogaster LD33453 full length cDNA.  
 ACCESSION AY058637  
 VERSION AY058637.1 GI:16198126  
 KEYWORDS FLI\_CDNA.  
 SOURCE Drosophila melanogaster.  
 ORGANISM Drosophila melanogaster.  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Phylotroidea; Drosophilidae; Drosophila.  
 REFERENCE 1 (bases 1 to 2122)  
 Stapleton, M., Brokslein, P., Hong, L., Abmayan, A., Carlson, J., Champe, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E., George, R., Gonzalez, M., Gartin, H., Li, P., Liao, G., Miranda, A., Mungall, C.J., Nuno, J., Paele, J., Paragas, V., Park, S., Phouanavong, S., Wan, K., Yu, C., Lewis, S.E., Rubin, G.M. and Celisner, S.  
 Direct Submission  
 Submitted (08-OCT-2001) Berkeley Drosophila Genome Project, Lawrence Berkeley National Laboratory, One Cyclotron Road, Berkeley, CA 94720, USA  
 Sequence submitted by:  
 Berkeley Drosophila Genome Project  
 Lawrence Berkeley National Laboratory  
 Berkeley, CA 94720  
 This clone was sequenced as part of a high-throughput process to sequence clones from Drosophila Gene Collection 1 (Rubin et al., Science 2000). The sequence has been subjected to integrity checks for sequence accuracy, presence of a polyA tail and contiguity within 100 kb in the genome. Thus we believe the sequence to reflect accurately this particular cDNA clone. However, there are artifacts associated with the generation of cDNA clones that may have not been detected in our initial analyses such as internal priming, priming from contaminating genomic DNA, retained introns



due to reverse transcription of unspliced precursor RNAs, and reverse transcriptase errors that result in single base changes. For further information about this sequence, including its location and relationship to other sequences, please visit our web site (<http://fruitfly.berkeley.edu>) or send email to [cdna@fruitfly.berkeley.edu](mailto:cdna@fruitfly.berkeley.edu).

## FEATURES

source location/Qualifiers

1. 2122  
/organism="Drosophila melanogaster"  
/strain="y; cn bw sp"  
/db\_xref="taxon:7227"

## gene

1. 2122  
/gene="alpha-Est1"  
/note="alignment with genomic scaffold AE003671"

## CDS

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166..1863  
/note="Longest ORF"

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SAGASVHALMTEDTGLFKAIMQSSSMCEANPESGRMAYRLACOLGSGSENE  
KEFVYIOLKAPASEMAAGITLVSOEERQVLPFPVPEYPTTRCCVPRCHREML  
PEAMGNDLPLILGNSFEGFLSYOSTLHDEHMLSAFVLPRIETRSKOSHLKDL  
ROFKNDFNDATRGHNEFECILHLSYFHLHNGHILRVLSMEVQTIORLVGMVAA  
SPHFHNFQVOMGKHVRGVSHADLISYFHLHNGHILRVLSMEVQTIORLVGMVAA  
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## BASE COUNT

536 a 524 c 563 g 499 t

## ORIGIN

Query Match 20.7%; Score 353.2; DB 3; Length 2122;  
Best Local Similarity 52.4%; Pred. No. 2.3e-92;

Matches 878; Conservative 0; Mismatches 778; Indels 18; Gaps 4;

27 TCGCCTGAACCTATGCTTTAATGATGTCATTAATATACACAACTACCGTCTGAGTAC 86  
192 TCTCTGAATAATGGCCACCAAGCTCATTTGGCCACCAAGATGTCATATCGCTTGGCAC 251  
87 AATGAACCAATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 146  
252 AAGACAGACGAGTGTGTGACGACGAGGATGCGGAGTGTGCGGACATGCGGAAGGAC 311  
147 CGTCT--ACGATGATTTCTTACTACATTTTCGAGATGATGATGATGATGATGATGATGAT 203  
312 ACTCTACGACGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 371  
204 GGGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 263  
372 GGGGAGCTGGCTTCCGAGCCCGCCACGACATCCCGTGGTGGGGGTGGGGGATG 431  
264 CTGTGGCCAGCCACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 323  
432 CACCTATCCGCGCGCCAGCCGATGATGATGATGATGATGATGATGATGATGATGATGAT 491  
324 GAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 383  
492 CCGGATTTGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 551  
384 TGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 443  
552 CGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 611  
444 TGTGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 503  
612 CAGTCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 671

504 TGTGTGGTTCCTTACCTGAAATCGGAATATCTCATGTCCTCCGCGGACGCTGCT 563  
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732 CAAGACCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 791  
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684 GATTAACCAAGACGCGGTGTATGATGATGATGATGATGATGATGATGATGATGATGAT 743  
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744 GGTCTATGAGGCTTCTACAGATGATGATGATGATGATGATGATGATGATGATGATGAT 803  
912 CTGCGAGTGGGCAATGAGCAAGTGTGAGGCGATGATGATGATGATGATGATGATGATGAT 971  
804 CTATTAAGGAGAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 863  
972 ATACTCGGCGAGTGAAG 1031  
864 TGATTTGATCAAG 923  
1032 CGAATAGGCGGCAAGAGGATATGATGATGATGATGATGATGATGATGATGATGATGAT 1091  
924 GTTCTCTTGGACCCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 983  
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1044 CTCTTACAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1103  
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1164 GGAATCCCTGAGAGGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1223  
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1224 TCTGATTAATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1283  
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1284 CTTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1343  
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1629 TAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1688  
1524 CACCAACGAGCAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1583  
1689 CCGAAGAGCAATATCCCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1739  
1584 CATTAATAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1643

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Db 1740 ACTAGTGA---GAAAGGCCCGACAGATGTCCTCAATATGGAACAAACAGAGTTCAT 11796
QY 1644 GGAATTTGCCGAATATGATTAATTAACAAATGGCCAGTATATTCGATTAATAA 1697
Db 1797 TGTGCTGCCGAGTGCMAACGAATGCGATTTGGATTAAGACTATACATTAATAA 1850

RESULT 14
AX260182
LOCUS AX260182 1809 bp DNA linear PAT 26-OCT-2001
DEFINITION Sequence 144 from Patent WO0172774.
ACCESSION AX260182
VERSION AX260182.1 GI:16509196
KEYWORDS
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE
1. Deak P., Glover, D.M. and Midgley, C.
AUTHORS Cell cycle progression proteins
TITLE Patent: WO 0172774-A 144 04-OCT-2001;
JOURNAL Cyclacel Limited (GB)
FEATURES
Location/Qualifiers
source 1..1809
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
BASE COUNT 500 a 435 c 444 g 430 t
ORIGIN

Query Match 20.6%; Score 352.8; DB 6; Length 1809;
Best Local Similarity 54.3%; Pred. No. 3e-92;
Matches 876; Conservative 0; Mismatches 687; Indels 51; Gaps 6;

QY 101 TAATCATATCTGAATATGACAAATTAAGGTTTAAAGCATGACCTCTACGATGAT 160
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QY 161 CTATACAGTTTTCGAGATATACCTTATGCTAACGCTCCGATGGGTAGTTGATCA 220
Db 299 GCTACTTCACTTTCGAGAAATACCTTCGCAAGCCCTCGGTGGAGATCTGGCTTCA 358
QY 221 AGGCAACCCAGGCGCTTACCAGTGAAGGTTGATGATGCTGGGCCAACCA 280
Db 359 AGGCCCCGGAACAGTGAAGCCATGGGATCAGAAATGGATTGCACTTCCCGGACACA 418
QY 281 GATCGGTACAGACATTTCAATAGTGGCAACCCACAGTTCGGAGATGCTATACC 340
Db 419 AGCCCTTCAGACACACATGTTTTCAGAAATATGCGGGCTCAGAGACTGCTCTAC 478
QY 341 TGAATGTATACCAATGACTTGAACCCAGCAAAAGCGCTCCGTTATGTTTATCC 400
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QY 401 ATGCGGAGATTTTATTTTGGGGAAGCAAAATGTAAGTGTGTTCCGACTACTTA 460
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QY 461 TGAAGAAACCCGTGCTTGTGTAACCGTGAATATGCTTTGGTGTGTTGTTCTTA 520
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QY 581 CTTGAGATGAGTCAAGAGTAAATATGCAATTTGGTGGGATGATGAATATTAACG 640
Db 692 CCTGCGATGAGTCAAAACAAATGAGCATTCGGCGGTGATTCCAACATATTAAC 751
QY 641 TCTTGGCGAAAGTGTGCTGAGGCTCAACCATTAATGATGATTAACCAAGACCC 700

Db 752 TCTTTGGGAAAGTCCCGGAGAGCTGACCACTTCTTGCACTAAGTCCCAACAG 811
QY 701 GTGTTTATTCATGCTGATATCATGATGTCGGTAAATTCATGCTCATATGGCTCA 760
Db 812 AAGTCTTATCCCAAAACATATGCTTATGTCGGGCAAGTGTGTCCTGACCAAC 871
QY 761 CAGATGCGAAAGTGTGCTGCTACCAATGCGCAAAAGCTGTGTTAAGGAGAGACA 820
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QY 1355 AAATATTAACCCATGCTATTTATGCTTTGGCCGTGCTGATTAAGGTGAAGCCATG 1414
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QY 1595 CCGATATGCTCTTAATATGTTAATATGAGGATGAATGAAATGATTAATTTGACAG 1654
Db 1695 -CGTAACCAACTTAAATGCTCAATATGAGGATCAGTTGAATGATATGCGCTTCAG 1753
QY 1655 AATGATGATTAATTAACCAATGGCAAGTATTTGATTAATAAAGAGAAATGT 1708
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RESULT 15

```





	RESULT 1	
XX	AAT68597	
XX	AAT68597 standard; DNA; 1710 BP.	
XX	AAT68597;	
XX	08-AUG-1997 (first entry)	
XX	Md-alpha-E7 gene.	
XX	Malathion carboxylesterase; organophosphate; insecticide;	
XX	pesticide; remediation; bioremediation; decontamination; ds.	
XX	Musca domestica Rutgers strain.	
OS		
FH	Key	Location/Qualifiers
FT	mutation	752
FT	/tag= a	
FT	/note= "Trp-251 TGG codon is altered to a Ser"	
FT		codon in resistant mutants"
PN	W09719176-Al.	
XX		
PD	29-MAY-1997.	
XX		
PF	22-NOV-1996;	96WO-AU00746.
XX		
PR	23-NOV-1995;	95AU-0006751.
XX		
PA	(CSTR ) COMMONWEALTH SCI & IND RES ORG.	
PI	Boyce T, Brownlie JC, Campbell PM, Claudianos C;	

PI Newcomb RD, Oakesholt JG, Robin GC, Russell RJ, Smyth K;  
XX WPI: 1997-298113/27.  
DR P-PSDB: AAM17767.  
XX  
PT DNA encoding enzyme that degrades organophosphate pesticides -  
XX useful for decontamination of soil, water, food etc  
XX  
PS Claim 6: Fig 3: 52pp; English.

A 1710 bp DNA molecule (AAT68597) comprises the Md-alpha-E7  
coding sequence of the Musca domestica Rutgers strain. It was  
isolated by amplification of genomic DNA using alpha-esterase  
consensus primers (see also AAT68598-99) and use of a 534 bp  
amplicon to screen a genomic library of M. domestica. A  
mutation of the gene, resulting in substitution of serine for tryptophan  
at amino acid position 251 (see also AAM17767), confers malathion  
resistance. The resistant enzyme acts as a malathion  
carboxylesterase and can be formulated for use in degrading  
environmental carboxylester or dimethyl general organophosphates.

Sequence 1710 BP; 498 A; 369 C; 394 G; 449 T; 0 other;

Query Match 100.0%; Score 1710; DB 18; Length 1710;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1710; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 ATGACTTTTGAAGCAATTCATATTTGCGCTGAACATATGCTTAATGATGTCAT 60  
QY 61 AAATACACAACTACGCTGAGTACAAATGAAGCAATATATGATATGTA 120  
DB 61 AAATACACAACTACGCTGAGTACAAATGAAGCAATATATGATATGTA 120  
QY 121 CAAATTAAGGGTGTAAAGCAATGACCGTCTACGATGATCTTCAACAGTTTCA 180  
DB 121 CAAATTAAGGGTGTAAAGCAATGACCGTCTACGATGATCTTCAACAGTTTCA 180  
QY 181 ATACCATGCTAAGCCTCCAGTGGGTGAGTTGAGTTCAAGGACCCGAGGCTGTA 240  
DB 181 ATACCATGCTAAGCCTCCAGTGGGTGAGTTGAGTTCAAGGACCCGAGGCTGTA 240  
QY 241 CCATGGAGGGTGTACGTATGCTGTGGGCCAGCCAGATCGGTACAGACATTTT 300  
DB 241 CCATGGAGGGTGTACGTATGCTGTGGGCCAGCCAGATCGGTACAGACATTTT 300  
QY 301 ATAGTGGCAAAACCCACAGGTTGGAGATTGCTATACCTGAATGTGTATACCAATGAC 360  
DB 301 ATAGTGGCAAAACCCACAGGTTGGAGATTGCTATACCTGAATGTGTATACCAATGAC 360  
QY 361 TTGAACCCAGACAAAGGGGCTCTGTATGATGTTTCAATCCATGATGTTATTTTC 420  
DB 361 TTGAACCCAGACAAAGGGGCTCTGTATGATGTTTCAATCCATGATGTTATTTTC 420  
QY 421 GGGGAGCAAAATGTAAGTGTGGTCCGACTATTATGAAGAAACCCGTTGTTG 480  
DB 421 GGGGAGCAAAATGTAAGTGTGGTCCGACTATTATGAAGAAACCCGTTGTTG 480  
QY 481 GTAACGTCATATGCTTTGGGTGTTGGTTCCTTACCTGTAATCGGAAATCTC 540  
DB 481 GTAACGTCATATGCTTTGGGTGTTGGTTCCTTACCTGTAATCGGAAATCTC 540  
QY 541 AATGTCCTCCGACACGCTGCTCAAGATCAAGTAATGCTTGAAGTGGTCAAGT 600  
DB 541 AATGTCCTCCGACACGCTGCTCAAGATCAAGTAATGCTTGAAGTGGTCAAGT 600  
QY 601 AATATGTCATTTGGGTGGGTGATGACAAATATACCGTCTTGGCGAAAGTCTGT 660  
DB 601 AATATGTCATTTGGGTGGGTGATGACAAATATACCGTCTTGGCGAAAGTCTGT 660  
QY 661 GGGGCTCAACCATTTACATGATGATACGACAGACCCGTTGTTATTCATCGTGT 720  
DB 661 GGGGCTCAACCATTTACATGATGATACGACAGACCCGTTGTTATTCATCGTGT 720

DB 661 GGGGCTCAACCATTTACATGATGATACGACAGACCCGTTGTTATTCATCGTGT 720  
QY 721 ATCATGATGTCGCGTAATTCATGTCGTCATAGGGGCTCTACAGATGCGCAATGCTGG 780  
DB 721 ATCATGATGTCGCGTAATTCATGTCGTCATAGGGGCTCTACAGATGCGCAATGCTGG 780  
QY 781 CTCACCATGCGCAAAAGTGTGGCTATAGGAGAGACATGAAAAAGATCTCGGAA 840  
DB 781 CTCACCATGCGCAAAAGTGTGGCTATAGGAGAGACATGAAAAAGATCTCGGAA 840  
QY 841 TTCCATATGAAGCAATCCCTATGATGATGATGATGATGATGATGATGATGATGATGAT 900  
DB 841 TTCCATATGAAGCAATCCCTATGATGATGATGATGATGATGATGATGATGATGATGAT 900  
QY 901 GAAAGATGCAAAATTAAGTGTATGTTGCTTTGAGACCCCTAGAACATACCGAGACA 960  
DB 901 GAAAGATGCAAAATTAAGTGTATGTTGCTTTGAGACCCCTAGAACATACCGAGACA 960  
QY 961 GCGGACGTGTGTGACCCCAACCAATCAGAAATGATGATGATGATGATGATGATGATGAT 1020  
DB 961 GCGGACGTGTGTGACCCCAACCAATCAGAAATGATGATGATGATGATGATGATGATGAT 1020  
QY 1021 ATACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080  
DB 1021 ATACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080  
QY 1081 CAAATATCCGAGGTGTGTAAGAGTGTGAATCTGTGTGAATTTATGATGATGATGATGAT 1140  
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QY 1141 GCTGACAGTGAAGAGAGTGTGCGGAAACCGTGAAGAGGCTGCAATGTAAGGAGCC 1200  
DB 1141 GCTGACAGTGAAGAGAGTGTGCGGAAACCGTGAAGAGGCTGCAATGTAAGGAGCC 1200  
QY 1201 CATGTGATGAGGAGAAACACTACTGTGATTAATTTATGATGATGATGATGATGATGAT 1260  
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QY 1261 TTCTCTTCCCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320  
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QY 1321 ATTTATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380  
DB 1321 ATTTATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380  
QY 1381 CGTTTGGGCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440  
DB 1381 CGTTTGGGCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440  
QY 1441 AACATTTTGTGAAGAGCGCTGCAAGAGAAAGCGCAATACAAACCATGTAAGCGCATG 1500  
DB 1441 AACATTTTGTGAAGAGCGCTGCAAGAGAAAGCGCGCAATACAAACCATGTAAGCGCATG 1500  
QY 1501 GTTGGCATTTGAGAGCAATGTCGCAACACCGGCAACCATACAGCAATGATATAGCCGGC 1560  
DB 1501 GTTGGCATTTGAGAGCAATGTCGCAACACCGGCAACCATACAGCAATGATATAGCCGGC 1560  
QY 1561 ATGGAAGACCTGACCTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620  
DB 1561 ATGGAAGACCTGACCTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620  
QY 1621 ATGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680  
DB 1621 ATGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680  
QY 1681 AGTATATTCGATTAAGAGAGATGTTT 1710  
DB 1681 AGTATATTCGATTAAGAGAGATGTTT 1710  
RESULT 2  
AA091561

ID AA091561 standard; cDNA; 1713 BP.  
 AC AA091561.  
 XX 22-DEC-1995 (first entry)  
 XX OP-sensitive esterase E3 Lc743 clone.  
 DE Esterase; E3: bioremediation; organophosphate; carbamate;  
 XX Insecticide; pesticide; water decontamination; meat decontamination;  
 KW ss.  
 XX Lucilia cuprina.  
 OS  
 XX Key Location/Qualifiers  
 FT CDS 1..1713  
 FT /tag- a  
 FT  
 XX MO9519440-A1.  
 XX 20-JUL-1995.  
 XX 13-JAN-1995; 95MO-AU00016.  
 XX 13-JAN-1994; 94AU-0003347.  
 XX (CSIR ) COMMONWEALTH SCI & IND RES ORG.  
 XX Boyce TM, Campbell PM, Newcomb RD, Oakeshott JG;  
 PI Parker AG, Robin GC, Russell RJ, Smyth K;  
 XX WPI; 1995-263870/34.  
 DR P-PSDB; AAR78142.  
 XX Pure E3 esterase from *Lucilia cuprina* and related DNA - used to  
 PT eliminate residues of organophosphate and carbamate pesticides from  
 PT water, meat etc.  
 XX  
 XX Claim 5; Page 12-17; 38pp; English.  
 XX cDNA from organophosphate (OP)-sensitive *L. cuprina* pupa cDNA  
 CC library was amplified using cluster-specific esterase primers.  
 CC Isolated clone Lc743, a probable full-length cDNA, was expressed  
 CC using a baculovirus vector in insect cells and shown to encode  
 CC an OP-susceptible E3 esterase, useful in bioremediation.  
 XX  
 XX Sequence 1713 BP; 516 A; 305 C; 370 G; 522 T; 0 other;  
 SQ  
 Query Match 55.9%; Score 956.6; DB 16; Length 1713;  
 Best Local Similarity 73.4%; Pred. No. 2e-285;  
 Matches 1223; Conservative 0; Mismatches 444; Indels 0; Gaps 0;

Db 344 GTGCTATACGATTAATTAATCCGAAACTAAACGTCCTTTAGTATACATACATG 403  
 Qy 404 GCGAGATTTTATTTTCGCGCAAGCAATCTACTGGTTGGCCGACATCTTATGA 463  
 Db 404 GTGTGTTTATTTATTCGGAATAATCATGATGATGATGCTGATTTTTCATTA 463  
 Qy 464 AGAAACCCGTCCTGTGTACCGTCGAATATGCTTTGGGTGTGTGGTTCCTTACC 523  
 Db 464 AAAAGATGTGCTGTGTATTAACATACATATGCTTTGGGACCTGATTTTCAAGT 523  
 Qy 524 TGAATCGAAAAATCTCATGTCCCGGCAAGCTGGCTCAAGATCAAGTAATGGCT 583  
 Db 524 TAAATTCAGAAACCTTAATGTGCGGTAAATGCGCCTTAAAGTCAAGTATGGCT 583  
 Qy 584 TGAATGGGTACAGATTAATATGTCATTTTGGTGGCGATGACATATTTACGCT 643  
 Db 584 TGCCTTGATTAATAAATAATTTGGCCACTTGTGGTGCATTCGGAATATTTACAGT 643  
 Qy 644 TCGCGAAAGTGTGTGGGGCTCAACCCATTACATGATGATTAACGCAAGACCCGTG 703  
 Db 644 TTGCTGAAGAGTCCGCGGTGCTCTACCATGATGATTAACGCAAGACCCGTG 703  
 Qy 704 GTTATTCATCTGTGTATCATGATGTGCGTAAATTCATGCTCTATGGGCTCTACAG 763  
 Db 704 GTCTTTCATCTGTGTATCATGATGTGCGTAAATTCATGCTCTATGGGCTCTACAG 763  
 Qy 764 AATGCCAAGTGTGTGCGCTCAACCCATTACATGATGATTAACGCAAGACCCGTG 823  
 Db 764 AATGCCAAGTGTGTGCGCTCAACCCATTACATGATGATTAACGCAAGACCCGTG 823  
 Qy 824 AAAAGATATCTGTGAATTCCTTAATGAAGCAATCCCTTATGATTTGATTAAGAGAG 883  
 Db 824 AATGCCAAGTGTGTGCGCTCAACCCATTACATGATGATTAACGCAAGACCCGTG 883  
 Qy 884 CACAAGTTTGAACCCCAAGATGCAATATGATGATGATGATGATGATGATGATG 943  
 Db 884 AAAAGATATCTGTGAATTCCTTAATGAAGCAATCCCTTATGATTTGATTAAGAGAG 943  
 Qy 944 TAGAACATATACGACAGCCGCTGTGTGTACCAACCAATCAGAAATGCTGAAGA 1003  
 Db 944 TTGACCATATAGACCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1003  
 Qy 1004 GCGCTGGGGAATTCATCCCATATGATGATGATGATGATGATGATGATGATG 1063  
 Db 1004 CCGCTGGGGAATTCATCCCATATGATGATGATGATGATGATGATGATGATG 1063  
 Qy 1064 CCAATATATTCGCAACCAATATCCGAGGTGTAAAGATGTAATTCCTGTGAT 1123  
 Db 1064 TCACTTCAATTTCTTAAGCAATGCTATGCTTTAAGATGTAATTCCTGTGAT 1123  
 Qy 1124 ATGTGCTTGGAGT 1183  
 Db 1124 TTGTGCAAGTGAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1183  
 Qy 1184 CCAATATATTCGCAACCAATATCCGAGGTGTAAAGATGTAATTCCTGTGAT 1243  
 Db 1184 CTAATATATTAAGGCTCAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1243  
 Qy 1244 TTGTGCTTATTTCTATTTCTTCCCATGATGCTTCCATATTTGGCTTCAAC 1303  
 Db 1244 TTGTGCTTATTTCTATTTCTTCCCATGATGCTTCCATATTTGGCTTCAAC 1303  
 Qy 1304 ACACAGT 1363  
 Db 1304 ACACAGT 1363  
 Qy 1364 ACCCTATGCTATTTATGCTTTTGGCGGTAAAGCTTAAAGCTTAAAGCTTAAAG 1423  
 Db 1364 ATCCCTATGCTATTTATGCTTTTGGCGGTAAAGCTTAAAGCTTAAAGCTTAAAG 1423  
 Qy 1424 TAACCTATGCTTGTGTGAACATTTTGTGCAAGACCTGCAAGGAAGGCGCGAATCA 1483  
 Db 1424 TAACCTATGCTTGTGTGAACATTTTGTGCAAGACCTGCAAGGAAGGCGCGAATCA 1483



(CSIR) COMMONWEALTH SCI &amp; IND RES ORG

704 GTTATTCATCGTGGTATCATGATGTCCGGTAATTCATGTGCTCATGGGCTTACAG 763

Db 704 GTCTTTTCATCGTGTATCTAATATGCGGTAATGCTATTTGCTCATTTGGGCTAATATCC 763  
 Qy 764 AATGCCAAAGTCGTGCGCTCACATATGCGCAACGTTGGCTATATAGGAGAGACATATG 823  
 Db 764 AATGTCAACATCGTCCCTTACCTTACCAATTTGGCGGCTATATAGGAGATATATG 823  
 Qy 824 AAAAGATATCTGGAATTCCTAATGAAAGCAATCCCTATGATTTGATGATCAAGAGAGC 883  
 Db 824 ATAAGATGTTTGGAAATTTCTTATGAAAGCAAGCCACAGGATTTAATAAACCTTAGG 883  
 Qy 884 CACAGTTTGGACACCGCAAGATGCAAAATAGTCATGTTCCCTTTGGACCCACTG 943  
 Db 884 AAAAGTTTATCTCTAAGAGAGCGTACAAATAGTCATGTTCTTTGGTCCACTG 943  
 Qy 944 TAGAACATACAGACAGCCGCTGTGTGATCCCAACCAATCAGAAATGATGAGAGA 1003  
 Db 944 TTGAGCCATATCAGACCGCTGATTTGTCTTACCAACATCCTCGGGAATAGTTTAA 1003  
 Qy 1004 GCGCTGGGGAATTCGATACCCATTTGATAGCAATACCTCTACAGAGTTGCTTT 1063  
 Db 1004 CTGCTTGGGTAATTCGATACCCACTATGATGAGGTAACACTTATGAGGCTATTTT 1063  
 Qy 1064 CCAATATCAATTCGCAACCAATATCCGAGTGTAAAGATTTGAAATCCCTGTGATTT 1123  
 Db 1064 TCACTTCATTTCTTAAGCAAAATGCTTATGCTTTAAAGAAATGGAATTTGTCTCATTT 1123  
 Qy 1124 ATGTGCTTGGAGTGTGCTGACAGTAAACGAGTGCCTCCGGAACCTTGAGAGGCTG 1183  
 Db 1124 TTGTGCCAAGTAAATGCTGATGCTGTAAGCAGCCGCCAGAGACCTTGAAATGGAGT 1183  
 Qy 1184 CCAATTTGAAAAAGCCCATGATGATGAGGAAACACCTACTCTGATTAATTTATGAGC 1243  
 Db 1184 CTAATATTTAAAGGCTGATGTAACAGAGAAACCAACAGCTGATTAATTTATGATC 1243  
 Qy 1244 TTTGCTCTATTTCTATTTCTCTCCCATGATGCTGCTCAATTTGCTGTCAAC 1303  
 Db 1244 TTTGCTCTATTTCTATTTCTCTCCCATGATGCTGCTCAATTTGCTGTCAAC 1303  
 Qy 1304 ACACAGCTGGACCTCCATTTATTTGATGCTTGCATTTGATTTGCAAGAAATTTATTA 1363  
 Db 1304 ACACCTCGGTAACCCCTGCTACTGTAATGCTTGTGATTTGATTTGCAAGATTTATTA 1363  
 Qy 1364 ACCCTATGATTAATGCTGTTGGCGCTGTAAGGTTAAGGCTAAGCCGCTGATGAC 1423  
 Db 1364 ATCCCTATGATTAATGCTGTTGGCGCTGTAAGGTTAAGGCTAAGCCGCTGATGAT 1423  
 Qy 1424 TAACCTATCTTTCTGGAACATTTTGTGGAACGCTGCCCAAGGAAAGCCGCAATACA 1483  
 Db 1424 TAACCTATTTCTTTGGAATCAATTTGGCCAAACGATGCTTAAGAAATCGGCTGATACA 1483  
 Qy 1484 AAACATTTGAACGATGCTGATATGATATGATATGCAATTTGCAACCTGCTATATTA 1543  
 Db 1484 AAACATTTGAACGATGCTGATATGATATGATATGCAATTTGCAACCTGCTATATTA 1543  
 Qy 1544 GCAATGATATAGCGGCAAGGAAACCTACCTGGATGCCATTAATAAATCCGATGATG 1603  
 Db 1544 GCAATGATATAGCGGCAAGGAAATGTTTCTGGGATGCCATTTAAGAAATCCGAGAG 1603  
 Qy 1604 TCTATTAATGTTTAATATCGGCGATGATGAAAGTTATGATTTGCAAAATGATGTA 1663  
 Db 1604 TATACAGGTTTGAATATTTATGAGCAATTTGAAATGATTTGCTGTAATGATTA 1663  
 Qy 1664 AAATTAACATGCGCAAGTATTTGATTAAGAAAGAGAGATTTT 1710  
 Db 1664 AGATTAACATGCGAATGATTTTGAAGAAACATGAGATTTATTT 1710

RESULT 4  
 AA091566  
 ID AA091566 standard; cDNA; 1713 BP.  
 XX  
 AC AA091566;

XX  
 DT 22-DEC-1995 (first entry)  
 DE OP-resistant esterase Lc7L103con.  
 DE Esterase; E3; bioremediation; organophosphate; carbamate;  
 KW Insecticide; pesticide; water decontamination; meat decontamination;  
 KW ss.  
 XX  
 XX Lucilia cuprina.  
 OS  
 FH Key 1.1713  
 FT CDS /tag= a  
 FT  
 PN W09519440-A1.  
 PD 20-JUL-1995.  
 XX  
 XX 13-JAN-1995; 95MO-AU00016.  
 PF 13-JAN-1994; 94AU-0003347.  
 PR  
 XX  
 PA (CSIR) COMMONWEALTH SCI & IND RES ORG.  
 PI Boyce TM, Campbell PM, Newcomb RD, Oakeshott JG;  
 PI Parker AG, Rodin GC, Russell RJ, Smyth K;  
 XX  
 XX WPI; 1995-263870/34.  
 DR  
 XX  
 PT Pure E3 esterase from Lucilia cuprina and related DNA - used to  
 PT eliminate residues of organo:phosphate and carbamate pesticides from  
 PT water, meat etc.  
 PS Example 4; Page 12-17; 38pp; English.  
 CC RT-PCR was used to clone a cDNA allele of Lc-alpha-E7 (encoding  
 CC OP-susceptible esterase E3 of L. cuprina) from a diazinon  
 CC resistant strain, Llandillo 103. 4 isolated clones were  
 CC sequenced (Lc7L103 A-D, AA091562-65) that encoded diazinon-resistant  
 CC esterases; a consensus sequence is given in AA091566.  
 XX  
 SQ Sequence 1713 BP; 512 A; 307 C; 369 G; 525 T; 0 other;  
 Query Match 55.8%; Score 955; DB 16; Length 1713;  
 Best Local Similarity 73.3%; Pred. No. 6; le-285;  
 Matches 1222; Conservative 0; Mismatches 445; Indels 0; Gaps 0;  
 Qy 44 TTAATGATGTCATTAATTAATACCAAACTACCTGATGATCAATGAACCAATAA 103  
 Db 44 TTAATGATGTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 103  
 Qy 104 TCGATGATGATTAATGCAATTAAGGCTTAAAGCAATGACCGTCTAGATGATCTT 163  
 Db 104 TCGATGATGATTAATGCAATTAAGGCTTAAAGCAATGACCGTCTAGATGATGATCTT 163  
 Qy 164 ACTGACATTTGAGAGTATACCGGTAAGGCTTTAAAGCTTTAACTGTTAGATGATGATCTT 223  
 Db 164 ACTGACATTTGAGAGTATACCGGTAAGGCTTTAAAGCTTTAACTGTTAGATGATGATCTT 223  
 Qy 224 CACCCAGCGCGCTGATACATGAGGAGGTAGCTGATTTGCGCCAGCAAGAT 283  
 Db 224 CACCCAGCGCGCTGATACATGAGGAGGTAGCTGATTTGCGCCAGCAAGAT 283  
 Qy 284 CCGTACGACAGATTTATTAAGTGCAACCCAGAGTTGGAGGATTTGCTATACCTGA 343  
 Db 284 CCGTACGACAGATTTATTAAGTGCAACCCAGAGTTGGAGGATTTGCTATACCTGA 343  
 Qy 344 ATGTATACCAATGATTTGATGACCAAGCAAAAGGCTGCTTATGTTTATCATCCAG 403  
 Db 344 GCGTCTATACCAATGATTTGATGACCAAGCAAAAGGCTGCTTATGTTTATCATCCAG 403  
 Qy 404 GCGGAGATTTTATTTTGGGGAAGCAATGTAATGTTGTTGCTCCGACTTATTAAGA 463





PT water, meat etc.

XX Example 4: Page 12-17; 38pp; English.

CC RT-PCR was used to clone a cDNA allele of Lc-alpha-E7 (encoding  
CC Op-susceptible esterase E3 of *L. cuprina*) from a diadion  
CC resistant strain, Llandillo 103. 4 Isolated clones were  
CC sequenced (LC7L103 A-D, A091562-65) that encoded diadion-resistant  
CC esterases. The esterases, or cells expressing them, are used  
CC in bioresmediation.

XX Sequence 1713 BP; 513 A; 307 C; 369 G; 524 T; 0 other.

Query Match

Best Local Similarity 55.8%; Score 955; DB 16; Length 1713;  
Matches 1222; Conservative 73.3%; Pred. No. 6,1e-285;  
0; Mismatches 445; Indels 0; Gaps 0;

44 TTAATGATGTCATTAATACAAACCTGCTGATGACCAATGAAACCAATAA 103  
44 TTAATGATGTCATTAATACAAACCTGCTGATGACCAATGAAACCAATAA 103  
104 TCGATGATGTCATTAATACAAACCTGCTGATGACCAATGAAACCAATAA 163  
104 TCGATGATGTCATTAATACAAACCTGCTGATGACCAATGAAACCAATAA 163  
104 CTGATGATGTCATTAATACAAACCTGCTGATGACCAATGAAACCAATAA 163  
164 ACTACAGTTTGGAGGTATACCGTACGCAACCGCGAGTGGAGCTGAGATTAAAG 223  
164 ACTACAGTTTGGAGGTATACCGTACGCAACCGCGAGTGGAGCTGAGATTAAAG 223  
224 CACCCAGCGCTGTACCATGAGGAGGTGATGATGCTGTGGGCGCCAGCAAGAT 283  
224 CACCCAGCGCTGTACCATGAGGAGGTGATGATGCTGTGGGCGCCAGCAAGAT 283  
284 CGGATACAGACATTTCAATAGTGAAGCAACCCAGAGTTGCGAGATTGCTATACCTGA 343  
284 CGGATACAGACATTTCAATAGTGAAGCAACCCAGAGTTGCGAGATTGCTATACCTGA 343  
284 CAGTGCAGTTGATTTATTTACAGCAAAAGTGTGGCTGAGAGATTGCTATACCTGA 343  
344 ATGTGATACCAATGACTTGAACCAAGCAAAAGCGCTGCTGTTATGTTTCAATGATG 403  
344 ATGTGATACCAATGACTTGAACCAAGCAAAAGCGCTGCTGTTATGTTTCAATGATG 403  
344 GCGCTATACCAATGACTTGAACCAAGCAAAAGCGCTGCTGTTATGTTTCAATGATG 403  
404 GCGGATGATTTATTTGCGGAGCAATGCTGATGCTGCTGCTGCTGCTGCTGCTGCTG 463  
404 GCGGATGATTTATTTGCGGAGCAATGCTGATGCTGCTGCTGCTGCTGCTGCTGCTG 463  
404 GTGGGATTTATTTATCGGTGCAAAATGCTGATGATGATGCTGCTGCTGCTGCTGCTG 463  
464 AGAAACCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 523  
464 AGAAACCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 523  
524 TGAATGCGAAATCTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 583  
524 TGAATGCGAAATCTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 583  
584 TGAATGCGAAATCTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 643  
584 TGAATGCGAAATCTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 643  
644 TCGGCGAAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 703  
644 TCGGCGAAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 703  
704 GTTATTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 763  
704 GTTATTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 763  
764 AATGCCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 823  
764 AATGCCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 823  
824 AAAAAGTATCCCTGGAATTCCTATGAAAGCAATCCCTATGATTTGATGCAAAAGAGAGAC 883  
824 AAAAAGTATCCCTGGAATTCCTATGAAAGCAATCCCTATGATTTGATGCAAAAGAGAGAC 883  
824 ATAGAGATGTTTGGAGTCTTTTGAAGCCAGACAGATTAATTAATTAATCTTGAAG 883

884 CACAATGTTGACACCGCAAGAAATGCAAAATAGATGCTTCTGTTGACCCAGCTG 943  
884 CACAATGTTGACACCGCAAGAAATGCAAAATAGATGCTTCTGTTGACCCAGCTG 943  
944 TAGAACCATACACAGACAGCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1003  
944 TAGAACCATACACAGACAGCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1003  
1004 GCGCTGGGGAATGCTATCCCAATGATGATGCAATGCTGCTGCTGCTGCTGCTGCTGCT 1063  
1004 GCGCTGGGGAATGCTATCCCAATGATGATGCAATGCTGCTGCTGCTGCTGCTGCTGCT 1063  
1004 ATGCTTGGGGAATGCTATCCCAATGATGATGCAATGCTGCTGCTGCTGCTGCTGCTGCT 1063  
1064 CCAATGATTTGCAAAATATCCGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1123  
1064 CCAATGATTTGCAAAATATCCGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1123  
1064 TCACTTGTGTTTCTTAAACCAATGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1123  
1124 ATGCTTGGGGAATGCTATCCCAATGATGATGCAATGCTGCTGCTGCTGCTGCTGCTGCT 1183  
1124 ATGCTTGGGGAATGCTATCCCAATGATGATGCAATGCTGCTGCTGCTGCTGCTGCTGCT 1183  
1184 CCAATGATTTGCAAAATATCCGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1243  
1184 CCAATGATTTGCAAAATATCCGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1243  
1244 TTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1303  
1244 TTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1303  
1304 ACACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1363  
1304 ACACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1363  
1364 ACCCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1423  
1364 ACCCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1423  
1364 ATCCCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1423  
1424 TAACTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1483  
1424 TAACTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1483  
1484 AATCCATTTGCAAAATATCCGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1543  
1484 AATCCATTTGCAAAATATCCGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1543  
1544 GCAATGATTTGCAAAATATCCGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1603  
1544 GCAATGATTTGCAAAATATCCGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1603  
1604 TCTATTAATGTTTAAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1663  
1604 TCTATTAATGTTTAAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1663  
1664 AATTTAAACATGCGCAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1710  
1664 AATTTAAACATGCGCAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1710

RESULT 7  
ID AA091564 standard; cDNA: 1713 BP.

XX AA091564;

XX 22-DEC-1995 (first entry)

XX OP-resistant esterase LC7L103C allele.

XX Esterase; E3; bioresmediation; organophosphate; carbamate;

XX insecticide; pesticide; water decontamination; meat decontamination;

XX ss.  
XX Lucilia cuprina.

FH Key Location/Qualifiers  
 FT CDS 1..1713  
 FT /\*tag- a  
 PN MO9519440-A1.  
 PD 20-JUL-1995.  
 XX 13-JAN-1995; 95WO-AU00016.  
 XX 13-JAN-1994; 94AU-0003347.  
 PA (CSIR ) COMMONWEALTH SCI & IND RES ORG.  
 PI Boyce TM, Campbell PM, Newcomb RD, Oakeshott JG;  
 PI Parker AG, Robin GC, Russell RJ, Smyth K;  
 DR WPI; 1995-263870/34.  
 XX Pure E3 esterase from *Lucilia cuprina* and related DNA - used to  
 PT eliminate residues of organo:phosphate and carbamate pesticides from  
 PT water, meat etc.  
 PS Example 4; Page 12-17; 38pp; English.  
 CC RT-PCR was used to clone a cDNA allele of Lc-alpha-E7 (encoding  
 CC Op-susceptible esterase E3 of *L. cuprina*) from a diazinon  
 CC resistant strain, Llandillo 103. 4 Isolated clones were  
 CC sequenced (LC7L103 A-D, AA091562-65) that encoded diazinon-resistant  
 CC esterases. The esterases, or cells expressing them, are used  
 CC in bioremediation.  
 XX  
 SQ Sequence 1713 bp; 512 A; 308 C; 368 G; 525 T; 0 other;  
 Query Match 55.8%; Score 953.4; DB 16; Length 1713;  
 Best Local Similarity 73.2%; Pred. No. 1.9e-284;  
 Matches 1221; Conservative 0; Mismatches 446; Indels 0; Gaps 0;

QY 584 TGAGATGGTCAGAGTAATATTCATTTTCGGGCGATGAGCAATATTACGCTC 643  
 DB 584 TCGGTTGGATTAAATAATATGCGCACTTTGGTGCAATCCGATATATTACAGTCT 643  
 QY 644 TCGCGAAGATGCTGGTGGGGCCCTCAACCCATTACATGATGATTAACCGAACACCGCTG 703  
 DB 644 TTGGTGAAGTGGCGGGTGGCTTACCCACTACATGATGATTAACCGAACACCGCTG 703  
 QY 704 GTTTATTCATCGTGTATCATGATGTCGGGTATTCATGTCGTATGAGGCGCTCAGAG 763  
 DB 704 GTCTTTCCATCGTGTATCATGATGTCGGGTATTCATGTCGTATGAGGCGCTCAGAG 763  
 QY 764 AATGCCAAAGTCGTGGCGTCAACCATGAGCAAAAGTGTGCTAATAAGGAGAGACATG 823  
 DB 764 AATGTCACATCGTGGCTTACCTTACCCAAATTTGGTCGGCTAATAAGGAGATATG 823  
 QY 824 AAAAGATATCTGGAATTCCTAATGAAAGCCATCCCTATGATTTGATCAAAAGAGAGC 883  
 DB 824 ATAAAGATGTTTGGAGTTCCTTTGAAAGCCAGAGATTTAATAAACTTGAGG 883  
 QY 884 CACAGTTTGCACACCGGAGAAAGATGCAAAATAGGTCATGTTCTTTGGACCCACTG 943  
 DB 884 AAAAGTTTAACTCTAGAGAGAGCCGTAACAAATAGGTCATGTTCTTTGGTCCACTG 943  
 QY 944 TAGAACCATACACAGACCGGACTGTGTGTACCCAAACCATCAGAGAAATGTAAGA 1003  
 DB 944 TTGATCATATCAGACCGGCTGATGTGTGTACCCAAACCATCCTCGGAAATGTTAA 1003  
 QY 1004 GCGCTGGGGAATTCGATACCCACATGATTAAGCAATACCTCTGAGAAAGTTCTCT 1063  
 DB 1004 ATGCTTGGGGAATTCGATACCCACATGATTAAGCAATACCTCTGAGAAAGTTCTCT 1063  
 QY 1064 CCAAATCAATTTGCCAAACATATCCGAGGTTGTAAAGAGTTGAATCCTGTGTAAAT 1123  
 DB 1064 TCACCTGTGTTCTTAACCAATGCTATGCTTGTAAAGAAATGGAACCTGTGTAAAT 1123  
 QY 1124 ATGTCCTTGGAGTGGTGTACAGTACGACGAGTGGCCGGAACCTGGAGAGGCTG 1183  
 DB 1124 TTGTGCCAAGGATGTTGGCTGATGTCGACGACCGCCGAGAGACCTTGGAAATGG 1183  
 QY 1184 CCATTTGGAAGAAAGGCCCATGATGAGTGGGAAACCACTGATCGAATATTTATGAGC 1243  
 DB 1184 CTAATAATTAAGAAAGGCTATGTTACAGAGAAACCAACCGCGATATTTATGATG 1243  
 QY 1244 TTGCTCTATTTCTATTTCTCTTCCCATGATGCTTCTCAATTCGCTCAACC 1303  
 DB 1244 TTGCTCTCATCTATTTCTGTTCCCATGATGCTTCTCAATTCGCTTCAATG 1303  
 QY 1304 ACACAGCTGSCATCCCATTTATTTGATGCTTTCGATTTCCGATTCGGAAGAAATTTTA 1363  
 DB 1304 ACACCTCCGATACCCCGTCTACTTGTATGCTTCGACTTCGATTCGGAAGATCTTATTA 1363  
 QY 1364 ACCCTATGCTATTTATGCTTGGCGTGGCGTTAAAGGCTTAAGGCTAGGCTAGAGC 1423  
 DB 1364 ATCCCTATGCTATTTATGCTTGGCGTGGCGTTAAAGGCTTAAGGCTAGGCTAGAT 1423  
 QY 1424 TAACCTATCTCTCTGGAACATTTTGTGGAAGCCCTGCCAAAGGAAGCCCGGATATCA 1483  
 DB 1424 TAACCTATTTCTCTGGAACATTTTGTGGAAGCCCTGCCAAAGGAATTCCTGTAATACA 1483  
 QY 1484 AAACCATGGAACGATGTTGGCATTTTGGACGAAATTCGCCACCGGCAAAACCATACA 1543  
 DB 1484 AAACATTTGAACGATGCTGTATGATGATACAAATTTGCCACCGGATATCTTATTA 1543  
 QY 1544 GCAATGATATGCGCGGATGGAACCTCACCTGGATCCCATTAATAAATTCGATGATG 1603  
 DB 1544 GCAATGATATGCGCGGATGGAACCTCACCTGGATCCCATTAATAAATTCGATGATG 1603  
 QY 1604 TCTATTAATGTTTAATATTCGCGATGATTAAGATTTATGATTTCCGAGAAATGATATA 1663  
 DB 1604 TGTACAACTGTTTGAATATTTAGTATGATTAAGAAATGATGATGCTGGAATATGATA 1663

QY 1664 AATTAACAATGGCGCAAGATATTCGATATAAAGAGCAATGTTT 1710  
 Db 1664 AGATTAACAATGGCAATGATGTTTGAACAAACATAGAGATTATTT 1710

## RESULT 8

ID AAO91563  
 ID AAO91563 standard; cDNA; 1713 BP.

AAO91563;

22-DEC-1995 (first entry)

OP-resistant esterase Lc7L103B allele.

Esterase; E3; bioremediation; organophosphate; carbamate;

Insecticide; pesticide; water decontamination; meat decontamination;

Lucilia cuprina.

Key Location/Qualifiers

CDS 1..1713

W09519440-A1.

20-JUL-1995.

13-JAN-1995; 95WO-AU00016.

13-JAN-1994; 94AU-000347.

(CSTR) COMMONWEALTH SCI & IND RES ORG.

Boyce TM, Campbell PM, Newcomb RD, Oakeshott JG;

Parker AG, Robin GC, Russell RJ, Smyth K;

WPI; 1995-263870/34.

Pure E3 esterase from *Lucilia cuprina* and related DNA - used to

elutinate residues of Organo:phosphate and carbamate pesticides from

water, meat etc.

Example 4: Page 12-17; 38pp; English.

RT-PCR was used to clone a cDNA allele of Lc-alpha-E7 (encoding

OP-susceptible esterase E3 of *L. cuprina*) from a diazinon

resistant strain, Llandillo 103. 4 isolated clones were

sequenced (Lc7L103 A-D, AAO91562-65) that encoded diazinon-resistant

esterases. The esterases, or cells expressing them, are used

in bioremediation.

Sequence 1713 BP; 513 A; 308 C; 368 G; 524 T; 0 other;

Query Match 55.6%; Score 950.2; DB 16; Length 1713;

Best Local Similarity 73.1%; Pred. No. 1.9e-283;

Matches 1219; Conservative 0; Mismatches 448; Indels 0; Gaps 0;

QY 44 TTAATGCAATGGTCAATTAATACCAAACTACCGCTGATGACAAATGAACCCAAATAA 103  
 Db 44 TTAATGCAATGGTCAATTAATAGTTTAACTATGCTTAACCAATGAACCGTGGAG 103  
 QY 104 TCGATACGATATGGAATAATTAAGGTGTTAGCGAATACCGTCTACGATATCTT 163  
 Db 104 CTGAATGCAATATGCAAGTGAAGGCGTTAAACGTTAACTGTACGATATCTT 163  
 QY 164 ACTACAGTTTGGAGATATACCTATGCTAGCGTCCAGTGGGAGTGGATTCAGG 223  
 Db 164 ACTACAGTTTGGAGATATACCGTACCGCCACGCGAGTGGGAGTGGATTCAGG 223  
 QY 224 CACCCACGAGGCTGTACCATGAGGAGGTGATGATGCTGTGGGCGCAACAGAT 283  
 Db 224 CACCCACGAGGCTGTACCATGAGGAGGTGATGATGCTGTGGGCGCAACAGAT 283

Db 224 CACCCACGAGCAACACCTGGAGTGTGGGTGATTTGTGCATCATTAAGATAGT 283  
 QY 284 CGGTACACAGATTTTCAATAGTGCACAAACCCACAGTTGGAGATTTGCTATACCTGA 343  
 Db 284 CAGTGCAGATTTTCAATAGTGCACAAAGTGTGGTGCAGAGATTTGCTATACCTAA 343  
 QY 344 ATGTGTATACCAATGACCTGGAACCCAGCAAAAGCGCTGTATAGTGTTCATCCATG 403  
 Db 344 GCGTCTATACCAATATCTTAATCCGAACTAAACGCTCCGTTTGTATATACATCATG 403  
 QY 404 GCGGAGATTTTATTTGGCGGAGCAAAATGCTAATCTGTTGGTCCGACTACTTATGA 463  
 Db 404 GTGGGATTTTATTTATGCGTGAATAATCATCGTGTATGCTGATTTATTTATTA 463  
 QY 464 AGAAACCGT 523  
 Db 464 AAAAGATGT 523  
 QY 524 TGAATCGGAAATCTCATGTCCCGCAACGCTGCGCTCAAGATCAATAGTGGCT 583  
 Db 524 TAAATTCAGAAAGACCTTAATGTGCGCTAATGCGGCTTAAAGATCAAGTATGCGCT 583  
 QY 584 TGAGATGGGTCAAGATATATTTGCCATTTTGGTGGCGATGTAGACATATACCTCT 643  
 Db 584 TGGGTGGATTTAAATAATTAATGCGCAACTTGGTGCATCCCGATTAATTAACAGTCT 643  
 QY 644 TCGGCGAAAGTGTGTGGGCGCTCAACCCATTAATGATGATACCGAAGACCGCTG 703  
 Db 644 TTGGTGAAGATGCGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 703  
 QY 704 GTTTATTTCCATGTTGATCATGATGTGCGGTAAATTCATGTCTCATGCGCTCTACG 763  
 Db 704 GTCTTTCCATGTTGATCATGATGTGCGGTAAATTCATGTCTCATGCGCTCTACCG 763  
 QY 764 AATGCCAAAGTGTGCGCTCAACCATGCGCAACGCTGTGTGTGTGTGTGTGTGTGTGT 823  
 Db 764 AATGTCAACATGCTGCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 823  
 QY 824 AAAAGATATCTGGAATTCCTATGTAAGCAATCCCTATGATTTGATCAAAAGAGAGC 883  
 Db 824 ATAGGATATGTTGAGATTTCTTTTGAAGCCAAAGCAGATTAATTAATTAATTAATTA 883  
 QY 884 CACAGTTTGTACACCCGGAAGATGCAAAATTAAGTCAATGTTCTTTTGGACCCACTG 943  
 Db 884 AAAAGTTTAACTTGAAGAGACGTAACAATTAAGTCAATGTTCTTTTGGACCCACTG 943  
 QY 944 TAGAACATACCAAGACAGCGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1003  
 Db 944 TTGAGCATATTCAGACCGCTGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1003  
 QY 1004 GCGCTGTGGGAAATTTGATACCCCAATGATGATGCAATACCTCTTACGAAAGTTGCT 1063  
 Db 1004 ATGCTGTGGGAAATTTGATACCCCAATGATGATGCAATACCTCTTACGAAAGTTGCT 1063  
 QY 1064 CCAATCAATTTGCAAAACATATCGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1123  
 Db 1064 TCACTTGT 1123  
 QY 1124 ATGTGCTGTGGAGT 1183  
 Db 1124 TTGTGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1183  
 QY 1184 CCAATTTGTAAGAAAGCCCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1243  
 Db 1184 CTAAATTTTAAAGAGCTCATGTTACAGAGAAACACCAACCCCGCTTATTTATGATG 1243  
 QY 1244 TTGTGCTGTATTTCTATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1303  
 Db 1244 TTGTGCTGTATTTCTATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1303  
 QY 1304 ACACAGCTGCACTCCATTTATTTGTATGTTGTGTGTGTGTGTGTGTGTGTGTGTGT 1363  
 Db 1304 ACACCTCGGCTACACCCGCTACTTGTATGCTTGTGTGTGTGTGTGTGTGTGTGTGT 1363





Db 1082 CCAAGGAGATGATGAAAGCCGCTGGAGTAACTCCATCCCATCTTTATAGGAAACACT 1141  
 Qy 1045 TCCATGAGAGTTTCTTCCAAATTCATTTGCCAAACATATCCGAGGTTGTAAAGAG 1104  
 Db 1142 TCGTACGAGGCGCTGCTGGGTTCCAGAGTAAAGCTTATGCCAGAGTGTGACAG 1201  
 Qy 1105 TTGGAATCCGTGTGATATATGATGCTTGGAGTTGGCTGACAGTGAACGAGTCCCG 1164  
 Db 1202 CTGTATGTGTGACACCTTTCATCTCCAAAGATTTGTGGCCACGAGGCCAGTAAAGA 1261  
 Qy 1165 GAAACCCCTGAGAGGCTGCCATTTGTGAAAAAGGCCCATGTGTGATGGGAAACACTCT 1224  
 Db 1262 AACTGAGATTCGTGAGAGTGCACAGATTCGAGATTTCCAGTCCAGTCCAGAAAGCAC 1321  
 Qy 1225 CTGATATATTTTATGAGCTTTGCTCTATTTCTATTTCTCCCTCCCATGATGCTTTC 1284  
 Db 1322 CCAGATATTTATGATGATCTCTGTTGATTTCTACTCTCTGTTTCCGCTGAGGTTG 1381  
 Qy 1285 CTACATTTGCGCTTCAACACACAGCTGGCACTCCCATTTATTTGATGTTGATTTTC 1344  
 Db 1382 GTCCATTTCCCGACACGCGTACGCGGCTGGAGCTCCAGTATATTTCTATGATATGACT 1441  
 Qy 1345 GATTCGAGAAATTTATTAACCCCATGATATGATGCTTTGGCCGCTTGAAGCT 1404  
 Db 1442 GACTCCGAGAGCTCATTTTTCGATCCGATTTATGCGGTGGAGCGGTGTCAAGGGG 1501  
 Qy 1405 GTAGGCAATGCGGATGAGCTTATCTTCTTCTGAAACATTTTGTCAAAAGCCTGCA 1464  
 Db 1502 GTACGCGATGCGGAGATTTGATGATACCAATTCACGACGCTGCTGGCGGCTTGGCG 1561  
 Qy 1465 AAGGAAAGCCGCGATACAAACCATTTGACGATGTTGGCATTTGACGGAATTCGCC 1524  
 Db 1562 AAGGAAAGCCGCGATACAAACCATTTGACGATGTTGGCATTTGACGGAATTCGCC 1621  
 Qy 1525 ACCACGCGAATCCATACGATGATATGACGCGATGGAAGCACTGACCGGATGCC 1584  
 Db 1622 GCCAGGATATCCCTACAGCGAAGATCAACGATGATGACACTCTACCACTTATCA 1681  
 Qy 1585 ATAAAAAATCCGATGATGCTATTAATTTTAAATATCGGCGATGAATGAAGTTATG 1644  
 Db 1682 GTTCGCAATCCGAGAGGTATCAAGTGCCTCAACATCAGTATGAGCTGAAGTTATC 1741  
 Qy 1645 GATTTGCCGAAATGATTAATTTAAACATGCGGCAATATTTGATTAAGAAAGAGAA 1704  
 Db 1742 GATTCGCGTGTGAGTCCCAATTTGAAGTCTGGGAGAGCTCTATGACGAAACAAAGAT 1801  
 Qy 1705 TTGTT 1709  
 Db 1802 TTATT 1806

PR 23-MAR-2000; 2000US-191637P.  
 PR 11-JUL-2000; 2000US-0614150.  
 PA (PEKE ) PE CORP NY.  
 PI Venter JC, Adams M, Li PMD, Myers EM;  
 DR WPI; 2001-656860/75.  
 DR P-PSDB; ABB57996.  
 XX  
 PT New isolated nucleic acid detection reagent for detecting 1000 or more  
 PT genes from Drosophila and for elucidating cell signalling and cell-cell  
 PT interactions -  
 PS  
 PS Claim 1; SEQ ID NO 779; 21pp + Sequence Listing; English.  
 CC The invention relates to an isolated nucleic acid detection reagent  
 CC capable of detecting 1000 or more genes from Drosophila. The invention is  
 CC useful in developmental biology and in elucidating cell signalling and  
 CC cell-cell interactions in higher eukaryotes for the development of  
 CC insecticides, therapeutics and pharmaceutical drugs. The invention  
 CC discloses genomic DNA sequences (AB116176-AB130511), expressed DNA  
 CC sequences (AB101840-AB116175) and the encoded proteins  
 CC (ABB57737-ABB72072).  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pcl\_sequences.  
 SQ Sequence 1665 BP; 397 A; 446 C; 468 G; 354 T; 0 other;  
 Query Match 23.3%; Score 399.2; DB 23; Length 1665;  
 Best Local Similarity 53.6%; Pred. No. 1,1e-112;  
 Matches 880; Conservative 0; Mismatches 753; Indels 9; Gaps 2;  
 Qy 53 TGCATTAATTAATACAACTACCGTCTGATCAATGAAACCAATATGATATCTG 112  
 Db 5 TCGACTTTAAGTCCAAACAGACGATACGACGACGAAAGACTGCTGATGACCA 64  
 Qy 113 AATATGACAAATTAAGGTTGTTAAGCAATGACCGCTTACGATGATCTTACTACGTT 172  
 Db 65 CTTACGAGCAATCAAGAGGTGTTAAGGAAAGTCCATTCGCGGCACTGCTTCTGAGCT 124  
 Qy 173 TCGAGATATACCTTATGCTTACGCTCCAGTGGGTGATGATGATTCAGGACCCGACG 232  
 Db 125 TCGAGCGGATCCCTTTCGCAACACCGGTTGGGCAAGCTTCAAGGCTCCCGACG 184  
 Qy 233 GGCCTTACCATGAGGAGGTGATGATGATGCTGTTGGGCGACGACCAATGCGTACAGA 292  
 Db 185 CCGCGAGGCTGTGACGAGAGTCAAGAGCTGACCTCCAGGCTCCCAAGCCACTGACAG 244  
 Qy 293 CAGATTTCAATAGTGGCAACCCACAGGTTGAGGATGTTCTATACCTGATGTATATA 352  
 Db 245 AGCACTTCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 304  
 Qy 353 CCAATGCTTGAACCCAGCAAAAGGCGTCTTATGTTGTTTCACTGCGGAGATTT 412  
 Db 305 CAAAGATTTGTATCCCAACCAACCAATGCCCTGATGCTGATGATGATGATGATGATG 364  
 Qy 413 TTATTTTCGCGAAGCAAAATGTAACGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 472  
 Db 365 TCCAGTTTGGCGAGGCTCTCCGAGGATTTACAGTCCGATTTTGTGCTGCGAGAGATG 424  
 Qy 473 TGTCTTGTGTAACCGTACATATCTTTGGGTTGTTGGGTTTCTTACCTGAAATCGG 532  
 Db 425 TGTGTGCTATTTCTATCACTACAGTGTGAGCACTGGGATTTTGTGCTGAGATC 484  
 Qy 533 AAAATCTCAATGTCCCGGCAACGCTGCTCAAGATCAAGTAATGCGCTTGAATGGG 592  
 Db 485 CCGAATCGATGTGCGCGCAATGCGGACTCAAGATCAAGTGTGGCGCTGCGGTGG 544  
 Qy 593 TCAAGATATATTTGCAATTTTGGTGGGATGATAGCAATATTAACGCTTCCGCGGAA 652  
 Db 545 TCAAGGCCAATCTGTGCGTTTGGAGGCGATTTCCCGAATATATATTTTGGGAGCA 604

RESULT 10  
 ABL02099  
 ID ABL02099 standard; cDNA; 1665 BP.  
 XX  
 AC ABL02099;  
 XX  
 DT 26-MAR-2002 (first entry)  
 XX  
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 779.  
 XX  
 KW Drosophila; developmental biology; cell signalling; insecticide;  
 XX Pharmaceutical; gene; ss.  
 OS Drosophila melanogaster.  
 XX  
 PN WO2001/1042-A2.  
 XX  
 PD 27-SEP-2001.  
 XX  
 PF 23-MAR-2001; 2001WO-US09231.  
 XX

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QY 653 GTGCTGGTGGGGCCCTCAACCATTCATGATGATACCGAACAGACCCGTTTATTC 712
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Db 605 GTGCGGGAAGTGCCTCGTTCACACTACATGATGATACAGAGACAGCATGACTTTCC 664
QY 713 ATCGTGTATCATATGTCGGGTAATTCATGTCCTCATGGGCTCTACAGAAATCCAAA 772
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Db 665 ACAAGGCCATCTGCTGCGGTAATACGCTTCCCTCGGGAGTACTCTCAGAGAA 724
QY 773 GTGCTGGCTCACCAGCCCAACGTTGTGCTATTAAGGAGAGACATGAAGAAAGATA 832
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Db 725 ACTGGCCATATCGTGTGGCTCTCCAGCGGGGTTACGAGGTGAAGAACACCCGGATG 784
QY 833 TCTGGAATTCCTAATGAAGAACCAATCCATATGATTTGATCAAGAGAGCCACATTT 892
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Db 785 TCTGGAGATTCCTGAGAACCCCAAGGAGATCCGAATATCAAGAACCAATGAGAACTCT 844
QY 893 TGACACCCGGAAGAAATGCAAAATAGTCATGTTCCCTTTGGACCCACCTAGAACCAT 952
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Db 845 GCATTGACGAGAGAGAGAGAGGAGATGATGATCTCTTTGGCCGCTAATCGAACCT 904
QY 953 ACCAGACAGCCGACTGTGTGTACCCAAACCAATCAGAGAAATGATGAAGAGCCCTGGG 1012
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Db 905 ATGTAAACAGGCACTGTGTGTGCGGAGAGAAACCATGAAATGATGAGAACCCCTGGA 964
QY 1013 GAAATTCATACCCCATTTGATGAGCAATACCTCCTACGAAAGTTTGTTCCTCAATCAA 1072
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Db 965 GCATTAATATCCCATTTATCATTCGAGAGGCTTTCCCAAGAGGGGCTCTCTGTACTAG 1024
QY 1073 TTGCAAAACAATATCCGAGAGTTGTAAGAGTTGGAATCCTGTGTAATATGTCCTT 1132
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Db 1025 AGACCAAGACCAATCCGAAGGTCTAAGAGATGAGAGTGGAGACTGCGGGTTGTGGGCTTA 1084
QY 1133 GGGAGTGGCTGACGAGTAAGCACTGCCCCGAGAAACCTTGAGAGAGGCTGCCATTGGA 1192
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Db 1085 TCGAATTAATATGAGACAGAGGAAAGTGCCTGTGCGGAGATGACGATAGCTGAGAGC 1144
QY 1193 AAAAGGCCATGTGATGGAGGAAACACCT-----ACTCGATTAATTTATGAGCTTT 1246
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Db 1145 AGTGTACTACGCGCATTAAGACGCCCATCTGTGACACCTGATGATTAATCTTGATGATG 1204
QY 1247 GCTCTATTTTATTTCTCTCTCCCATGATGCTGCTCTCAATTTGGCTTCAACACA 1306
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Db 1205 TTCCACAGAGTACTTGTGTTCCCAATATACCGCAGATATTTGCCGCTGCACTGAGTGC 1264
QY 1307 CAGCTGGACCTCCATTTATTTGATCGTTGATTTGATTTGCGAAGAAATTAATACC 1366
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Db 1265 CTCGAGATGCGCGACGATTTGTACCGCTTGTGACTTGTGACTCCAGCA--CTTCAACC 1321
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Db 1322 ACCTGCGCATCTGATGTTGCGGCAAAAAGTGAAGGAGGACGTCGACGCGCATGCTGT 1381
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Db 1382 CCTACTTGTCTTACAACTGCTGCGGAGAGAACCTCAAGAACACACGCGGGAGTCAAGT 1441
QY 1487 CCATTGAAGCAATGTTGATGATTTGCGAGAAATTCGCCACACCATCAACAGA 1546
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Db 1442 GCATCGAGGCGCTGTGGAGACTGTGAGCACTTTGGCGCATGTGGAACCCCACTTGG 1501
QY 1547 ATGATATAGCCGCGCATGAAAAACCTCAGCTGGATCCCATTAATAAATTCGATGTCT 1606
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Db 1502 ATCCGGAACAGAGAGACCTGTGGACGCCGTCGATCCTCGCGCGCTGAGAAACACAGC 1561
QY 1607 ATTAAGTTTAATATATCGCGCATGATTAAGATTATGATTTGCCAAATAGGATTAATA 1666
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Db 1622 TGATGTCTGGAGAGTTCCTT 1643

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RESULT 11
ID ABL02103 standard; cDNA; 1593 BP.
XX
AC ABL02103;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 791.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
XX pharmaceutical; gene; ss.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PE 23-MAR-2001; 2001MO-US09231.
XX
PR 23-MAR-2000; 2000US-191637P.
XX
PR 11-JUL-2000; 2000US-0614150.
XX
PA (PEKE ) PE CORP NY.
XX
PI Venter JC, Adams M, Li PMD, Myers EM;
XX
DR WPI; 2001-656860/75.
XX
DR P-PSDB; ABB58000.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
PS Claim 1; SEQ ID NO 791; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (AB116176-AB130511), expressed DNA
CC sequences (AB101840-AB116175) and the encoded proteins
CC (ABBS7737-ABBS72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 1593 BP; 417 A; 394 C; 405 G; 377 T; 0 other;
XX
Query Match 23.3%; Score 398.8; DB 23; Length 1593;
Best Local Similarity 55.4%; Pred. No. 1,4e-112;
Matches 888; Conservative 0; Mismatches 692; Indels 24; Gaps 5;
QY 111 TGAATGAGCAAAATTAAAGGTGTTAAGCAATACCTCTACGATGATTTCTACTACAG 170
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Db 6 TGACTGCGCTCTCTGCGGGAGTGAAGAAACACATCTGGGAGAGAACTACTCTAG 65
QY 171 TTGAGAGTATACCTATGCTTAAGCCCTCCAGTGGGAGTGTGATTCAGATCCACCCA 230
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Db 66 TTTCGAGAGATACCTCTTCCCAAGCCTCCGCTGGAGATCTGCGCTTCAAGGCCCGGA 125
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QY 231 GCGGCTGTACCATGAGAGGGTGAAGTGTGCTGTGGGCCACCAACAGATCGTTACA 290
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Db 126 AGCAGTGGAGCGCATGAGTCAAGAAATGATGACTTCCGCGGACAGACAGCCCTTCA 185
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QY 291 GACGATTTCAATAGTGCACAAACCCACAGGTTTCGAGAGATGCTTATACCGAATGTGA 350
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Db 186 GACACACATGTTTTCAGAAAATACGCGGCTCAGAGAGACTGCTCTACTTAAATGTGTA 245
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QY 351 TACCAATGACTTGAACCCAGACAAAAGGCTCTGTTATGTTTCAATCCATGCGGAGGA 410

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Db 246 TGTCAAGATCTGACACCGGATTAACCTGCGTCCGATGATTGGATCTACGAGAGAG 305  
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 Db 306 CTATCAAGTTGGGGAAGCTTCTCGGATATGTAACAGTCCGACTTTTATCATTCGAAGA 365  
 Qy 471 CGTGCTCTGTAACCGTCAATATGCTTTGGGTGTGTGGTTCCTTACGCTGAATC 530  
 Db 366 TGTGCTCATAGTACCGTCTGATGACTGGTGGCTTGGGCTTCCCTGAGCTGGATGA 425  
 Qy 531 GGAATCTCANTGTCGCGGCAAGCGTGGCTCAAGATCAAGTAATGCGCTTGAATG 590  
 Db 426 TCCCACTCAAGCGTCCGGAATGCAAGTCTCAAGATCAAAATCATGCGCTCGCATG 485  
 Qy 591 GGTCAAGATTAATTTGCAATTTTGGTGGTGGATGATAGACATTTACCGTCTGGGGA 650  
 Db 486 GGTGCAACAAACATGAGAGCATTCGGCGGTATTCACAACATATTAACCTTTTGGCGA 545  
 Qy 651 AAGTGTGTTGGGCTCAACCCATTACATGATGATTAACCAAGACAGCGGTGTTAT 710  
 Db 546 AAGTGTGTTGGGCTCAACCCATTACATGATGATTAACCAAGACAGCGGTGTTAT 605  
 Qy 711 CCATGCTGATCATGATGCTCGGTAATTCATGCTGCTACAGGCTTACAGATGCCA 770  
 Db 606 CCACAAGCTATGATGATGCTCGGTAATTCATGCTGCTACAGGCTTACAGATGCCA 665  
 Qy 771 AAGTGTGCTTACCATGATGCTCGGTAATTCATGCTGCTACAGGCTTACAGATGCCA 830  
 Db 666 TATTTGGGCTTATAGGCTGGGCAAAATTTGGATATACCCGCTGATTAAGACACAGC 725  
 Qy 831 TATCTGGAATTCCTAATGAAGCAATCCATGATGATTTGATCAAGAAGGACCAAGT 890  
 Db 726 GATCTTTGATTTCTGCATCATGATGATGCGGAGATTTGCAAGGCGCACCGCAAGT 785  
 Qy 891 TTTGACACCGCAAGATGCAAAATAGTCAATGCTTCTTGGACCCACTGTAAGAC 950  
 Db 786 TCTCAGCAACGATGAAGACATCATGATCTTTTCCCTTGGACCTGCTGTAAGAC 845  
 Qy 951 ATACGACAGCGGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1010  
 Db 846 ATATCTACCGGACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 905  
 Qy 1011 GGGAAATTCGATACCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1070  
 Db 906 GAGTCACAGATACCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 965  
 Qy 1071 AATTGCCAAACATATCCGAGGTTGTAAGAGTGTGAATCTGCTGATTAATGAGC 1130  
 Db 966 AGAGTTTCAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 1025  
 Qy 1131 TTGGGAGTTGGCTGACAGTGAAGCAAGTCCCGGAAACCTGGAAGAGGCTGCTGAT 1190  
 Db 1026 GAGCGATCTCGGT--CTTAACCTAGATCCAACTGCTGAGAACTAGCGCTTGAAC 1082  
 Qy 1191 GAAAAAGGCGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1250  
 Db 1083 GAGAGAGGCGTATTTCCGCGAGCAACCTGTAACGAGCAAAACATGATGAAGTTTCGA 1142  
 Qy 1251 CTATTTTATTTCTCTTCCCATGATGATGATGATGATGATGATGATGATGATGAT 1304  
 Db 1143 GCTATGCTCATATGAGAGTCTGCGACCCATATATACAGGCGACCTTTGAACCTGTC 1202  
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 Db 1203 GCAATCCGCGCGACGATCTGATGATGATGATGATGATGATGATGATGATGAT 1259  
 Qy 1365 CCGCATGCTATATGCTTTGGCGGCTGCGGTTAAGGTTAAGGTTAAGGTTAAGGTT 1424  
 Db 1260 CGCATTTAGGATTTGCTTGGCGCATGATGATGATGATGATGATGATGATGATGAT 1319  
 Qy 1425 AACCTATCTTCTGGAACATTTTGTGAAGAGCGCTGCCAAGAGAAAGCGCGCATTC 1484

Db 1320 GTGCTATATTTCCACAGCATGTTGTCATCATCCGCTCCGATTCCTCCGAAACAA 1379  
 Qy 1485 AACATTCACAGCATGTTGTCATTCGAGGAATTTGCCACACCGCAACCATACAG 1544  
 Db 1380 GGTATTAACCGGAATGTCGAGCTTTGGACAGATTTGGACGACGACGAGATCCAACT 1439  
 Qy 1545 CAATGATATACCGGCAATGCAAACTCACCTGGATCCCATTAATAAATCCGATGAT 1604  
 Db 1440 CGAAGATATA-----AATCCTCAGTTTGCACCCATGAGAAA---CGTAACCA 1487  
 Qy 1605 CTATTAATGTTTAATATGCGCATGATTAATGAAGTATGATGATTTGCCAGAAATGA 1664  
 Db 1488 CTATTAATGTTTCAATATTTGGGATTCAGTTTGAAGTATGATGATGATGATGAT 1547  
 Qy 1665 AATTAACAAATGGGCAATGATATTCGATTAATAAAGAGGATGAT 1708  
 Db 1548 AATGAAACCTGTGTGATATGTTTCTAGCGCCCAACAAACTGT 1591

RESULT 12  
 ABL01859  
 ID ABL01859 standard; cDNA; 1863 BP.  
 XX  
 AC ABL01859;  
 XX  
 DT 26-MAR-2002 (first entry)  
 XX  
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 59.  
 XX  
 KW Drosophila; developmental biology; cell signalling; insecticide;  
 KW pharmaceutical; gene; ss.  
 XX  
 OS Drosophila melanogaster.  
 XX  
 PN W0200171042-A2.  
 XX  
 PD 27-SEP-2001.  
 PD  
 PF 23-MAR-2001; 2001WO-US09231.  
 XX  
 PR 23-MAR-2000; 2000US-191637P.  
 PR 11-JUL-2000; 2000US-0614150.  
 XX  
 PA (PEKE ) PE CORP NY.  
 XX  
 PI Venter JC, Adams M, Li PWD, Myers EW;  
 XX  
 DR WPI; 2001-656860/75.  
 DR  
 XX P-PSDB; ABB57756.  
 XX  
 PT New isolated nucleic acid detection reagent for detecting 1000 or more  
 PT genes from Drosophila and for elucidating cell signalling and cell-cell  
 PT interactions -  
 XX  
 PS Claim 1: SEQ ID NO 59; 21pp + Sequence Listing; English.  
 XX  
 CC The invention relates to an isolated nucleic acid detection reagent  
 CC capable of detecting 1000 or more genes from Drosophila. The invention is  
 CC useful in developmental biology and in elucidating cell signalling and  
 CC cell-cell interactions in higher eukaryotes for the development of  
 CC insecticides, therapeutics and pharmaceutical drugs. The invention  
 CC discloses genomic DNA sequences (ABL01840-ABL16175), expressed DNA  
 CC sequences (AB01840-ABL30511), and the encoded proteins  
 CC (AB01840-ABL30511).  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WPI  
 CC at ftp.wpi.int/pub/published\_pcl\_sequences.  
 CC  
 XX  
 SQ Sequence 1863 BP; 425 A; 493 C; 523 G; 422 T; 0 other;

Query Match 20.7%; Score 353.2; DB 23; Length 1863;  
 Best Local Similarity 52.4%; Pred. NO. 2.1e-98;  
 Matches 878; Conservative 0; Mismatches 778; Indels 18; Gaps 4;

QY 27 TCGCTGAACATGCTTTAAATGATGTCATTAATATACAAACATACCGTCTGAGTAC 86  
 Db 192 TCTGCTGAATGAGGACACCAAGCTCATTTGGCCACAAAGATGCTCAAGTATGCGCTTGGCAC 251  
 QY 87 AAATGAACCCAAATTAATCGATGATGATATGACAAATTAAGGCTGTAAGCAATGAC 146  
 Db 252 AAACGACGAGGAGGTGCTGACAGGAGATGCGGAGATGCGCAATGCGCAAGAC 311  
 QY 147 CGTCT---ACGATGATTTCTTACTACAGTTTGAGAGATATACCTATGCTAGACCTCCAGT 203  
 Db 312 ACTCTAGACGACGAGATGATGATCTGCGCTTGAGAGATCCCTTTTGACAGCGCGCGGT 371  
 QY 204 GGGTGAATGATGATCAAGGACCCAGCGGCTGTACCATGAGGAGGTGATGATGATG 263  
 Db 372 GGGGAGAGCTGCGCTTCCGAGCCCGCCAGCCACATCCCTGTTGGGGGGTGGCGGATG 431  
 QY 264 CTGAGGCGCAACCAAGATGAGTACAGACAGATTTATAGTGGCAAAACCCAGGTTG 323  
 Db 432 CACCTATCCGCGGCGCAAGCCGATGCAAAAGCACTTGTGCTCAGCATGCTGCAAGGAC 491  
 QY 324 GGAGGATTTGCTATACCTGATGATGATGATGATGATGATGATGATGATGATGATG 383  
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 QY 864 TGATTTGATCAAGAGGATGATGATGATGATGATGATGATGATGATGATGATG 923  
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 AC ABA90480;  
 XX  
 DT 12-FEB-2002 (first entry)  
 XX  
 DE Drosophila cell cycle progression protein coding sequence #115.  
 KW Antiproliferative; cytoskeletal; cardiac; immunosuppressive; meiosis;  
 KW antiinflammatory; antiproliferative; dermatological; antifungal; mitosis;  
 KW antiparasitic; antimetabolic; antineoplastic; antithrombotic; cell division;  
 KW cell cycle progression protein; tumour; proliferative disorder;  
 KW cardiovascular; autoimmune; dermatological disorder; ds.  
 XX  
 Drosophila sp.  
 OS  
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 PD 04-OCT-2001.  
 XX  
 PF 23-MAR-2001; 2001WO-GB01297.  
 XX  
 PR 24-MAR-2000; 2000GB-0007268.  
 XX  
 PA (CYCL-) CYCLACEL LTD.  
 XX  
 PI Deak P, Glover DM, Midgley C;  
 XX  
 DR WPI: 2002-055132/07.  
 XX



OS Drosophila melanogaster.  
 XX  
 XX W0200171042-A2.  
 XX  
 PD 27-SEP-2001.  
 XX  
 XX 23-MAR-2001; 2001WO-US09231.  
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 XX 23-MAR-2000; 2000US-191637P.  
 XX  
 XX 11-JUL-2000; 2000US-0614150.  
 XX  
 PA (PEKE ) PE CORP NY.  
 PI Venter JC, Adams M, Li PMD, Myers EW;  
 DR WPI; 2001-656860/75.  
 XX P-PSDB; ABB57963.  
 XX  
 XX New isolated nucleic acid detection reagent for detecting 1000 or more  
 PT genes from Drosophila and for elucidating cell signalling and cell-cell  
 PT interactions -  
 XX  
 PS Claim 1; SEQ ID NO 680; 21pp + Sequence listing; English.  
 XX  
 XX The invention relates to an isolated nucleic acid detection reagent  
 CC capable of detecting 1000 or more genes from Drosophila. The invention is  
 CC useful in developmental biology and in elucidating cell signalling and  
 CC cell-cell interactions in higher eukaryotes for the development of  
 CC insecticides, therapeutics and pharmaceutical drugs. The invention  
 CC discloses genomic DNA sequences (AB16176-AB16175), expressed DNA  
 CC sequences (AB101840-AB16175) and the encoded proteins  
 CC (AB57737-AB572072).  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp://wipo.int/pub/published\_pcl\_sequences.  
 XX  
 XX Sequence 6175 BP; 1732 A; 1242 C; 1350 G; 1851 T; 0 other;  
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 Query Match 20.4%; Score 349.4; DB 23; Length 6175;  
 Best Local Similarity 53.9%; Pred. No. 6.4e-97;  
 Matches 1038; Conservative 0; Mismatches 626; Indels 263; Gaps 5;  
 QY 46 AATGTCATGTCATTAATATACAACTACGCTCTAGTACAAATGAACCAATATATC 105  
 DB 3054 AGAACCATGACATTAATATACGACAGATATGCGCAGTACCAATGAACAGTTGTGCC 3113  
 QY 106 GATACGTAATATGACAAATTAAGGCTGTTAAGCAATGACCGTACAGATTTCTTAC 165  
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QY 441 GTTGTCCCGACTACTTATGAGAAACCGGTGCTTGGTAACCGTCAATATCGTT 500  
 DB 3534 GTATGCCCCGATTTACTTATGAGAGAGATTTGTCTCTGACAGATACAGTACCGACT 3593  
 QY 501 GGGTGTGTTGGT----- 513  
 DB 3594 TGGGGCTTTGGTATATCTATGCTGTATGCGCAATATTTTGAATTAATTTGTA 3653  
 QY 514 -----TTCCTTAGCCTCAATTCGAAATTCGATTCGCCGACAGCTGGCC 562  
 DB 3654 CTTACACGAGATTTATGAGCTTAAGTCCCGAGCTAATTTACAGGAATGTGTGCC 3713  
 QY 563 TCAAGATCAAGTAATGAGCTTGAAGATGAGTCAAGATATATGCAATTTTGGTGGC 622  
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 DB 3834 TGTATACCGATCAACCCAGAGGCTCTTTCATCGGCGCATCTTGAGGAGTGGCA 3893  
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 QY 860 CCTATGATTTGATCAAGAGAGACCCACATGTTTGAACCCGAAAGATTCAAATTAAG 919  
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 QY 920 TCAATTTCTTTTGGACCCACTGTAGACCATTCACAGACCGGCTGTGTATCCCA 979  
 DB 4074 TATGTTTCTTTTGGACCCACTGTAGACCATTCACAGACCGGCTGTGTATCCCA 4133  
 QY 980 AACCATCAAGAAATGTTGAAGAGCGCTGGGAAATTCATTCACCATTTATAGCA 1039  
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 QY 1040 ATACTCTCAGAGAGTTGCTTCCAAATCAAT----- 1074  
 DB 4194 ACACCTCTGACAGAGGCGCTGTGGGTTCCAGGTTAGATTTGGAAATTTTGTGAT 4253  
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 DB 4554 TGTGCTATTTCCGACAGAGGCTGAGGCTGAGCTCAGATTAATTTCTATGATATGACT 4613





Db 1021 TTGGCCCTTGGCCCGGTTATCGAGCCATATGTGGCGATGATGGCGTATCCCAAAATCG 1080  
OY 985 ATCAGAGAAATGATGAGAGAGCGCTGGGAAATTCGATACCCACATGTATAGCAATAC 1044  
Db 1081 CAGCAAGAGCAGCTGTCCAGCGCCCTGGGGTATTCATTCCTCATATCAGCGAACT 1140  
OY 1045 TCCTACGAAAGTTGCTTCCAAATCAATGCGCAACAATATCCG--GAGGTGTAAAA 1101  
Db 1141 TCGTTGGAAGACCTCTCTCTATTCGACACACCTGATGATCCGCTTTACATGCTGAGT 1200  
OY 1102 GAGTTGGAATCCTGTGTAATATATGCTTGGGAGTTGGCTGACAGTGAACGAGTCC 1161  
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OY 1162 CCGAAGACCTGAGAGAGGCTGCCATTTGAAAAAGGCCATGTGATGGGAAACACT 1221  
Db 1259 -CGGAGATGATGAGAGAGCTGAGAGAGTCTACTTTGACGATCCGACGGGCCAGCATG 1317  
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OY 1342 TTCGATTCGAGAAATTAATTAACCCCTATGCTATTTATGCGTTTGGCCGTGGCTTAA 1401  
Db 1438 ATGATTTGCCACA---CTTTAATCTACTATGCACTTTGAAGTGGGCAAAAAGTGAAG 1494  
OY 1402 GGTGTAGCCATGCGGATGAGCTAATCTCTCTGGAACATTTTGTGAAAGGCTG 1461  
Db 1495 GGTGTGTCGATGCGGATGAGCTAATCTCTGGAACATTTTGTGAAAGGCTG 1554  
OY 1462 CCAAGGAAAGCCGAGATACAAAACATTTGAGCAGATGTTGGCATTTGACGGAATTC 1521  
Db 1555 GACAAGAAATTTGCGCGAATACCGCAGCTGAGGAGCTGTTGGCATTTGACGGAATTC 1614  
OY 1522 GGCACACCGGCAACCATACGCAATGATATAGC 1556  
Db 1615 GGCACACCGGAGATCCCACTGTGAGATAATCCG 1649

Search completed: April 11, 2003, 01:07:10  
Job time : 263.473 secs



GenCore version 5.1.4-p5\_4578  
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OM nucleic - nucleic search, using sw model

Run on: April 11, 2003, 00:24:12 ; Search time 1660.57 Seconds  
(without alignments)  
16677.553 Million cell updates/sec

Title: US-09-776-910-14

Perfect score: 1710  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rtd:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	277.4	16.2	649	9	AI388926 GH19977.5
3	247.8	14.5	688	9	AI403569 GH23036.5
4	246.6	14.4	526	9	AI108080 GH06811.5
5	241.4	14.1	516	9	AI108156 GH06911.5
6	240.2	14.0	569	13	BI609541 RH14337.5

7	239.4	14.0	660	13	BI639486 SD22067.5
8	236	13.8	671	9	AI517692 GH28740.5
9	226.2	13.2	630	9	AI403830 GH23353.5
10	225.6	13.2	674	13	BI628316 RH56682.5
11	225.6	13.2	676	13	BI635372 SD16705.5
12	224.6	13.1	673	13	BI614181 RH43493.5
13	223	13.0	672	13	BI614443 RH43812.5
14	222.6	13.0	670	13	BI233202 RH29491.5
15	222.2	13.0	648	9	AI113763 GH10213.5
16	220.6	12.9	648	9	AI403098 GH22464.5
17	219	12.8	646	9	AI109901 GH09292.5
18	219	12.8	646	9	AI293416 LP06524.5
19	218.2	12.8	646	9	AI293416 LP06524.5
20	215.4	12.6	658	13	BI564586 RH6188.5
21	215.2	12.6	804	9	AA264069 LD07724.5
22	213	12.5	656	13	BI614821 RH44296.5
23	213	12.5	656	13	BI619037 RH44995.5
24	211.2	12.4	669	13	BI588370 RH29561.5
25	210.8	12.3	656	13	BI621302 RH52624.5
26	209.4	12.2	628	9	AI109573 GH08080.5
27	209.2	12.2	619	9	AI516869 GH27454.5
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29	208.8	12.2	647	13	BI575862 RH32195.5
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32	207.8	12.2	614	12	BG641228 SD1219.5
33	207.4	12.1	614	9	AI107729 GH05557.5
34	207.4	12.1	614	9	AI134360 GH11805.5
35	205.8	12.0	633	13	BI370683 RH57396.5
36	202.8	11.9	612	9	AA950522 LD30351.5
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39	199.2	11.6	614	13	BI617897 RH48369.5
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43	198	11.6	588	13	BI638519 SD0822.5
44	198	11.6	607	13	BI624437 RH63994.5
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## ALIGNMENTS

RESULT 1  
LOCUS AI062034 778 bp mRNA linear EST 19-APR-2001  
DEFINITION GH01076.5prime GH Drosophila melanogaster head P072 Drosophila melanogaster cDNA clone GH01076 5prime similar to U51050:  
Drosophila melanogaster alpha esterase (aef) gene, partial cds,  
mRNA sequence.

ACCESSION AI062034  
VERSION AI062034.1 GI:3337873

SOURCE  
ORGANISM Drosophila melanogaster  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Ephydroidea; Drosophilidae; Drosophila.

REFERENCE  
AUTHORS Harvey D., Brokstein P., Hong L., Evans-Holm M., Su C., Tsang G.,  
1 (bases 1 to 778)

TITLE BDGP/HMMI Drosophila EST project  
JOURNAL Unpublished (2001)  
COMMENT Contact: Stapleton, M.

BDGP  
Lawrence Berkeley National Lab  
One Cyclotron Rd, Berkeley, CA 94720, USA  
Fax: 510 486 6798  
Email: [http://www.fruitfly.org/EST\\_estfruitfly.berkeley.edu](http://www.fruitfly.org/EST_estfruitfly.berkeley.edu)  
Plate: 10 row: G column: 4  
High quality sequence stop: 363.  
Location/Qualifiers

## FEATURES





Matches 351: Conservative 0; Mismatches 174; Indels 0; Gaps 0;

QY 202 GTGGGAGATTGAGATTCAGACGACCCAGGCGCTGACCATGGAGGGTGTACGTAT 261  
 Db 1 GTGGGGAGATTGCGGTTTAAGGCCCTCAGAGGCCATCCCTGGGAGCGAGTTCGGAC 60  
 QY 262 TGTGTGGGCGACGACCAACAGATCGGTACAGACATTTCAATAGTGCACCAACAGT 321  
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 QY 562 CTCAGAGATCAAGTATGAGCTTGTAGATGGTCAAGATATATTCGCAATTTTCGCTGGC 621  
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 QY 622 GATGTAGACAAATATTAACCGCTTCGCGGAGAAAGTGTGGGGGCTCAACCCATTCATG 681  
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 QY 682 ATGATTAACCGAAGACCCGCTGTTTATTCATCGTGTATCATG 726  
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RESULT 5  
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 DEFINITION GH06911.5prime GH Drosophila melanogaster head pot2 Drosophila melanogaster cDNA clone GH06911.5prime similar to U51050.0 Drosophila melanogaster alpha esterase (aef) gene, partial cds, mRNA sequence.  
 ACCESSION A1108156  
 VERSION A1108156.1 GI:3476435  
 SOURCE EST.  
 ORGANISM fruit fly.  
 Drosophila melanogaster  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
 1 (bases 1 to 516)  
 Harvey, D., Brokslein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G., Lewis, S., and Rubin, G.M.  
 BDBP/HIMI Drosophila EST Project  
 Unpublished (2001)  
 Contact: Stapleton, M.  
 BDBP

REFERENCE  
 AUTHORS Lawrence Berkeley National Lab  
 One Cyclotron Rd, Berkeley, CA 94720, USA  
 Fax: 510 486 6798  
 Email: [http://www.fruitfly.org/EST\\_est@fruitfly.berkeley.edu](http://www.fruitfly.org/EST_est@fruitfly.berkeley.edu)  
 Plate: 69 row: A column: 11  
 High quality sequence stop: 425.

FEATURES  
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 /clone\_1ib="GH Drosophila melanogaster head pot2"

/sex="male and female"  
 /dev\_stage="adult"  
 /lab\_host="DH5 - alpha"  
 /note="Organ: head; Vector: pot2; Site\_1: EcoRI; Site\_2: XhoI; Sized fractionated cDNAs were directly ligated into POT2. Plasmid cDNA library."  
 BASE COUNT 119 a 125 c 150 g 122 t  
 ORIGIN

Query Match 14.1% Score 241.4; DB 9; Length 516;  
 Best Local Similarity 66.8%; Pred No 1.3e-61;  
 Matches 344; Conservative 0; Mismatches 171; Indels 0; Gaps 0;

QY 202 GTGGGAGATTGAGATTCAGACGACCCAGGCGCTGACCATGGAGGGTGTACGTAT 261  
 Db 1 GTGGGGAGATTGCGGTTTAAGGCCCTCAGAGGCCATCCCTGGGAGCGAGTTCGGAC 60  
 QY 262 TGTGTGGGCGACGACCAACAGATCGGTACAGACATTTCAATAGTGCACCAACAGT 321  
 Db 61 TGCAGCCGCGGAGGATTAAGCGCGTCCAGGTGACGTTCCGTTCCGATAGGTAGAGGC 120  
 QY 322 TCGGAGGATTGCTATACCTCAATGTGTATACCAATGACTTGAACCCAGCAAAAGCGT 381  
 Db 121 TCCGAGGAGTCTCTATCTCAATGTGTATACCAACATGTGAAGCCCGACAGGCTCGC 180  
 QY 382 CCGTATATGTTTTCATCATCGAGGAGATTATTTTCGCGGAGCAAAATTCGTAATCG 441  
 Db 181 CCGTATATGTTTTCATCATCGAGGAGATTATTTTCGCGGAGCAAAATTCGTAATCG 240  
 QY 442 TTTGGTCCGACCTACTTATGAGAAACCCGCTGCTTGTGTAACCGTCAATATCGTTTG 501  
 Db 241 TATGGCCCGGATTTATGAGAAAGATGTGTCTCTACAGATACAGTACCGACTT 300  
 QY 502 GGTGTGTGGGTTCTTACCTGAAATCGGAAATCTCAATGCCCCGCAACGCTGGC 561  
 Db 301 GGGGCTTTGGGATTTATGAGCTTAAGTCCCGGAGCTAATGACAGGAAATGCTGGC 360  
 QY 562 CTCAGAGATCAAGTATGAGCTTGTAGATGGTCAAGATATATTCGCAATTTTCGCTGGC 621  
 Db 361 CTCAGAGATCAAGTATGAGCTTGTAGATGGTCAAGATATATTCGCAATTTTCGCTGGC 420  
 QY 622 GATGTAGACAAATATTAACCGCTTCGCGGAGAAAGTGTGGGGGCTCAACCCATTCATG 681  
 Db 421 GATGTAGACAAATATTAACCGCTTCGCGGAGAAAGTGTGGGGGCTCAACCCATTCATG 480  
 QY 682 ATGATTAACCGAAGACCCGCTGTTTATTCATCGTGTATCATG 716  
 Db 481 ATGCTAACCGATCAAGACCAAGGCGCTTTTCATCG 515

RESULT 6  
 LOCUS B1609541 569 bp mRNA linear EST 07-SEP-2001  
 DEFINITION RH14337.5prime RH Drosophila melanogaster normalized Head p1C-1 Drosophila melanogaster cDNA clone RH14337.5 similar to alpha-Est7: FBan001112 GO: [carboxylesterase (GO:0004091); carboxylesterase (GO:0004091)] located on: 3R 84D5-84D5; 08/17/2001, mRNA sequence.

ACCESSION B1609541  
 VERSION B1609541.1 GI:1550506  
 SOURCE EST.  
 ORGANISM fruit fly.  
 Drosophila melanogaster  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
 1 (bases 1 to 569)  
 Champe, M., Chavez, C., Dorsett, V., Farrant, D., Frise, E., George, R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G., Mista, S., Munhall, C., J., Nunoo, J., Pacleb, J., Parasas, V., Park, S., Phouanavong, S., Wan, K., Yu, C., Lewis, S.E., Celniker, S., and Rubin, G.M.  
 BDBP/HIMI RH Drosophila EST Project





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QY 953 ACCAGACACCGACGCTGTGTGTACCAACAACAGAGAAATGGTGAAGAGCGCTGG 1012
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 430 TCTCCACGCCCAATGTGTATATCAAGCCCTCAAGAGATGATGAAGACCGCTTGA 489
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QY 1013 GAAATTCGATACCGACATGATGAGCAATACCTCTACGAGGTTTGTTCGAATCAA 1072
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Db 490 GTAATCCATCCCTCCCTGTTTATAGAAACACTTGTACGAGGCGCTGTGGTTCCAG 549
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1073 TTGCCAACAATATCCGAGCTTTGTAAGAAGTTGA 1109
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Db 550 AGGTAAGCTTATGCCGACGAGTGTGACGACGCTTGA 586
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RESULT 8
A1517692
LOCUS A1517692 671 bp mRNA linear EST 19-APR-2001
DEFINITION GH28740.Sprime GH Drosophila melanogaster head pot2 Drosophila
            melanogaster cDNA clone GH28740 Sprime similar to U51050:
            Drosophila melanogaster alpha esterase (aef) gene, partial cds,
            mRNA sequence.
ACCESSION A1517692
VERSION A1517692.1 GI:4420792
KEYWORDS EST.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 671)
            Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,
            Lewis,S. and Rubin,G.M.
            BDGP/HHMI Drosophila EST Project
            Unpublished (2001)
            Contact: Stapleton, M.
            BDBP
            Lawrence Berkeley National Lab
            One Cyclotron Rd, Berkeley, CA 94720, USA
            Fax: 510 486 6798
            Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
            Plate: 287 row: D column: 4
            High quality sequence stop: 538.
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        /organism="Drosophila melanogaster"
        /db_xref="taxon:7227"
        /clone_lib="GH Drosophila melanogaster head pot2"
        /sex="male and female"
        /dev_stage="adult"
        /lab_host="DHS - alpha"
        /note="Organ: head; Vector: pot2; Site:1: EcoRI; Site:2:
            XhoI; Sized fractionated cDNAs were directly ligated into
            pot2. Plasmid cDNA library."
BASE COUNT 155 a 170 c 193 g 153 t
ORIGIN
Query Match 13.8%; Score 236; DB 9; Length 671;
Best Local Similarity 64.4%; Pred. No. 6.7e-60;
Matches 353; Conservative 0; Mismatches 195; Indels 0; Gaps 0;

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Db 302 GAGTTGGGTTTAAGGCCCTCCAGAGCCCATTCCTCCGGAGAGAGTCCGCACTCAGC 361
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QY 268 GGGCCACCAACAGATCGGTACAGACGATTTATAGTGGCAACCCACAGGTTGGAG 327
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 362 CAGCCGAAGATTAAGGCCCTCCAGGTCACATTTGCTTCGATAGTAGAGGCTCCGAG 421
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 328 GATTGTATACCTGAATGTGTATACCAATGACTTGAACCCAGCAAAAGGCGCTCTT 387
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 422 GACTGCTCTATCTCAATGTGTACACCAACAATGTGAAGCCGACAAAGCTCGCCGGTT 481
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 388 ATGTTTTCATCCATGCGGAGATTTATTTGGGGAAGCAATGCTACGTGTGT 447
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 482 ATGTTTGGATTTACGAGAGAGGCTTCATTTATCGCGAGGCCAATCGGAATGTATGGC 541
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 448 CCCGACTACTTTATGAAGAAACCCGTGTCTGTGTACCGTCGAATATGTTGGGTGTG 507
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 542 CCGGATTAATCTTATGAAGAAAGATTTGTTCTGTCAGATACAGTACCGACTTGGGCT 601
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 508 TTGGGTTTCTCCTTACCTGAATCGAAATCTCAATGTCCTCCGCAACGCTGCTCAG 567
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 602 TTGGGATTTATGAGTCTTAAATCCCGAGCTAAATGTACAGAAATGCTGGCTCAAG 661
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QY 568 GATCAAGT 575
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Db 662 GATCAAGT 669
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RESULT 9
A1403830
LOCUS A1403830 630 bp mRNA linear EST 19-APR-2001
DEFINITION GH23353.Sprime GH Drosophila melanogaster head pot2 Drosophila
            melanogaster cDNA clone GH23353 Sprime similar to U51052:
            Drosophila melanogaster alpha esterase (aef) gene, partial cds,
            mRNA sequence.
ACCESSION A1403830
VERSION A1403830.1 GI:4246917
KEYWORDS EST.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 630)
            Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,
            Lewis,S. and Rubin,G.M.
            BDGP/HHMI Drosophila EST Project
            Unpublished (2001)
            Contact: Stapleton, M.
            BDBP
            Lawrence Berkeley National Lab
            One Cyclotron Rd, Berkeley, CA 94720, USA
            Fax: 510 486 6798
            Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
            Plate: 233 row: E column: 5
            High quality sequence stop: 548.
FEATURES
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        1..630
        /organism="Drosophila melanogaster"
        /db_xref="taxon:7227"
        /clone_lib="GH23353"
        /clone_lib="GH Drosophila melanogaster head pot2"
        /sex="male and female"
        /dev_stage="adult"
        /lab_host="DHS - alpha"
        /note="Organ: head; Vector: pot2; Site:1: EcoRI; Site:2:
            XhoI; Sized fractionated cDNAs were directly ligated into
            pot2. Plasmid cDNA library."
BASE COUNT 150 a 162 c 173 g 144 t
ORIGIN
Query Match 13.2%; Score 226.2; DB 9; Length 630;
Best Local Similarity 60.1%; Pred. No. 6.1e-57;

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Matches 375; Conservative 0; Mismatches 249; Indels 0; Gaps 0;

149 TCTACGATGATCTTACTACAGTTTGAGAGTATACCCATATGCTAGCCTCCAGTGGG 208  
 2 TCTACGCAACAACCTACTACTGCTGAGGCGCTCCGTTCCGCAAGCGGCGGCGG 61  
 209 AGTTGAATTCACAGCCGCCCTGTACATGGAGGGGTGTACGTGATGCTGTG 268  
 62 AGCTCCCTCTACAGGCGCGCGGTGAGGAGCCAGACACTGCTGATGTCAGCGGTGACAC 121  
 269 GCGCAGCAGACAGATCCGATGAGACAGATTTCAATTAAGTGGCAAAACCCACAGTTGCGAG 328  
 122 ATGTTCCGGCCCAAGCCCTGCCAGGTCAACATGCTTGAAGCGAGTGCAGCGAG 181  
 329 ATGTGCTATACCTGAATGTGTATACCAATGACTGAGACCAAGCAAGAGCGTCTGT 388  
 182 ACTGTCTGACTCAATGCTTACACACGAGGAGTTACTTCCACACAGCTTTGCCGTT 241  
 389 TGGTTTCATCCATGCGGAGATTTTATTTTGGCGGAGCAAAATGTAAGTGTGCTG 448  
 242 TGGTTTGGATCTATGCGCGGTGATTCAAATGGAGAGATCCGCGGATCTGACAGCC 301  
 449 CCGACTACTTATGAGAAACCCGCTGCTGTGTACACCGTCAATATGCTTGGGTGT 508  
 302 CGGACTACATATGATGAGACATGCTGATGCTGATATGCTATGCTGATGAGAGCC 361  
 509 TGGGTTTCTTACCTGGAATCGGAATTCATATGCTCCCGGAGCGCTGGCTCAGG 568  
 362 TGGGATTCCTTATGCTTGCAGACAGAAAGATGATGCTTCTGAGAACGCCGATTAAG 421  
 569 ATCAAGTAAATGCTGAGAGTGGTCAAGATATATTGCTTCTGCTGCTGCTGAG 628  
 422 ATCAAGTAAATGCTGAGAGTGGTCAAGATGCTTCTGCTGCTGCTGCTGCTG 481  
 629 ACATATTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 688  
 482 ATATATTAACCGTTTGTGTGAGAGTGTGAGAGTGCATCCACATATATATGATGCTGA 541  
 689 CCGACAGACCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 748  
 542 CGGATGAGGCGCAAGGCGCTATTTCAACAGATATATATGCTGAGTCCGACTGGCAG 601  
 749 CATGGGCTCTACAGATGGCAAA 772  
 602 CCGTGGCGAGACCCCAACCCACA 625

RESULT 10  
 B1628316 674 bp mRNA linear EST 10-SEP-2001  
 LOCUS  
 DEFINITION RH56682.5prime RH Drosophila melanogaster normalized Head p1C-1  
 Drosophila melanogaster cDNA clone RH56682.5 similar to alpha-Est7:  
 Fban0001112 GO: [carboxylesterase (GO:0004091)] carboxylesterase  
 (GO:0004091) located on: 3R 84D5-84D5; 08/22/2001, mRNA sequence.  
 B1628316  
 B1628316.1 GI:15530524  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 fruit fly,  
 Drosophila melanogaster  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 Ephydroidea; Drosophilidae; Drosophila.  
 1 (bases 1 to 674)  
 Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, B., Carlson  
 'J', Champs, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E., George  
 'R', Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G., Mista, S.,  
 Munhall, C.J., Nuno, J., Pacleb, J., Paragas, V., Park, S.,  
 Phouanenvong, S., Wan, K., Yu, C., Lewis, S.E., Celisner, S. and Rubin  
 'G.M.  
 BDBP/HMMI RH Drosophila EST Project  
 TITLE  
 JOURNAL  
 COMMENT  
 BDBP  
 Contact: Stapleton, M.

Lawrence Berkeley National Lab  
 One Cyclotron Rd, Berkeley, CA 94720, USA  
 Fax: 510 486 6798  
 Email: <http://www.fruitfly.org/EST>, [estfruitfly@berkeley.edu](mailto:estfruitfly@berkeley.edu)  
 Plate: RH.566 row: G column: 10  
 High quality sequence stop: 558.  
 location/Qualifiers

FEATURES  
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 1..674  
 /organism="Drosophila melanogaster"  
 /db\_xref="taxon:7227"  
 /clone="RH56682"  
 /clone\_lib="RH Drosophila melanogaster normalized Head  
 p1C-1"  
 /sex="male and female"  
 /dev\_stage="adult"  
 /lab\_host="DH5-alpha Tona"  
 /note="Organ: head; Vector: p1C1; Site: 1; XhoI: Site: 2;  
 BamHI: Library was kindly generated by Piero Carninci at  
 the RIKEN. The library was normalized and excised using  
 Cre recombinase. Plasmid cDNA library."  
 Cre recombinase. Plasmid cDNA library."

BASE COUNT 153 a 170 c 195 g 155 t 1 others

ORIGIN

Query Match 13.2%; Score 225.6; DB 13; Length 674;  
 Best Local Similarity 63.7%; Pred. No. 9.6e-57;  
 Matches 342; Conservative 0; Mismatches 195; Indels 0; Gaps 0;

28 CCCGGAACCTTGGCTTAAATGCTGCTCAATTAATACAAATACCCGCTGAGTACA 87  
 138 CGCTGGCGGTGGCGCTTAAACCATGACATTAAGTCCAGCATGTCGCACTGAC 197  
 88 AATGAACCCCAATATATGATATCTGATATGACAAATTAAGGTGTTAAGCGAATAC 147  
 198 AATGAACAGTGTGCGCGACACGAGATACGCGAAGTGAAGGATATCAAGCTATCT 257  
 148 GTCTAGATGATTTCTACTACAGTTTTCAGATATACCTTATGCTTAAGCTCAGTGG 207  
 258 CTCTAGATGTGCTCTACTTACCTTACAGTGTGATGAGTATCCGCTACCGCCAGCT 317  
 208 GAGTTAGATTCAGAGCACCACCGCGCTGTACATGGAGGAGGTGTACGTGATGCTGT 267  
 318 GAGTTGGGTTTAAAGCCCTCAGAGGCTTCCCTGGAGCGAGTGGAGCTGACGAC 377  
 268 GGGCAGCAGCAAGATCGGTATACAGATTTATTAAGGAGCCACCAAGGTTGCGAG 327  
 378 CACCCGAAGATTAAGCCCGTCCAGGTGCTGCTTCTGATTAAGGTAGAGGCTCCAG 437  
 328 GATTGCTATACCTGATATGATATACCAATGACTGACCCAGACAAAGGCTCTGTT 387  
 438 GAGTGCCTATATCTCAATGTGTACACCAATATGTAAGCCCGAGAGGCTGCCGTT 497  
 388 ATGTTTTCATCCATGCGGAGATTTTATTTTCGGGAGCAAAATGCTGACTGTTTGT 447  
 498 ATGTTTGGATTCAGGAGAGGAGCTTCATATATGCGGAGGCCAATGCGAATGCTAT 557  
 448 CCCGACTACTTAAAGAAACCCGCTGCTGTGTAACCGTCAATATGCTTGGGTGTG 507  
 508 TTGGTTTCTTACCTGCAATGGAATATCTCAATGCTCCGGGAGCAAGCTGGCTC 564  
 558 CCGGATTAATTAAGAAAGATGTTGCTCGTCAACATACAGTACGACTGGGCTG 617  
 618 NTGGGATTTATGAGCTTAAGTCCCGGAGCTAAATATGACAGGAATATGCTGGCTC 674

RESULT 11  
 B1635372 676 bp mRNA linear EST 10-SEP-2001  
 LOCUS  
 DEFINITION SD16705.5prime SD Drosophila melanogaster Schneider L2 cell culture  
 p072 Drosophila melanogaster cDNA clone SD16705.5 similar to  
 alpha-Est7: Fban0001112 GO: [carboxylesterase (GO:0004091)]  
 carboxylesterase (GO:0004091) located on: 3R 84D5-84D5; 05/18/2001  
 mRNA sequence.  
 B1635372

ACCESSION  
 B1635372

VERSION B1635372.1 GI:15537582  
 KEYWORDS EST.  
 SOURCE fruit fly.  
 ORGANISM Drosophila melanogaster  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
 REFERENCE 1 (bases 1 to 676)  
 AUTHORS Harvey, D., Broksstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G., Lewis, S. and Rubin, G.M.  
 TITLE BDGP/HMT Drosophila EST project  
 JOURNAL Unpublished (2001)  
 COMMENT Contact: Stapleton, M.  
 BDGP  
 Lawrence Berkeley National Lab  
 One Cyclotron Rd, Berkeley, CA 94720, USA  
 Fax: 510 486 6798  
 Email: [http://www.fruitfly.org/EST\\_est@fruitfly.berkeley.edu](http://www.fruitfly.org/EST_est@fruitfly.berkeley.edu)  
 Plate: SD.167 row: A column: 5  
 High quality sequence stop: 641.

## FEATURES

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 /lab\_host="DHS-alpha"  
 /note="Vector: pot2; Site\_1: EcorI; Site\_2: XhoI; Sized fractionated cDNAs were directly ligated into pot2. Plasmid cDNA library."  
 BASE COUNT 155 a 173 c 194 g 154 t  
 ORIGIN

Query Match 13.2%; Score 225.6; DB 13; Length 676;  
 Best Local Similarity 63.8%; Pred. No. 9,6e-57;  
 Matches 342; Conservative 0; Mismatches 194; Indels 0; Gaps 0;

28 CGCGTGAACCTATGCTTAATGATGCTGATCAATTAATACAAACACCTGCTGACTACA 87  
 141 CGCTGG 111  
 88 AATGAACCAATTAATGATGCTGATCAATTAATGATGCTGATGCTGATGCTGATGCTG 147  
 201 AATGAACCAATTAATGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 260  
 148 GTCTAGATGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 207  
 261 CTCTAGATGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 320  
 208 GATTTAGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATG 267  
 321 GATTTAGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATG 380  
 268 GGGCCAGCAAGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 327  
 381 CAGCCCAAGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATG 440  
 328 GATTTAGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATG 387  
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 388 ATGCTTTAGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 447  
 501 ATGCTTTAGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 560  
 448 CCGGACTACTTATGAACCAACCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 507  
 561 CCGGACTACTTATGAACCAACCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 620  
 508 TTGGGTTCTTACCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 563  
 621 TTGGGTTCTTACCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 676

## RESULT 12

B1614181 673 bp mRNA linear EST 07-sep-2001  
 RH43493:5prtime RH Drosophila melanogaster normalized Head p1c-1  
 B1614181  
 LOCUS  
 DEFINITION

B1614181  
 (GO:0004091) located on 3R 84D5-84D5; 08/18/2001, mRNA sequence.  
 B1614181  
 GI:15509706  
 EST.

## ACCESSION

B1614181  
 GI:15509706  
 EST.

## KEYWORDS

fruit fly.  
 Drosophila melanogaster  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

## REFERENCE

1 (bases 1 to 673)  
 Stapleton, M., Broksstein, P., Hong, L., Tyler, D., Berman, B., Carlson, J., Champagne, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E., George, R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G., Mista, S., Mungall, C.J., Nunoo, J., Pacle, J., Paragas, V., Park, S., Phouanavong, S., Wan, K., Yu, C., Lewis, S.E., Celnik, S. and Rubin, G.M.  
 BDGP/HMT RH Drosophila EST project  
 Unpublished (2001)  
 Contact: Stapleton, M.  
 BDGP  
 Lawrence Berkeley National Lab  
 One Cyclotron Rd, Berkeley, CA 94720, USA  
 Fax: 510 486 6798  
 Email: [http://www.fruitfly.org/EST\\_est@fruitfly.berkeley.edu](http://www.fruitfly.org/EST_est@fruitfly.berkeley.edu)  
 Plate: RH 434 row: H column: 9  
 High quality sequence stop: 553.

## FEATURES

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 /clone="RH43493"  
 /clone.lib="RH Drosophila melanogaster normalized Head p1c-1"  
 /sex="male and female"  
 /dev\_stage="Adult"  
 /lab\_host="DHS-alpha Tona"  
 /note="Organ: head; Vector: p1c1; Site\_1: XhoI; Site\_2: BamHI; Library was kindly generated by Piero Carninci at the RIKEN. The library was normalized and excised using Cre recombinase. Plasmid cDNA library."  
 BASE COUNT 153 a 169 c 195 g 155 t  
 ORIGIN

Query Match 13.1%; Score 224.6; DB 13; Length 673;  
 Best Local Similarity 63.6%; Pred. No. 1,9e-56;  
 Matches 341; Conservative 0; Mismatches 195; Indels 0; Gaps 0;

28 CGCGTGAACCTATGCTTAATGATGCTGATCAATTAATACAAACACCTGCTGACTACA 87  
 138 CGCTGG 111  
 88 AATGAACCAATTAATGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATG 147  
 198 AATGAACCAATTAATGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 257  
 148 GTCTAGATGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 207  
 258 GTCTAGATGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 317  
 208 GATTTAGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 267  
 318 GATTTAGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 377  
 268 GGGCCAGCAAGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 327

Db	378	CAGCCGAGGAAATGAAGCCGCTCCAGGTGCAGTTCGCTTCGATAAGGTGAGGGCTCCGAG	437
QY	328	GATGTCTATACCTAATAGTGTATACCAATGACTTGAACCCAGACAAAAGCGTCTCTTT	387
Db	438	GACTCCCTCTATCTCAATGTGTATACACCAACATGTGAAGCCCGACAAAGGCTTGCCCGGT	497
QY	388	ATGCTTTTCAACCATGCGGGAGATTTTATTTTGGGCGAAGCAATCGTAACGTGGTTGGT	447
Db	498	ATGCTTTTGGATTCACGAGGAGGAGCGTTCAATTATCGGCGAGGCCAATTCGGGAATGGTATGCG	557
QY	448	CCCGACTACTTTATATCAAGAACCCGTGGCTTTGGTAAACCGTCAATATTCGTTTGGGTGTG	507
Db	558	CCGGATTACTTTATCAAGAAAGATGTTTNTCTCGTCACAGATACACTACCGACTTGGGGCT	617
QY	508	TTGGTTTTCCTTAGCGCTGAAATCGGAAATATCATGTATCCCGGGACGCTGGCCT	563
Db	618	TTGGATTTATACGTCTTAAGTCCCGGACGCTAAATATGTATCCAGGAATATGCTGTGCTT	673

RESULT	13
B1614443	
LOCUS	
DEFINITION	B1614443 672 bp mRNA linear EST 07-SEP-2001
ACCESSION	RH43812.3prime RH Drosophila melanogaster normalized Head P1C-1
VERSION	Phan001112 GO:(carboxyesterase cDNA clone RH43812 similar to alpha-BST);
KEYWORDS	(GO:0004091) GO:(catalyzed on: 3R 84D5::08/18/2001, mRNA sequence.
SOURCE	B1614443 B1614443 GI:15509668
	EST,
	fruit fly.

ORGANISM  
Drosophila melanogaster  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Ephydroidea; Drosophilidae; Drosophila.  
1 (bases 1 to 672)

REFERENCE

**AUTHORS**  
Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, B., Carlson  
J., Champagne, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E., George  
R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G., Mitra, S.,  
Mundall, C. J., Nunoo, J., Paclob, J., Pargacs, V., Park, S.,  
Phouanavong, S., Wan, K., Yu, C., Lewis, S. E., Celniker, S.,  
G.M.

**TITLE**  
BDGP/HHMI RH *Drosophila* EST Project

**JOURNAL**  
Unpublished (2001)

**COMMENT**  
Contact: Stapleton, M.

Lawrence Berkeley National Lab  
One Cyclotron Rd, Berkeley, CA 94720, USA  
Fax: 510 486 6798  
Email: [http://www.fruitfly.org/EST\\_estefruitfly.berkeley.edu](http://www.fruitfly.org/EST_estefruitfly.berkeley.edu)  
Plate: RH.438 row: A column: 12  
High quality sequence stop: 554.  
Location/Qualifiers  
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pric-1"
/sex="male and female"
/dev_stage="Adult"
/lab_host="DH5-alpha Tona"
/note="Organ: head; Vector: pFUC1; Site.1: XhoI; Site.2:
BamHI. The library was kindly generated by Piero Carninci at
the RIKEN. The library was normalized and excised using
Cre recombinase. Plasmid cDNA library."
BASE COUNT      154 a      154 g      155 t
ORIGIN           154 c      194 g

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Best Local Similarity	63.6%	Pred. No. 5.9e-56;	
Matches 340; Conservative	0;	Mismatches 199;	Indels 0; Gaps 0;

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QY 88 AATGAACCCCAATTAATGATACGTCAATATGACCAATTAAGGGTGTGAACGCAATACC 147

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QY 148 GTCTACGATATTTCTTACTACAGTTTTCGAGAGTATACCTTGTCTAAGCCTCCAGTGGCT 207

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QY 328 GATTGTCTAATCTGAATGTATACCAATGACTGAACCCAGCAAAAGAGCGTCTGT 387

Db 438 GACTGCTCTATCTCATGTGTACCAACAATGTGAAGCCCGACAAGGCTCGCCGGTT 497

QY 388 ATGATTTCATCCANTGGCGAGATTATTTTCGGCGAGCAAAATCTAATCTGTTGGT 447

Db 498 ATGTTTGGATTACGAGAGAGGCTTCATTATCCGCGAGGCAATCGGGAATGTTATGCG 557

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Db 618 TTGGGATTTATGAGTCTTAAGTCCCCCGAGCTAAATGTACCAAAATATGCTGGCG 672

RESULT 14					
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LOCUS					
DEFINITION	B1233202,	670 bp	mRNA	linear	EST J1-JUL-2001
	BE29491.5	spine RE	Drosophila melanogaster	normalized	Embryo Pfc-1
	Drosophila		melanogaster cDNA clone BE29491.5	similar to	alpha-B5C7
	PBano001112	located on:	3R 84D5-84D5; 04/12/2001,	mRNA sequence.	
ACCESSION	B1233202				
VERSION	B1233202.1				
KEYWORDS	EST.				
SOURCE	Fruit fly.				
ORGANISM	Drosophila melanogaster				

REFERENCE	TITLE
AUTHORS	JOURNAL
	COMMENT
1 (bases 1 to 670) Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, B., Carlson J., Champ, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E., George R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G., Mitra, S., Mungall, C. J., Nunoo, J., Pacle, J., Paragas, V., Park, S., Phonuanavong, S., Wan, K., Yu, C., Lewis, S. E., Celniker, S. and Rubin , G. M.	BDGP/HMT RE Drosophila Est Project Unpublished (2001) Contact: Stapleton, M.

BDGP  
Lawrence Berkeley National Lab  
One Cyclotron Rd. Berkeley, CA 94720, USA  
Fax: 510 486 6798  
Email: [http://www.fruitfly.org/EST\\_est@fruitfly.berkeley.edu](http://www.fruitfly.org/EST_est@fruitfly.berkeley.edu)  
Plate: RE.294 row: H column: 7  
High quality sequence stop: 534.

FEATURES

source

location/Qualifiers

1. 670

organism="Drosophila melanogaster"

db\_xref="taxon:7227"

clone="RE29491"

clone\_lib="RE Drosophila melanogaster normalized Embryo



GenCore version 5.1.4-p5.4578  
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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	956.6	55.9	1713	US-08-669-524-1	Sequence 1, Appl
3	956.6	55.9	1713	US-09-068-960-1	Sequence 1, Appl
4	956.6	55.9	1713	US-09-068-960-7	Sequence 7, Appl
5	956.6	55.9	1713	US-09-068-960-9	Sequence 9, Appl
6	955	55.8	1713	US-09-068-960-3	Sequence 3, Appl
7	952.2	55.7	1713	US-08-668-524-2	Sequence 2, Appl
8	951.8	55.7	1713	US-08-668-524-5	Sequence 5, Appl
9	162.6	9.5	1584	US-08-747-221B-51	Sequence 51, Appl
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11	162.6	9.5	1584	US-09-005-051-51	Sequence 51, Appl
12	162.6	9.5	1584	US-09-005-051-52	Sequence 52, Appl
13	162.6	9.5	2007	US-08-747-221B-36	Sequence 36, Appl
14	162.6	9.5	2007	US-08-747-221B-38	Sequence 38, Appl
15	162.6	9.5	2007	US-09-005-051-36	Sequence 36, Appl
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24	127	7.4	1792	US-08-747-221B-20	Sequence 20, Appl
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ALIGNMENTS

RESULT 1  
US-09-068-960-14  
Sequence 14, Application US/09068960A  
Patent No. 6235515  
GENERAL INFORMATION:  
APPLICANT: Commonwealth Scientific and Industrial Rsrch. Org.  
TITLE OF INVENTION: MALATHION CARBOXYESTERASE  
FILE REFERENCE: Attorney Docket No. 6235515 50179-051  
CURRENT FILING DATE: 1998-05-20  
EARLIER FILING DATE: 1998-05-20  
EARLIER APPLICATION NUMBER: PCT/AU96/00746  
EARLIER FILING DATE: 1996-11-22  
EARLIER APPLICATION NUMBER: AU 6751  
NUMBER OF SEQ ID NOS: 43  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 14  
LENGTH: 1710  
TYPE: DNA  
ORGANISM: Musca domestica  
US-09-068-960-14

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## RESULT 2

US-08-669-524-1

Sequence 1, Application us/08669524

Patent No. 5843758

## GENERAL INFORMATION:

APPLICANT: RUSSELL, Robyn J.

APPLICANT: NEWCOMB, Richard D.

APPLICANT: ROBIN, Geoffrey C.

APPLICANT: BOYCE, Thomas M.

APPLICANT: CAMPBELL, Peter M.

APPLICANT: PARKER, Anthony G.

APPLICANT: OAKESHOT, John G.

APPLICANT: SMYTH, Kerrie A.

TITLE OF INVENTION: ENZYME BASED BIOMEDIATION

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lowe Price Leblanc &amp; Becker

STREET: 99 Canal Center Plaza, Suite 300

CITY: Alexandria

STATE: Virginia

COUNTRY: USA

ZIP: 22314

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/669,524

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Price, Robert L.

REGISTRATION NUMBER: 22,685

REFERENCE/DOCKET NUMBER: 1451-021

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-684-1111

TELEFAX: 703-684-1124

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1713 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-669-524-1

## Query Match

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Matches 1223; Conservative 0; Mismatches 444; Indels 0; Gaps 0;

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Db	1424	TAACTATTTCTTCTGGAAATCAATTTGGCCAAACGTAATGCTTAAAGAAATCGCTGAATACA	1483
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Best Local Similarity	73.4%;	Pred. No. 2,4e-304;		
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 DB 584 TGAATTCGGAATATCTCATATGTCCTGCAACGCTGCTCAAGGATGCAATATG 643  
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 DB 824 AAAAAAGATGTGTGCTGCTGCAACGCTGCTCAAGGATGCAATATG 883  
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 DB 884 CACAAGTGTGTGCTGCTGCAACGCTGCTCAAGGATGCAATATG 943  
 QY 944 TAGAAGTGTGTGCTGCTGCAACGCTGCTCAAGGATGCAATATG 1003  
 DB 944 TAGAAGTGTGTGCTGCTGCAACGCTGCTCAAGGATGCAATATG 1003  
 QY 1004 GCGGCGAAGTGTGTGCTGCTGCAACGCTGCTCAAGGATGCAATATG 1063  
 DB 1004 GCGGCGAAGTGTGTGCTGCTGCAACGCTGCTCAAGGATGCAATATG 1063  
 QY 1064 CCAATATGCTGCTGCTGCAACGCTGCTCAAGGATGCAATATG 1123  
 DB 1064 CCAATATGCTGCTGCTGCAACGCTGCTCAAGGATGCAATATG 1123  
 QY 1124 ATGTCGCTGCTGCTGCTGCAACGCTGCTCAAGGATGCAATATG 1183  
 DB 1124 ATGTCGCTGCTGCTGCTGCAACGCTGCTCAAGGATGCAATATG 1183  
 QY 1184 CCAATATGCTGCTGCTGCAACGCTGCTCAAGGATGCAATATG 1243  
 DB 1184 CCAATATGCTGCTGCTGCAACGCTGCTCAAGGATGCAATATG 1243  
 QY 1244 TTTGCTGCTGCTGCTGCTGCAACGCTGCTCAAGGATGCAATATG 1303  
 DB 1244 TTTGCTGCTGCTGCTGCTGCAACGCTGCTCAAGGATGCAATATG 1303  
 QY 1304 ACAAGTGTGTGCTGCTGCAACGCTGCTCAAGGATGCAATATG 1363  
 DB 1304 ACAAGTGTGTGCTGCTGCAACGCTGCTCAAGGATGCAATATG 1363  
 QY 1364 ACCGCTGCTGCTGCTGCTGCAACGCTGCTCAAGGATGCAATATG 1423  
 DB 1364 ACCGCTGCTGCTGCTGCTGCAACGCTGCTCAAGGATGCAATATG 1423  
 QY 1424 TAACTATGCTGCTGCTGCTGCAACGCTGCTCAAGGATGCAATATG 1483  
 DB 1424 TAACTATGCTGCTGCTGCTGCAACGCTGCTCAAGGATGCAATATG 1483

QY 1484 AAACATTTGAAGCAGTGTGCTGCAACGCTGCTCAAGGATGCAATATG 1543  
 DB 1484 AAACATTTGAAGCAGTGTGCTGCAACGCTGCTCAAGGATGCAATATG 1543  
 QY 1544 GCAATGATGCTGCTGCTGCAACGCTGCTCAAGGATGCAATATG 1603  
 DB 1544 GCAATGATGCTGCTGCTGCAACGCTGCTCAAGGATGCAATATG 1603  
 QY 1604 TCTATGATGCTGCTGCTGCAACGCTGCTCAAGGATGCAATATG 1663  
 DB 1604 TCTATGATGCTGCTGCTGCAACGCTGCTCAAGGATGCAATATG 1663  
 QY 1664 AAATTTAACAATGCTGCTGCAACGCTGCTCAAGGATGCAATATG 1710  
 DB 1664 AAATTTAACAATGCTGCTGCAACGCTGCTCAAGGATGCAATATG 1710

RESULT 6  
 US-09-068-960-3  
 ; Sequence 3, Application US/09068960A  
 ; Patent No. 6235515  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Commonwealth Scientific and Industrial Resrch. Org.  
 ; TITLE OF INVENTION: MALATHION CARBOXYL ESTERASE  
 ; FILE REFERENCE: Attorney Docket No. 6235515 50179-051  
 ; CURRENT APPLICATION NUMBER: US/09/068,960A  
 ; EARLIER FILING DATE: 1998-05-20  
 ; EARLIER APPLICATION NUMBER: PCT/AU96/00746  
 ; EARLIER FILING DATE: 1996-11-22  
 ; EARLIER APPLICATION NUMBER: AU 6751  
 ; EARLIER FILING DATE: 1995-11-23  
 ; NUMBER OF SEQ ID NOS: 43  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 3  
 ; LENGTH: 1713  
 ; TYPE: DNA  
 ; ORGANISM: Lucilia cuprina  
 US-09-068-960-3

Query Match 55.8%; Score 955; DB 4; Length 1713;  
 Best Local Similarity 73.3%; Pred. No. 8, 2e-304;  
 Matches 1222; Conservative 0; Mismatches 445; Indels 0; Gaps 0;

QY 44 TTAATGCTGCTGCTGCAACGCTGCTCAAGGATGCAATATG 103  
 DB 44 TTAATGCTGCTGCTGCAACGCTGCTCAAGGATGCAATATG 103  
 QY 104 TCGATGCTGCTGCTGCAACGCTGCTCAAGGATGCAATATG 163  
 DB 104 TCGATGCTGCTGCTGCAACGCTGCTCAAGGATGCAATATG 163  
 QY 164 ACTAGCTGCTGCTGCTGCAACGCTGCTCAAGGATGCAATATG 223  
 DB 164 ACTAGCTGCTGCTGCTGCAACGCTGCTCAAGGATGCAATATG 223  
 QY 224 CACCCGAGGCTGCTGCTGCAACGCTGCTCAAGGATGCAATATG 283  
 DB 224 CACCCGAGGCTGCTGCTGCAACGCTGCTCAAGGATGCAATATG 283  
 QY 284 CCGTACAGGCTGCTGCTGCAACGCTGCTCAAGGATGCAATATG 343  
 DB 284 CCGTACAGGCTGCTGCTGCAACGCTGCTCAAGGATGCAATATG 343  
 QY 344 ATGCTATGCTGCTGCTGCAACGCTGCTCAAGGATGCAATATG 403  
 DB 344 ATGCTATGCTGCTGCTGCAACGCTGCTCAAGGATGCAATATG 403  
 QY 404 GCGGATGCTGCTGCTGCAACGCTGCTCAAGGATGCAATATG 463  
 DB 404 GCGGATGCTGCTGCTGCAACGCTGCTCAAGGATGCAATATG 463  
 QY 464 AGAAACCGTGTGCTGCTGCAACGCTGCTCAAGGATGCAATATG 523  
 DB 464 AGAAACCGTGTGCTGCTGCAACGCTGCTCAAGGATGCAATATG 523

Db 464 AAAAGATGATGATGATTAACATCAATATCGTTGGAGCTAGCTTTCTAAGT 523  
 QY 524 TGAATATGGAATATCAATATGTCGGGCAACGCTGGCTCAAGATCAATATGCTT 583  
 Db 524 TAAATATGAGACCTTAATATGTCGGGCAACGCTGGCTCAAGATCAATATGCTT 583  
 QY 584 TGAGATGGGTCAGAGATATATGTCGTTGGGCGGATGATCAATATATACCTCT 643  
 Db 584 TGGCTGGATTAATAATATGTCGTTGGGCGGATGATCAATATATACCTCT 643  
 QY 644 TCGGCGAAGTGTGGGCGGCTCAACCATATGATGATTAACCAACAGCCGCTG 703  
 Db 644 TTGGTGAAGTGTGGGCGGCTCAACCATATGATGATTAACCAACAGCCGCTG 703  
 QY 704 GTTATTCATCTGTGATCATGATGTCGGGTAATTCATGCTCATGGGCTCATAG 763  
 Db 704 GTCTTTCCATCTGTGATCATGATGTCGGGTAATTCATGCTCATGGGCTCATAG 763  
 QY 764 AATGCCAAGTGTGGGCTCAACCATATGATGATTAACCAACAGCCGCTG 823  
 Db 764 AATGCCAAGTGTGGGCTCAACCATATGATGATTAACCAACAGCCGCTG 823  
 QY 824 AAAAGATATCTGGAATTCCTAATGAAGCCATTCCTATGATTTGATCAAGAGAGC 883  
 Db 824 ATTAAGATGTTTGGATTTCTTAATGAAGCCATTCCTATGATTTGATCAAGAGAGC 883  
 QY 884 CACAGTGTGACACCCGGAAGATGCAAAATTAAGTATGTTCTTTGGACCCACTG 943  
 Db 884 AAAAGTGTGATCTTAAGAGAGCCGATCAAAATTAAGTATGTTCTTTGGACCCACTG 943  
 QY 944 TAGACCATACAGAGAGCCGATCTGTGTACCCAAACCAATCAAGAAATGATGA 1003  
 Db 944 TAGACCATACAGAGAGCCGATCTGTGTACCCAAACCAATCAAGAAATGATGA 1003  
 QY 944 TTGAGGATATGACAGCCGATCTGTGTACCCAAACCAATCAAGAAATGATGA 1003  
 Db 944 TTGAGGATATGACAGCCGATCTGTGTACCCAAACCAATCAAGAAATGATGA 1003  
 QY 1004 GCGCTTGGGAAATGATATCCCAATGATGATGATGATGATGATGATGATGAT 1063  
 Db 1004 GCGCTTGGGAAATGATATCCCAATGATGATGATGATGATGATGATGATGAT 1063  
 QY 1064 CCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1123  
 Db 1064 TCACTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1123  
 QY 1124 ATGTCCTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1183  
 Db 1124 ATGTCCTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1183  
 QY 1184 CCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1243  
 Db 1184 CCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1243  
 QY 1244 TTTGCTCTATTTCTATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1303  
 Db 1244 TTTGCTCTATTTCTATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1303  
 QY 1304 ACACAGCTGCT 1363  
 Db 1304 ACACAGCTGCT 1363  
 QY 1364 ACCCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1423  
 Db 1364 ACCCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1423  
 QY 1424 TAACTATCT 1483  
 Db 1424 TAACTATCT 1483  
 QY 1484 AAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1543  
 Db 1484 AAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1543  
 QY 1544 GCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1603  
 Db 1544 GCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1603

QY 1604 TCAATTAATGTTAAATATGCGGATGATTAAGTATGATGATTTGCCAATGATA 1663  
 Db 1604 TATACAGTGTGATTAATGATGATGATTAAGTATGATGATTTGCCAATGATA 1663  
 QY 1664 AATTAACATGCGCAAGTATGATTAAGTATTAAGTATTAAGTATTAAGT 1710  
 Db 1664 AGATTAACATGCGCAAGTATGATTAAGTATTAAGTATTAAGTATTAAGT 1710  
 RESULT 7  
 US-08-669-524-2  
 ? Sequence 2, Application US/08669524  
 ? Patent No. 5843758  
 ? GENERAL INFORMATION:  
 ? APPLICANT: RUSSELL, Robyn J.  
 ? APPLICANT: NEWCOMB, Richard D.  
 ? APPLICANT: ROBIN, Geoffrey C.  
 ? APPLICANT: BOYCE, Thomas M.  
 ? APPLICANT: CAMPBELL, Peter M.  
 ? APPLICANT: PARKER, Anthony G.  
 ? APPLICANT: OAKSHOTT, John G.  
 ? APPLICANT: SMYTH, Kerrie A.  
 ? TITLE OF INVENTION: ENZYME BASED BIOREMEDIATION  
 ? NUMBER OF SEQUENCES: 22  
 ? CORRESPONDENCE ADDRESS:  
 ? ADDRESSEE: Lowe Price Leblanc & Becker  
 ? STREET: 99 Canal Center Plaza, Suite 300  
 ? CITY: Alexandria  
 ? STATE: Virginia  
 ? COUNTRY: USA  
 ? ZIP: 22314  
 ? COMPUTER READABLE FORM:  
 ? MEDIUM TYPE: Floppy disk  
 ? COMPUTER: IBM PC compatible  
 ? OPERATING SYSTEM: PC-DOS/MS-DOS  
 ? SOFTWARE: Patent Release #1.0, Version #1.30  
 ? CURRENT APPLICATION DATA:  
 ? APPLICATION NUMBER: US/08/669,524  
 ? FILING DATE:  
 ? CLASSIFICATION: 435  
 ? ATTORNEY/AGENT INFORMATION:  
 ? NAME: Price, Robert L.  
 ? REGISTRATION NUMBER: 22,685  
 ? REFERENCE/DOCKET NUMBER: 1451-021  
 ? TELECOMMUNICATION INFORMATION:  
 ? TELEPHONE: 703-684-1111  
 ? TELEFAX: 703-684-1124  
 ? INFORMATION FOR SEQ ID NO: 2:  
 ? SEQUENCE CHARACTERISTICS:  
 ? LENGTH: 1713 base pairs  
 ? TYPE: nucleic acid  
 ? STRANDEDNESS: single  
 ? TOPOLOGY: linear  
 ? MOLECULE TYPE: DNA (genomic)  
 ? US-08-669-524-2  
 Query Match 55.7%; Score 952.2; DB 2; Length 1713;  
 Best Local Similarity 72.5%; P-adj. No. 6.8e-303;  
 Matches 1209; Conservative 0; Mismatches 458; Indels 0; Gaps 0;

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QY 224 CACCCAGGCGCTGTACCATGAGAGGTGTACGATTTGCTGGGCGCACCAACAGAT 283
Db 224 CACCCAGGCGGACCAACCCCTGGATGGTGGCTGATTTGCAATCAATAAAGATAGT 283
QY 284 CCGTACAGACAGATTTCAATAGTGGCAACCAAGCTTGGAGAGATGCTATACCTGA 343
Db 284 CAGTCAAGATTTATTTATNACNMGCAAGTGTGGCTCAGAGAGATGCTATACCTGA 343
QY 344 ATGTATACCAATGACTTGAACCCAGACAAAGGCGCTGTATGTTTATTCATCAGT 403
Db 344 GNGCTATACCAATATATTAATCCGAACTAAACCTCCCGTTTATGTAATACATCATG 403
QY 404 GCGAGATTTATTTGGGCAACCAATGTATCTGTTGGTCCGACACTTATATGA 463
Db 404 GTGGGATTTATTTATGCGGTAACATCATGTATGATGTATGCTCCGATTTATTTATTA 463
QY 464 AGAACCCTGCTGTGTGAACCTGCAATATGTTGGTGGTGGTGGTGGTGGTGGTGGT 523
Db 464 AAAAGATGTGGTGTGTGAATACATATATGTTGGAGCTGTAGGTTTCTAAGTT 523
QY 524 TGAATGCAAAATCTCATGTCCTCCGCAACCTGCGCTCAAGATCAAGTAAAGGCT 583
Db 524 TAAATGCAAGACCTTAATGTCCCGNATATCCGCTTAAAGATCAAGTCAAGTGGCT 583
QY 584 TGAGATGGTCAAGAGTAAATATGCTATTTGCTGGTGGTGGTGGTGGTGGTGGTGGT 643
Db 584 TGGGTGGATTAATAAATATGCGCAACTTGTGGCAATCCGATATATATATACAGTCT 643
QY 644 TCGGCAAGTGTGTGGGCGCTCAACCTATATATGATGATGATGATGATGATGATGATG 703
Db 644 TTGGTCAAGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 703
QY 704 GTTATTCATGCTGTATCATGATGCTCGGTAATTCATGCTGCTGCTGCTGCTGCTGCT 763
Db 704 GTCTTTTCATGCTGTATCATGATGCTGGGTAATGCTGCTGCTGCTGCTGCTGCTGCT 763
QY 764 AATGCCAAGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 823
Db 764 AATGCCAAGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 823
QY 824 AAAAGATATCTGCAATTCCTTAATGAAAGCCATCCCTATGATGATGATGATGATGATG 883
Db 824 AATAGAGATGTTTGGANTTTCTTNTGAAAGCCAGCAAGATTAATTAATTAATTAATTA 883
QY 884 CACAAGTTTGACACCCGAAGAAATGCAAAATAGTATGTTTCTTCTTGGACCCACTG 943
Db 884 AAAAGTTTATCTGTAGAAAGGCTACAAATAGTATGTTTCTTCTTGGTCCACTG 943
QY 944 TAGAACCATACAGACAGCGAGCTGTGTGTAACCAACCAATCAAGAAATGCTGAAGA 1003
Db 944 TTGANCCATATCAGACCGCTGATGTGTCTTACCAACCAATCTCTGGGAAATGCTTAAN 1003
QY 1004 GCGCTGGGGAATTCATATCCCAATGTATAGCAATACCTCTCAAGAGTGGTGGCTTT 1063
Db 1004 NTGCTGGGGAATTCATATCCCAATGTATAGTATGTTGTAACCTCATATGAGGTCTATTTT 1063
QY 1064 CCAATATTCATTCGCAACATATCCGAGGTGTGAAGAGTGGATTCCTGTGGAAT 1123
Db 1064 TCACCTCCTTTCATTCGCAACATATCCGAGGTGTGAAGAGTGGATTCCTGTGGAAT 1123
QY 1124 ATGTCCTGGGAGTGGTGTGACAGTGAAGCAAGTGGCCGGAACCTGTGAGAGGCTG 1183
Db 1124 TTGTGCAAGTGAATGGTGTGATGTAAGCAAGCCGCCAGAGACCTTGGAAATGGGTG 1183
QY 1184 CCAATTCGAAAAAGCCCTGTGATGAGTGGGAAACCACTACTCTGTGATATTTTATGAGC 1243
Db 1184 TTAATATTAAGAGCTCATGTTTACAGAGAAACCAACGACGATTAATTTATGATC 1243
QY 1244 TTGCTCCTATTTCTATTTCTCTCCCATGACATCGCTTCTCAATTTGGCTTCAAC 1303
Db 1244 TTGCTCCTCCTATTTCTATTTCTCTCTCCCATGACATCGCTTCTCAATTTGGCTTCAAT 1303
QY 1304 ACACAGCTGGACCTCCCATTTATTTGATGCTTTGATTTGATTTGCAATTTGCTTCAAT 1363

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Db 1304 ACNCTCCGGTACACCCCTGCTTGTATGCTTCCGACTTNGATTCGGAATCTTATTA 1363
QY 1364 ACCCTATGCAATATATGCTTTTGGCCGTGCTTAAAGGTGAAGCATGCGGATGAC 1423
Db 1364 ATCCCTATGCAATATATGCTTTTGGCCGTGCTTAAAGGTGAAGCATGCGGATGAC 1423
QY 1424 TAACCTATGCTTCTGCAACCTTTTGTGCAAGCCCTGCCAAAGAAAGCCGGAATGA 1483
Db 1424 TAACCTATGCTTCTGCAACCTTTTGTGCAAGCCCTGCCAAAGAAAGCCGGAATGA 1483
QY 1484 AAACATTTGAAGCATGTTGTGCAATTTGCAAGCATTTGCAAGCATTTGCAAGCATTT 1543
Db 1484 AAACATTTGAAGCATGTTGTGCAATTTGCAAGCATTTGCAAGCATTTGCAAGCATTT 1543
QY 1544 GCAATGATATAGGCGGATGGAACCACTCACTGGGATCCATTAATAAATCCGATGATG 1603
Db 1544 GCAATGATATAGGCGGATGGAACCACTCACTGGGATCCATTAATAAATCCGATGATG 1603
QY 1604 TCTATTAATGTTTAAATATCGGATGATGATGAAAGTATGATTTGGCAGAAATGATA 1663
Db 1604 TATCAAGTGTGTAATATTTAGANGATGATGAAATGATTTGATGATGATGATGATG 1663
QY 1664 AAATTAACAATGGGCAATATATTCGATTAAGAGCAATGTTT 1710
Db 1664 AGATTAACAATGGGCAATATATTCGATTTGAATAACATAGAGATTTATTT 1710

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RESULT 8
US-09-068-960-5
; Sequence 5, Application US/09068960A
; Patent No. 6235515
; GENERAL INFORMATION:
; APPLICANT: Commonwealth Scientific and Industrial Resrch. Org.
; TITLE OF INVENTION: MALATHION CARBOXYL ESTERASE
; FILE REFERENCE: Attorney Docket No. 6235515 50179-051
; CURRENT FILING DATE: 1998-05-20
; EARLIER FILING DATE: 1996-11-22
; EARLIER APPLICATION NUMBER: PCT/AU96/00746
; EARLIER FILING DATE: 1995-11-23
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1713
; TYPE: DNA
; ORGANISM: Lucilia cuprina
US-09-068-960-5

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Query Match 55.7%; Score 951.8; DB 4; Length 1713;
Best Local Similarity 73.2%; Pred. No. 9,3e-303;
Matches 1220; Conservative 0; Mismatches 447; Indels 0; Gaps 0;

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QY 44 TTAATGATGTCATTAATATACCAACTACGCTGTGATGCAAAATGAACCAATAA 103
Db 44 TTAATGATGTCATTAATATGTTTAAACTATGTTAACTAACAATGAACCAATGA 103
QY 104 TCGATACGAAATATGCAAAATTAAGGTGTTTAAAGCAATGACGCTGACATATCTT 163
Db 104 CTGAAACTGAAATATGCAAAATTAAGGTGTTTAAAGCAATGACGCTGACATATCTT 163
QY 164 ACTAGATTTGCAAGATATACCTTATGCTTAAGCTCCAGTGGGTGAGTATGATTCAGG 223
Db 164 ACTAGATTTGCAAGATATACCTTATGCTTAAAGCTCCAGTGGGTGAGTATGATTCAGG 223
QY 224 CACCCAGGCGCTGTACCATGAGAGGTGTAGCTGATTTGCTGGGCGCACCAAGAT 283
Db 224 CACCCAGGCGGACCAACACCTGGATGCTGATTTGCTGGGCGCACCAAGAT 283
QY 284 CCGTACAGACAGATTTCAATAGTGGCAAAACCAAGGTTGGAGAGATTTGCTATACCTGA 343
Db 284 CAGTCAAGATTTATTAAGGCGCAAAAGTGTGGCTCAGAGATTTGCTATACCTGA 343

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Db      38 TAAAGGAAAGAGCAATTAAGTGAAGAAAGAAATGTGTTCCATAGTATTTCGTGCAATTC 97
QY      185 CCTATGCTAAGCCTCCAGGAGTGGATGAGATTCAGAGCCAGCCGCTGATACAT 244
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      98 CATATGCCAAGACCTCCTAGGTGATCTAAGATTTAAGCCACCTCACTGAGAACTT 157
QY      245 GGGAGGCTGTACGTATGCTGTGGGCCAGCCAGACAGATCGGTACAGACATTTTCATTA 304
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      158 GGTGAGGTGTTCTTATGCTAGTAAGAAAGAGGAATAGTGTGATGATCAGTACATTTATTA 217
QY      305 GTGGCAAAACCCAGAGTTCGGAGATGTCTATACCTGATGTGTATACCAATGACTTAA 364
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      218 AAAAAATTAAAGTGGGCTGAAGATGTTTATACCTCAATGCTATGACCAAAAAACAT 277
QY      365 ACCGAGCAAAAGGCGCTCTGATGTTTATGCTTATCAGTGGCAGATTTTATTTTCGGCG 424
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      278 CAGAGAAATCACTTTCTCCAGTAATGATGATGATACATGAGAGAGGCTTCTCATGAGAT 337
QY      425 AAGCAATCTGAATGCTTGGTTCGCCGACTACTTATGAAAGAAACCCGTGCTTGGTAA 484
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      338 CTGAAATATGATATGATGATGCTCGAATATTGATGATGATGATGATGATGATGATGAT 397
QY      485 CCGTCAATATGCTTGGGTGCTGCTGCTTACCTGATGATGATGATGATGATGATGATGATG 544
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      398 CTTTCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 451
QY      545 TCCCGGAGGAGGCTGCGCTCAAGGATCAAGTATGATGATGATGATGATGATGATGATGATG 604
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      452 CCGCTGGCAGATGTTGTTGATGAGCAGGTTGAGCTTAAATGGTAAAAACAAATA 511
QY      605 TTGCAATTTGCTGCGCATGTAGCAATATTACGCTTTCGCGGAAAGCTGTGCGGG 664
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      512 TTGCAATCCTTTGGTGTGAGCCCAACATGTGACTATTTTGGAGATCAGCAGGTGGTG 571
QY      665 CCTCAACCATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 723
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      572 CAAGTGTCTATTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 630

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## RESULT 10

US-08-747-221B-52/c

; Sequence 52, Application US/08747221B

; Patent No. 6063610

; GENERAL INFORMATION:

; APPLICANT: Silver, Gary W.

; APPLICANT: Wisniewski, Nancy

; TITLE OF INVENTION: No. 6063610e1 Carboxylesterase Nucleic Acid

; NUMBER OF SEQUENCES: 66

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Carol Talkington Verser, Ph.D.

; ADDRESS: Heskia Corporation

; STREET: 1825 Sharp Point Drive

; CITY: Fort Collins

; STATE: Colorado

; COUNTRY: USA

; ZIP: 80525

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: Windows 95

; SOFTWARE: Wordperfect for Windows, Version 7.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/747/221B

; FILING DATE: No. 6063610e1ember 12, 1996

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Verser, Carol Talkington

; REGISTRATION NUMBER: 37/459

; REFERENCE/DOCKET NUMBER: FC-1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 970/493-7272

; TELEFAX: 970/484-9505

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; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1584 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-747-221B-52

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Query Match 9.5%; Score 162.6; DB 3; Length 1584;  
Best Local Similarity 55.8%; Pred. No. 4.5e-43;  
Matches 334; Conservative 0; Mismatches 259; Indels 6; Gaps 1;

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QY      125 TTAAGGCTTAAAGCAATGACCGTCTACGATGATTTCTTACATGCTTTCGAGATATAC 184
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Db      1547 TAAAGGAAAGAGCAATTAAGTAAGAAAGAAATGTTCCATAGTATTTCGAAATTC 1488
QY      185 CCTATGCTAAGCCTCCAGTGGGTGAGTGAATTCAGAGCACCAGCGCGCTGTACCAT 244
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1487 CATATGCCAAGCCTCCTGATGATCTAAGATTTAAGCCACCTCACTGAGAACTT 1428
QY      245 GGGAGGCTGTACGTATGCTGTTGGGCCAGCCAGATCGGTACAGACAGATTTTCATTA 304
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1427 GGTACAGTGTCTTCTGATGCTAGTAAGAAAGGCAATGTTGATGATGATGATGATG 1368
QY      305 GTGGCAAAACCAAGGCTGAGAGATGCTATACCTGATGATGATGATGATGATGATGATG 364
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1367 AAAAAATTAAAGTAGAGGCGTGAAGATGTTTATACCTCAATGCTATGACCAAAACAT 1308
QY      365 ACCGAGCAAAAGGCGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 424
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1307 CAGAGAAATCACTTCTCCAGTAATGATGATGATGATGATGATGATGATGATGATG 1248
QY      425 AAGCAATCTGAATGCTTGGTTCGCCGACTACTTATGAAAGAAACCCGTGCTTGGTAA 484
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1247 CTGAAATATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1188
QY      485 CCGTCAATATGCTTGGGTGCTGCTGCTTACCTGATGATGATGATGATGATGATGATG 544
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1187 CTTCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1134
QY      545 TCCCGGAGGAGGCTGCGCTCAAGGATCAAGTATGATGATGATGATGATGATGATGATG 604
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1133 CCGCTGGCAATGTTGTTGATGAGCAGGTTGAGCTTAAATGGTAAAAACAAATA 1074
QY      605 TTGCAATTTGCTGCGCATGTAGCAATATTACGCTTTCGCGGAAAGCTGTGCGGG 664
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1073 TTGCAATCCTTTGGTGTGAGCCCAACATGTGACTATTTTGGAGATCAGCAGGTGGTG 1014
QY      665 CCTCAACCATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 723
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Db      1013 CAAGTGTCTATTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 955

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## RESULT 11

US-09-005-051-51

; Sequence 51, Application US/09005051

; Patent No. 6291222

; GENERAL INFORMATION:

; APPLICANT: Silver, Gary W.

; APPLICANT: Wisniewski, Nancy

; TITLE OF INVENTION: No. 6291222e1 Carboxylesterase Nucleic Acid

; NUMBER OF SEQUENCES: 66

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Carol Talkington Verser, Ph.D.

; ADDRESS: Heskia Corporation

; STREET: 1825 Sharp Point Drive

; CITY: Fort Collins

; STATE: Colorado

; COUNTRY: USA

; ZIP: 80525

; COMPUTER READABLE FORM:





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; TELECOMMUNICATION INFORMATION:
;
; TELEPHONE: 970/493-7272
;
; TELEFAX: 970/484-9505
;
; INFORMATION FOR SEQ ID NO: 38:

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; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 2007 nucleotides
;
; TYPE: nucleic acid
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; STRANDEDNESS: single
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; TOPOLOGY: linear
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; MOLECULE TYPE: CDNA
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;
US-08-747-221B-38

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Query Match	9.5%;	Score 162.6;	DB 3;	length 2007;
Best Local Similarity	55.8%;	Pred. No. 5.3e-43;		
Matches 334;	Conservative	0;	Mismatches 259;	Indels 6; Caps 1

Oy	125	TTAAGGGTTAAACCGAATACCGCTACAGATATCTTACTACAGTTTCGAGATATAC	184
Dd	1960	TAAAGCAAAAGACCAATATAGTGAAGAAAGAAATGTCTTCATAGTATTTCTGCAATTC	1901
Oy	185	CTATGCTAAACCTCCAGTGGGTAGTTGAGATTCAAGGACCCAGCGGCTGTACCAT	244
Dd	1900	CATATGCCAAMCCTCTGTAGTGATCTAAGATTATTAAGCACCTCAACCTGCAGAACCTT	1841
Oy	245	GGGAGGCTGTACGTGATTTGCTGTGGGCCACGACCAAGATCGGTACAGACAGTTTCATA	304
Dd	1840	GGTCAGGCTGTTCTGAATGCTAGTAAGAAAGGAATAGTTGTAGATCAGTACATTTTATTA	1781
Oy	305	GTGGCAAAACCAACAGGTTCGGAGATGTGTATACCTGATGTATACATGACTCTGA	364
Dd	1780	AAAAATTTAAGTGTGGGGCTGAGAATTTGTTATACCTCATGTCTTATGTACCAAAAACAT	1721
Oy	365	ACCAGACAAAAGCGCTGCTGTTATGTTTTCATCCATGGCGAGATTTTATTTTTCGGCG	424
Dd	1720	CAGAAATCACTTCTTCAGTATAGTATGATGATGATGAGAGAGGCTTCTTCATGGAT	1661
Oy	425	AAGCAATCGTACTGTTTGTGTCGACATCTTTATGAAGAAACCCGTGCTTGTGTA	484
Dd	1660	CTGGAAATAGGATATGATGATGTCCTGAATTTTGAATGATATGGAATTTCTTCGTATA	1601
Oy	485	CGGTCAATATCGTTTGGGGTGTGGGTTTCTGTACCGTGAATATCGAAATCTCAATG	544
Dd	1600	CTTTCAATTATGATATAGGTGTTTGTGGATTTTGAACCTCGGGAATAGAGAA-----G	1547
Oy	545	TCCCGGACAGCGTGGCCCTCAGAGTCAAGTAAATGACCTTGAATGGGTCAAGAGTAA	604
Dd	1546	CGCTGGCAATGTGTGTTGATGTGACAGGTTGAGCTGTAAATATGGGTAAACAACTA	1487
Oy	605	TTGCCATTTTGGGTGGCGATGTAGACAATTTACCGTCTTGGCGAAAGTGTGGTGGG	664
Dd	1488	TTGCATCTCTTGGTGGTGACCCCAACATCTGACTATTTTGGAGAAATACGAGGTGGTG	1427
Oy	665	CGTCAACCATTAATAGATGATTAACGCAACAGACCGGTGGTTATTCATCGGTGAT	723
Dd	1426	CAAGTTCATATTTAGTATGTTATCAACATCTTCCACAGAGACTTTTCAATTAAGGATC	1368

RESULT 15  
US-09-005-051-36  
; Sequence 36, Application US/09005051

1 GENERAL INFORMATION:  
2 APPLICANT: Silver, Gary W.  
3 APPLICANT: Wisniewski, Nancy  
4 TITLE OF INVENTION: No. 6291222e1 Carboxylesterase Nucleic Acid  
5 TITLE OF INVENTION: Molecules, Proteins and Uses Thereof  
6 NUMBER OF SEQUENCES: 66  
7 CORRESPONDENCE ADDRESS:

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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INFORMATION FOR SEQ ID NO: 36:

LENGTH: 2007 nucleotides

TYPE: nucleic acid  
STRANDEDNESS: single

TOPOLOGY: linear

FEATURE:

LOCATION: 11..159

05-03-003-001-30

Query Match	Post Local Similarity
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100	0.99

Matches 334; Conserva

QY 125 TTAAAGGTGTTAACC

Query Match	9.5%	Score 162.6;	DB 4	Length 2007;
Best Local Similarity	51.8%	Pred. No. 5.3e-43;		
Matches 334;	Conservative 0;	Mismatches 259;		Indels 6; Gaps 1;

Oy	125	TTAAGGCTGTTAAGCGAATGACCGCTCACGATGATTTCTTACTACAGTTTCGAGAGTATAC	184
Db	48	TAAAGGAAAGAGCAAAATTAGTGAAAAAGAAATGTCTTCATAGTATTTCTGGAATTC	107
Oy	185	CCATGCTAAGCCCTCCATCGGTGGGTGAGTTGAGATTCAGAGCAAGCCAGCGGCGCTTACCAT	244
Db	108	CATATGCCAACCTCTCTTAGTGTATCTTAAGATTTAAAGCCACCTCAACCTGCACACCTT	167
Oy	245	GGGAGGCTGACGTGATTTGCTGTGGGCCAGCCACAGATCGGTACAGACAGATTTCAATA	304
Db	168	GGTCGAGTCTTCTTATGATCTAGTAAAGAGGGAATAGTTGAGTATCAGTACATTTTATTA	227
Oy	305	GTGGCAAAOCCACAGCTTGGAGATTTGCTATACCTGAATGTAATGTAATCAATGACTTGA	366
Db	228	AAAAAATTAAAGTAGGGCGCTGAAGATTGTTATATCCTTAAGTCTAATGTAATACCAAAACAT	287
Oy	365	ACCCAGACAAAAGGCGCTCTGTATTAGTTTTCATCCATGCGCGAGATTTATTTTCGGCG	424
Db	288	CAGAGAAATCACTTCTTCCAGTAATATGTAATGATATGATCATGAGAGAGCGTTCTTCATGGAT	347
Oy	425	AAGCAATGTAACGTGTTGGTTCGCCGACTTATTATGAGAAACCGCTGTCTTGGTAA	484
Db	348	CTGGAATAATGATATGTAATGATGCTCTGGAATTTGATGATTAAGAAATTTCTGCTTA	407
Oy	485	CCGTGCAATATGCTTGGGTGTGGGTCTTCCTTAGCTGAATTCGAAATTCGAAATTCGAATG	544
Db	408	CTTTCAATTATGATTAGTATGGTGTGTTGGGATTTTGAACCTGGGATATAGAAATA-----G	465
Oy	545	TCCCGCGCACGCTGCGCTCAAGATATCAAGTAATGCGCTTAGATGGGTCAAGAGATAATA	604
Db	462	CGCCTGGCAATGTTGGTTGATGAGCAAGGTTGAAGCTCTAAATGGGTAAAAAACAATA	523
Oy	605	TTTGCAATTTTGGGTGGCGATGTAGACAATATTACCGTCTTGGCGGAAAGTGTGTGGGG	664
Db	522	TTGCAATCTTTGGTGGTGACCCCAACAATGTGACTATTTTGGAAATCACACAGGTGGTG	583
Oy	665	CCTCAAACCATACATGATGATGAATACCGAAGACACCGGTGGTTATCTCATGCTGTATAC	723
Db	582	CAAGTGTTCATTTATGATGTTATAGATCTTTCCAAAGACTTTTTCATATAAGGATAC	640

Mon Apr 14 10:18:11 2003

Search completed: April 11, 2003, 08:51:41  
Job time : 46.4409 secs

us-09-776-910-14.rni

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Page 14

[illegible]

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OY 559 GGCCTCAAGATCAAGTATGCTTGGATGCTCAAGATATATATTCATTTCCT 618
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 565 GGTCTCCGGATCAGTAAACCTGTGGCTGGCTGCAAGAAAGCAAGATTTCCGA 624
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 619 GGGCATGTAGACATATATACCTCTTGGCGCAAGTGTGTGGGCTCAACCATTC 678
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 635 GGAGACCCAGGACATACCATACGCGGAGAGCCCTGGTGCATCAGTGGCATCTA 684
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 679 ATGATGATACCGACAGACCCGCTTATTCATCGTGTATCATCATGATGCTCCG 738
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DB 685 CTGACTCTTTTCAAGCTACGAGAGCTTTTCAAAAGAGCATTCATGAGCGGACA 744
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OY 739 TCCATGTGCTATGGGCTCTAC 761
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DB 745 GGAATGAGCTACTTCTTACTAC 767
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## RESULT 2

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US-09-738-626-1254
: Sequence 1254, Application US/09738626
: Publication No. US20020197605A1
: GENERAL INFORMATION:
: APPLICANT: NAKAGAWA, SATOSHI
: APPLICANT: MIZOGUCHI, HIROSHI
: APPLICANT: ANDO, SEIKO
: APPLICANT: HAYASHI, MIKIRO
: APPLICANT: OCHIAI, KEIKO
: APPLICANT: YOKOI, HARUHIKO
: APPLICANT: TATEISHI, MOKO
: APPLICANT: SENOH, AKIHIRO
: APPLICANT: IKEDA, MASATO
: APPLICANT: OZAKI, AKIO
: TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
: FILE REFERENCE: 249-125
: CURRENT APPLICATION NUMBER: US/09/738,626
: CURRENT FILING DATE: 2000-12-18
: PRIOR APPLICATION NUMBER: JP 99/377484
: PRIOR FILING DATE: 1999-12-16
: PRIOR APPLICATION NUMBER: JP 00/159162
: PRIOR FILING DATE: 2000-04-07
: PRIOR APPLICATION NUMBER: JP 00/280988
: PRIOR FILING DATE: 2000-08-03
: NUMBER OF SEQ ID NOS: 7059
: SOFTWARE: Patentin ver. 3.0
: SEQ ID NO 1254
: LENGTH: 1611
: TYPE: DNA
: ORGANISM: Corynebacterium glutamicum
US-09-738-626-1254

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Query Match      5.2% Score 88.4; DB 9; Length 1611;
Best Local Similarity 49.7%; Pred. No. 1.4e-16;
Matches 314; Conservative 0; Mismatches 306; Indels 12; Gaps 3;

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OY 177 GAGTATACCTATGTAAAGCTCCAGTGGGTGAGTGAATCAAGCACCCAGCGGC 236
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DB 78 GGGAAATTCCTACGGCCGCAACACAGCGGGAATAATGCTTCGCGGCAACCCGCGC 137
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 237 TGTACACGAGGAGGTGATGATGCTGTGGCCAGCCCAAGATGGTACAG--AC 293
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 138 CAAGAAATGGGAGCGGTGCGGATGCTCAATGTTCCGTAAGTCTCTCAGGCCAAC 197
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 294 AGATTTCATTAAGTGGCAACCAACGAGTTCGAGAGATGCTATACCTGATGTATAC 353
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 198 GTATCCCTGAGACAGATTAAGTTCGGGTTCAAGAGACTGCTTAACCTCGATGTCGCG 257
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 354 CATGACTTGAACCAAGGCGCTGTTATGTTTCAATCCATGGCGAGATTT 413
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 258 GCGTGATTT-----CCGAAGAAAGCTTCGTGTGTGTATCTCCAGCGGCTTCCTT 311
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 414 TATTTGGGCAAGCAATCTGTAAGTGT---GTCGCGACTACTTATGAAGAAACC 470
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DB 312 CATCATGGCTCATCAAGCAAAAGCGCTGCGGATATATACCTGTCAACAACATGAA 371
OY 471 CGTGCTTGTGTAACCGTGCATATATGCTTGGTGTGGTTCCTAGCTGAAGAAC 530
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DB 372 TGTGTCTAGCTGTGCGTTAATTTCCGCTGGCGCTTGGGCTATCTGATCTGGCTTC 431
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OY 531 GGAATATCTAATGTCCCGCGCAAGCTGACTCAAGATCAAGTAAATGCTTGGATG 590
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 432 CGTGGGGAGAGATTTGGTATGCCAACCCCGGCTCCACGATACAGCTCTGGCCCTGAG 491
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OY 591 GGTCAAGAGTAAATATGTCATTTGGTGGGCAATGTAAGCAATATACCTGTTGGGCA 650
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DB 492 GGTACGCGTAAATATGAAAGCATTCGCTGGGATCTGTGAACAGTCACTCATGAGGCA 551
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 651 AAGTGTGTTGGGCTCAACCATTTACATGATATACCAAGACCGGTGTTATTT 710
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 552 ATCCGGCGGCGCTGACAGAGTGTGCTCATGATGTGTGCGCGTGAGAGGACTATT 611
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 711 CCATGCTGATCATATGTCGCTGTAATTCATGCTGATGAGGCTCTACGAATGCCA 770
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 612 CCACCGCGCATGCCCCAATCCGCGCGGTCTGTGTGCACTCATCTACCAAGCAAA 671
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 771 AAGTGTGCGCTCACCATGCGCAACGTTTG 802
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 672 ATTCTGGCAGCGTAAGTGTATCTACCGCATG 703
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

## RESULT 3

```

US-09-917-800A-1511
: Sequence 1511, Application US/09917800A
: Patent No. US20020119462A1
: GENERAL INFORMATION:
: APPLICANT: Mendrick, Donna
: APPLICANT: Porter, Mark
: APPLICANT: Johnson, Kory
: APPLICANT: Castile, Arthur
: APPLICANT: Elashoff, Michael
: TITLE OF INVENTION: Molecular Toxicology Modeling
: FILE REFERENCE: 44921-5038-US
: CURRENT APPLICATION NUMBER: US/09/917,800A
: CURRENT FILING DATE: 2001-07-31
: PRIOR APPLICATION NUMBER: US 60/222,040
: PRIOR FILING DATE: 2000-07-31
: PRIOR APPLICATION NUMBER: US 60/222,880
: PRIOR FILING DATE: 2000-11-02
: PRIOR APPLICATION NUMBER: US 60/290,029
: PRIOR FILING DATE: 2001-05-11
: PRIOR APPLICATION NUMBER: US 60/290,645
: PRIOR FILING DATE: 2001-05-15
: PRIOR APPLICATION NUMBER: US 60/292,336
: PRIOR FILING DATE: 2001-05-22
: PRIOR APPLICATION NUMBER: US 60/295,798
: PRIOR FILING DATE: 2001-06-06
: PRIOR APPLICATION NUMBER: US 60/297,457
: PRIOR FILING DATE: 2001-06-13
: PRIOR APPLICATION NUMBER: US 60/298,884
: PRIOR FILING DATE: 2001-06-19
: PRIOR APPLICATION NUMBER: US 60/303,459
: PRIOR FILING DATE: 2001-07-09
: NUMBER OF SEQ ID NOS: 1740
: SOFTWARE: Patentin Ver. 2.1
: SEQ ID NO 1511
: LENGTH: 2141
: TYPE: DNA
: ORGANISM: Rattus norvegicus
: FEATURE:
: OTHER INFORMATION: Genbank Accession No. US20020119462A1 X65296
US-09-917-800A-1511

```

```

Query Match      4.3% Score 74.2; DB 10; Length 2141;
Best Local Similarity 54.3%; Pred. No. 4.4e-12;
Matches 220; Conservative 0; Mismatches 173; Indels 12; Gaps 3;

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OY	498	TTTGGGCTGTGGTTGCGTTCCTTACCTGGAATCGGAAATCTCAATGTGCCCGGCAACGC	557
Db	580	CTGGGCACTGGGGAATCTTTCAC-----ACAGGGGATGAACACAGCGGGGGAACCTG	633
OY	558	TGCGCTTCAGAGATCAAGTAAATGAGCCCTTGAGTGGGTCACAGATAATATATGCATTTTCGG	617
Db	634	GGGTCACCTGGACAGAGTGGCTGCCCTCGCTGCGTCAAGACACACATTTGCCAGCTTTTG	693
OY	618	TGGCGATGTAGACAATATATACGTTCTTCGGCGAAAGTGTGTGGGG	664
Db	694	AGGGAACCCAGCGCTGTGTACCATCTTTGGAGAGATCAAGCGGAGGAG	740

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; ORGANISM: Homo sapiens
;
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (72)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (2098)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (2114)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (2117)
; OTHER INFORMATION: n equals a,t,g, or c
;
US-09-925-301-335

```

```

Prior File(s) With Similarity >= 90%
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2147
LENGTH: 1966
TYPE: DNA
ORGANISM: Homo sapiens
FEATURES:
OTHER INFORMATION: Genbank Accession No. US20020142981A1 L07765
US-09-880-107-2147

Query Match          4.3%; Score 73.8; DB 10; Length 1966;
Best Local Similarity 57.1%; Pred. No. 5.5e-12;
Matches 198; Conservative 0; Mismatches 137; Indels 12; Gaps

QY      321 TTCGAGGATGTGTATACCTGAATGTGTA---TACCATGACTTTGAACCCAGACAAAGG 377
        ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db       403 TTTCGAAGAAGTGCTTTACCTCAATATTACACCTCCTCGCTACCTTGACGAAGAAAAACG 462

QY      378 GCGTCCTGTATGCTTTATCATGCATGGGGGAGATTTTATTTCGGCCACAACCAATCGTA 437
        || | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db       463 GCTGCCGATGATGTTGATCACGACGAGGGGGCTGATGGTGGCGGCATCA---AC 519

QY      438 CTGGTTGGTCCCGCATACTATTATGAAGAAACCCGTGCTCTGGGTAAACCGTGCAATTCG 497
        || | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db       520 CTATGATGGCGCTGCCCTTGCTGCTCCATCAAAAACGTGGGTGGTAGCAATTCATATCG 579

```

[illegible]

Db 797 AGGGAACCCAGGCTCTGTGACCATCTTTGGAGAGTCAACCGGAGAG 843

RESULT 6  
US-09-894-991-1

; Sequence 1, Application US/09894991  
; Patent No. US20020090619A1  
; GENERAL INFORMATION:  
; APPLICANT: Pfeiffer, Douglas R.  
; APPLICANT: Murphy, Anne M.  
; APPLICANT: Jung, Dennis W.  
; APPLICANT: Bradshaw, Patrick C.  
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MITOCHONDRIAL  
; FILE REFERENCE: 660088.430  
; CURRENT APPLICATION NUMBER: US/09/894,991  
; CURRENT FILING DATE: 2001-06-29  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1470  
; TYPE: DNA  
; ORGANISM: Bacillus subtilis  
US-09-894-991-1

Query Match 4.2%; Score 71.6; DB 10; Length 1470;  
Best Local Similarity 52.6%; Pred. No. 2.2e-11;  
Matches 265; Conservative 0; Mismatches 214; Indels 25; Gaps 4;

QY 179 GTATACCTTATGCTTAACCTCCAGTGGTGTGATTTCAAGTCAACCCAGCGGCTG 238  
Db 77 GCATCCCTTATGCCAAGCCGCTGTGCAACATGCGCTTTTAAAGCAGCTGAGCGGCTG 136  
QY 239 TACCATGGAGGGGTGACGTGATTTGGTGGC-----CAGCCACAG 281  
Db 137 AAGTGTGGGAAGATGCTTGTATGATCCACAGCGTACGCTCTATTGGCCGAGCGGCTG 196  
QY 282 ATCGGTACAGAGATTTTCATATAGTGGCAACCCAGGTTGGAGATTTGTATACCT 341  
Db 197 ATTTGCTCTACGTGTGTATACAGAGCTGCCCGCCAG--TCCGAGATTTGCTGTATGT 254  
QY 342 GAATGTATACCAATGACTGTACCAACCAAGAGGCTGCTGTATAGTTTTCATCA 401  
Db 255 CAATGTATTTGGCCCTGAC--ACTCCAAGTCAAAATCTCTGTCATGCTGTGATCA 311  
QY 402 TGCGGAGATTTTATTTTGGGGAAGCAATGTACTGTTGGTCCGACTTAT 461  
Db 312 CGAGGCGCTTTTATCTTGTGAGCGGCAAGTACCATTTGATGACGATCAAACTTGC 371  
QY 462 GA---AGAAACCCGTGCTTGTGTAACGTCATATGCTTGGTGGTGGTGGTTCCT 518  
Db 372 GGCACAGGAGAGATCATTTGCTTACATGATGATGCTGCGGCGGCTTTGGCTTTT 431  
QY 519 TAGCCGTAATGGAAATCTAATGTCCTCCGCAACGCTGCTCAAGATCAATAT 578  
Db 432 GCACCTTGTCTTGTGATGAGCGCTATTCGATTAACCTTGGCTTTTAAACCAAGCGC 491  
QY 579 GGCCTTGAATGCTCAAGATATATGTCATTTTGGTGGGATGATAGCAATATATAC 638  
Db 492 CCGGCTGAATGCTGGGGAAGATATCTACGCTTTGGCGGTATCCGATTAACGTAAC 551  
QY 639 CCGTCTTGGCGGAAGTGTGCTG 662  
Db 552 AGTATTTGGAGATCCCGCGCGG 575

RESULT 7  
US-09-894-991-7  
; Sequence 7, Application US/09894991  
; Patent No. US20020090619A1  
; GENERAL INFORMATION:  
; APPLICANT: Pfeiffer, Douglas R.

; APPLICANT: Murphy, Anne M.  
; APPLICANT: Jung, Dennis W.  
; APPLICANT: Bradshaw, Patrick C.  
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MITOCHONDRIAL  
; FILE REFERENCE: 660088.430  
; CURRENT APPLICATION NUMBER: US/09/894,991  
; CURRENT FILING DATE: 2001-06-29  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 1470  
; TYPE: DNA  
; ORGANISM: Bacillus subtilis  
US-09-894-991-7

Query Match 4.2%; Score 71.6; DB 10; Length 1470;  
Best Local Similarity 52.6%; Pred. No. 2.2e-11;  
Matches 265; Conservative 0; Mismatches 214; Indels 25; Gaps 4;

QY 179 GTATACCTTATGCTTAACCTCCAGTGGTGTGATTTCAAGTCAACCCAGCGGCTG 238  
Db 77 GCATCCCTTATGCCAAGCCGCTGTGCAACATGCGCTTTTAAAGCAGCTGAGCGGCTG 136  
QY 239 TACCATGGAGGGGTGACGTGATTTGGTGGC-----CAGCCACAG 281  
Db 137 AAGTGTGGGAAGATGCTTGTATGATCCACAGCGTACGCTCTATTGGCCGAGCGGCTG 196  
QY 282 ATCGGTACAGAGATTTTCATATAGTGGCAACCCAGGTTGGAGATTTGTATACCT 341  
Db 197 ATTTGCTCTACGTGTGTATACAGAGCTGCCCGCCAG--TCCGAGATTTGCTGTATGT 254  
QY 342 GAATGTATACCAATGACTGTACCAACCAAGAGGCTGCTGTATAGTTTTCATCA 401  
Db 255 CAATGTATTTGGCCCTGAC--ACTCCAAGTCAAAATCTCTGTCATGCTGTGATCA 311  
QY 402 TGCGGAGATTTTATTTTGGGGAAGCAATGTACTGTTGGTCCGACTTAT 461  
Db 312 CGAGGCGCTTTTATCTTGTGAGCGGCAAGTACCATTTGATGACGATCAAACTTGC 371  
QY 462 GA---AGAAACCCGTGCTTGTGTAACGTCATATGCTTGGTGGTGGTGGTTCCT 518  
Db 372 GGCACAGGAGAGATCATTTGCTTACATGATGATGCTGCGGCGGCTTTGGCTTTT 431  
QY 519 TAGCCGTAATGGAAATCTAATGTCCTCCGCAACGCTGCTCAAGATCAATAT 578  
Db 432 GCACCTTGTCTTGTGATGAGCGCTATTCGATTAACCTTGGCTTTTAAACCAAGCGC 491  
QY 579 GGCCTTGAATGCTCAAGATATATGTCATTTTGGTGGGATGATAGCAATATATAC 638  
Db 492 CCGGCTGAATGCTGGGGAAGATATCTACGCTTTGGCGGTATCCGATTAACGTAAC 551  
QY 639 CCGTCTTGGCGGAAGTGTGCTG 662  
Db 552 AGTATTTGGAGATCCCGCGCGG 575

RESULT 8  
US-09-917-800A-1450  
; Sequence 1450, Application US/09917800A  
; Patent No. US20020119462A1  
; GENERAL INFORMATION:  
; APPLICANT: Mendrick, Donna  
; APPLICANT: Porter, Mark  
; APPLICANT: Johnson, Kory  
; APPLICANT: Castle, Arthur  
; APPLICANT: Elashoff, Michael  
; APPLICANT: Gene Logic, Inc.  
; TITLE OF INVENTION: Molecular Toxicology Modeling  
; FILE REFERENCE: 44921-5038-US  
; CURRENT APPLICATION NUMBER: US/09/917,800A  
; CURRENT FILING DATE: 2001-07-31  
; PRIOR APPLICATION NUMBER: US 60/222,040



PRIOR FILING DATE: 2000-07-31  
PRIOR APPLICATION NUMBER: US 60/222,880  
PRIOR FILING DATE: 2000-11-02  
PRIOR APPLICATION NUMBER: US 60/290,029  
PRIOR FILING DATE: 2001-05-11  
PRIOR APPLICATION NUMBER: US 60/290,645  
PRIOR FILING DATE: 2001-05-15  
PRIOR APPLICATION NUMBER: US 60/292,336  
PRIOR FILING DATE: 2001-05-22  
PRIOR APPLICATION NUMBER: US 60/295,798  
PRIOR FILING DATE: 2001-06-06  
PRIOR APPLICATION NUMBER: US 60/297,457  
PRIOR FILING DATE: 2001-06-13  
PRIOR APPLICATION NUMBER: US 60/298,884  
PRIOR FILING DATE: 2001-06-19  
PRIOR APPLICATION NUMBER: US 60/303,459  
PRIOR FILING DATE: 2001-07-09  
NUMBER OF SEQ ID NOS: 1740  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1450  
LENGTH: 1885  
TYPE: DNA  
ORGANISM: Rattus norvegicus  
FEATURE:  
OTHER INFORMATION: Genbank Accession No. US20020119462A1 U10697  
US-09-917-800A-1450

Query Match 4.2%; Score 71; DB 10; Length 1885;  
Best Local Similarity 53.8%; Pred. No. 3.9e-11;  
Matches 218; Conservative 0; Mismatches 175; InDels 12; Gaps 3;

QY 321 TTCGAGGATTGTCTAATCGAATGTATACCAAT--GACTTGAACCCAGACAAAG 377  
DB 350 TTCTGAGATTGTCTCTAATTAATTTACCTCTGACACTTTACAAAGAAATAGCAG 409  
QY 378 GGGTCTGTATGTTTCATGCGGAGATTATTTTCGCGCCAGCAAAATCGTAA 437  
DB 410 GCTGCCAGTCAGTGTGTGATTCATGAGGTGGAATGACACTGGGCGCATCA--AC 466  
QY 438 CTGTTGGTCCGACACTTATGAAAGAACCCGTGGTCTTGTGTAACCGTGCATATCG 497  
DB 467 CTATGATGGCCGGTCTCTGCTATGAAAGACGTGGTGAAGTGCATTCAGTATCG 526  
QY 498 TTTGGTGTGGTGGTTCCTTAGCCCTGAATCGGAATATCAATGTCCTCCCGGACGC 557  
DB 527 CTTGGGCACTGGGGATTCTTCAGCAGGCGGATGAAACACAGCAGG-----GGAACGTG 580  
QY 558 TGGCCTCAAGGATCAAGTAATGAGCTTGAGATGGGTGAGATGATATTGCAATTTTCG 617  
DB 581 GGGTCATTTGACCAAGTGGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 640  
QY 618 TGGCGATGTAGCAATTAATTAATGCTTTCGCGGAAAGTGTGGGCGCTCAACCATTA 677  
DB 641 GGGTGACCCAGCTGTGACCATTTTGGAGAGTACAGAGAGAGTTTCAATGCTCTCTGT 700  
QY 678 CATGATGATTAACCAAGACGACCCGTGGTTCATTCATGCTGTAT 722  
DB 701 TCTGTGTGTGTCCTCCACTGACCAAGAACCTCTCTCCACAGGGCCCAT 745

## RESULT 9

US-09-418-176-1  
Sequence 1, Application US/09418176  
Publication No. US20030040040A1  
GENERAL INFORMATION:  
APPLICANT: Das, Goutam  
TITLE OF INVENTION: DNA Molecules for Expression of  
TITLE OF INVENTION: Polypeptides  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: White & Case  
STREET: 1155 Avenue of the Americas  
CITY: New York

STATE: New York  
COUNTRY: United States  
ZIP: 10036-2787  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/418,176  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/624,398  
FILING DATE: 04-APR-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/SE96/00318  
FILING DATE: 12-MAR-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: SE 9501939-4  
FILING DATE: 24-MAY-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Theima A. Chen Cleland  
REGISTRATION NUMBER: 40,948  
REFERENCE/DOCKET NUMBER: 1103326-0206  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 819-8200  
TELEFAX: (212) 354-8113  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2428 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
TISSUE TYPE: mammary gland  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 82..2319  
OTHER INFORMATION: /product= "bile-salt-stimulated  
OTHER INFORMATION: lipase"  
FEATURE:  
NAME/KEY: exon  
LOCATION: 985..1173  
FEATURE:  
NAME/KEY: exon  
LOCATION: 1174..1377  
FEATURE:  
NAME/KEY: exon  
LOCATION: 1378..1575  
FEATURE:  
NAME/KEY: exon  
LOCATION: 1576..2415  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 151..2316  
FEATURE:  
NAME/KEY: polyA\_signal  
LOCATION: 2397..2402  
FEATURE:  
NAME/KEY: repeat\_region  
LOCATION: 1736..2283  
FEATURE:  
NAME/KEY: 5'UTR  
LOCATION: 1..81  
FEATURE:  
NAME/KEY: repeat\_unit  
LOCATION: 1736..1788  
FEATURE:

NAME/KEY: repeat\_unit  
LOCATION: 1789..1821  
FEATURE:  
NAME/KEY: repeat\_unit  
LOCATION: 1822..1854  
FEATURE:  
NAME/KEY: repeat\_unit  
LOCATION: 1855..1887  
FEATURE:  
NAME/KEY: repeat\_unit  
LOCATION: 1888..1920  
FEATURE:  
NAME/KEY: repeat\_unit  
LOCATION: 1921..1953  
FEATURE:  
NAME/KEY: repeat\_unit  
LOCATION: 1954..1986  
FEATURE:  
NAME/KEY: repeat\_unit  
LOCATION: 1987..2019  
FEATURE:  
NAME/KEY: repeat\_unit  
LOCATION: 2020..2052  
FEATURE:  
NAME/KEY: repeat\_unit  
LOCATION: 2053..2085  
FEATURE:  
NAME/KEY: repeat\_unit  
LOCATION: 2086..2118  
FEATURE:  
NAME/KEY: repeat\_unit  
LOCATION: 2119..2151  
FEATURE:  
NAME/KEY: repeat\_unit  
LOCATION: 2152..2184  
FEATURE:  
NAME/KEY: repeat\_unit  
LOCATION: 2185..2217  
FEATURE:  
NAME/KEY: repeat\_unit  
LOCATION: 2218..2250  
FEATURE:  
NAME/KEY: repeat\_unit  
LOCATION: 2251..2283  
PUBLICATION INFORMATION:  
AUTHORS: Nilsson, Jeanette  
AUTHORS: Blackberg, Lars  
AUTHORS: Carlsson, Peter  
AUTHORS: Enerback, Sven  
AUTHORS: Herneil, Olle  
AUTHORS: Bjursell, Gunnar  
TITLE: cDNA cloning of human-milk  
TITLE: bile-salt-stimulated lipase and evidence for its  
TITLE: Identity to pancreatic carboxylic ester hydrolase  
JOURNAL: Eur. J. Biochem.  
VOLUME: 192  
PAGES: 543-550  
DATE: Sept.-1990  
US-09-418-176-1

Query Match 4.1%; Score 70.4; DB 9; Length 2428;  
Best Local Similarity 55.6%; Pred. No. 7.2e-11;  
Matches 159; Conservative 0; Mismatches 121; Indels 6; Gaps 1;

QY 471 CGTGGCTGTGTAACCGGCAATATGCTTGGGTGTTGGTTCCTTAGCCTGAATC 530  
DB 555 CGTCACTGCTGACCTTAACTACCGGTGCGCCCTTGGTTCCTCAGC-----AC 608  
QY 531 GGAATATCTCAATGTCGCCGCAACGCTGCGCTCAAGATCAAGTAAGCCTTGAGATG 590  
DB 609 TGGGAGCGCAATCTGCCAGTAATATGCTTGGGATCAGACATGCGCATTCCTTG 668  
QY 591 GGTCAAGAGTAATATTCCTTTCGCTGGCGATGTAGACAAATATACCGCTTCGCGCA 650

DB 669 GGTGAAGAGTAATATCGCGGCTTCGGGGGGGACCCCAACAATACAGCTCTTCGGGGA 728  
QY 651 AAGTCTGTGGGGCTTCACCCATTTACATGATGATTAACCAACAGACCCGTGTTTAT 710  
DB 729 GTCTGTGAGAGTGCACAGCTCTCTGTGACAGACCCCTTCCTTCAACAAGGGCTCAT 788  
QY 711 CCATCGTGTATCATGATGTCGGTAATTCATGCTGCTCATGGGCC 756  
DB 789 CCGGAGCATCAGCCAGAGCGGCTGCGCTTGAATCCTTGGGTC 834

RESULT 10  
US-09-969-347-220  
Sequence 220, Application US/09969347  
Patent No. US20020115085A1  
GENERAL INFORMATION:  
APPLICANT: Ebner, Reinhard  
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Sign  
TITLE OF INVENTION: Sets  
FILE REFERENCE: 689290-69  
CURRENT APPLICATION NUMBER: US/09/969,347  
PRIOR FILING DATE: 2001-10-02  
PRIOR APPLICATION NUMBER: US/60/237,598  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: US/60/237,604  
NUMBER OF SEQ ID NOS: 318  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 220  
LENGTH: 2428  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-969-347-220

Query Match 4.1%; Score 70.4; DB 10; Length 2428;  
Best Local Similarity 55.6%; Pred. No. 7.2e-11;  
Matches 159; Conservative 0; Mismatches 121; Indels 6; Gaps 1;

QY 471 CGTGGCTGTGTAACCGGCAATATGCTTGGGTGTTGGTTCCTTAGCCTGAATC 530  
DB 555 CGTCACTGCTGACCTTAACTACCGGTGCGCCCTTGGTTCCTCAGC-----AC 608  
QY 531 GGAATATCTCAATGTCGCCGCAACGCTGCGCTCAAGATCAAGTAAGCCTTGAGATG 590  
DB 609 TGGGAGCGCAATCTGCCAGTAATATGCTTGGGATCAGACATGCGCATTCCTTG 668  
QY 591 GGTCAAGAGTAATATTCCTTTCGCTGGCGATGTAGACAAATATACCGCTTCGCGCA 650  
DB 669 GGTGAAGAGTAATATCGCGGCTTCGGGGGGGACCCCAACAATACAGCTCTTCGGGGA 728  
QY 651 AAGTCTGTGGGGCTTCACCCATTTACATGATGATTAACCAACAGACCCGTGTTTAT 710  
DB 729 GTCTGTGAGAGTGCACAGCTCTCTGTGACAGACCCCTTCCTTCAACAAGGGCTCAT 788  
QY 711 CCATCGTGTATCATGATGTCGGTAATTCATGCTGCTCATGGGCC 756  
DB 789 CCGGAGCATCAGCCAGAGCGGCTGCGCTTGAATCCTTGGGTC 834

RESULT 11  
US-09-917-800A-480  
Sequence 480, Application US/09917800A  
Patent No. US20020119462A1  
GENERAL INFORMATION:  
APPLICANT: Mendrick, Donna  
APPLICANT: Porter, Mark  
APPLICANT: Johnson, Kory  
APPLICANT: Castle, Arthur  
APPLICANT: Elashoff, Michael  
APPLICANT: Gene Logic, Inc.  
TITLE OF INVENTION: Molecular Toxicology Modeling  
FILE REFERENCE: 44921-5038-US

```

CURRENT APPLICATION NUMBER: US/09/917,800A
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/222,040
PRIOR FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: US 60/222,880
PRIOR FILING DATE: 2000-11-02
PRIOR APPLICATION NUMBER: US 60/290,029
PRIOR FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: US 60/290,645
PRIOR FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: US 60/292,336
PRIOR FILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: US 60/295,798
PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: US 60/297,457
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/298,884
PRIOR FILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: US 60/303,459
PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 1740
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 480
LENGTH: 1902
TYPE: DNA
ORGANISM: Rattus norvegicus
FEATURE:
OTHER INFORMATION: Genbank Accession No. US20020119462A1 AB010635
US-09-917-800A-480

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Query Match          4.1%; Score 69.6; DB 10; Length 1902;
Best Local Similarity 52.8%; Pred No. 1e-10;
Matches 225; Conservative 0; Mismatches 189; Indels 12; Gaps 3;

322 TCGGAGATTGCTATACCTGATGTATACCAATGACTTGACCCAGA---CAAAAG 378
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
389 TCTGAGAGACGCTGATATCTCAACATCTATACCAAGCCCATGCCAGAGGCTCTAC 448
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
379 CGTCTGTTATGTTTTCATCCATGCGGAGATTTTATTTGGGGAAGCAATGCTAAC 438
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
449 CTGCTGTGATGTGTGATCCACGAGAGTGATGTTATAGAAAGG---TTCATG 505
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
439 TGGTTGGTCCGCACTTATGAGAAACCGTGTCTGTGTAACCGTGCATATCGT 498
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
506 TGTGATGATCTCTATTGGAGATCAATGAGACTTGTGTGCTTCCATTCAGATATCGT 565
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
499 TTGGTGTGTTGGTTCTTACCTGAAATCGAAATCTCATGTCCCGGCAACGCT 558
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
566 CTGGGTCTCCGGGCTTTTTCAGC-----ACTGAGATGAGCATCCAGAGGCAACTGG 619
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
559 GGCCTCAAGATCAATGATGCGCTTGAGATGGGTCAAGAGTAATATGCAATTTTCGGT 618
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
620 GGATACCTGGACCAAGGCGCTCCCTCGATGGGTCCAGAGAAATATCGCCCTTTTGA 679
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
619 GGCATGTAGACAATATATACGCTTTCGGGAAAGTGTGCGGCTCAACCCATTCAC 678
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
680 GCGAACCTATACCGGGTCACTATTTTGGCGTGTCTGACAGTGGCAACAGTGTCTCA 739
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
679 ATGATGATACCGAAGACAGCCCGTGTGTTATTCATGATGATGATGATGATGAT 738
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
740 CATGTTATATCCCATGCTCAAGGCTCTTCATGATGATGATGATGATGATGATG 799
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
739 TCCATG 744
    ||| |||
800 GCCCTG 805

```

```

RESULT 12
US-09-917-800A-1324
; Sequence 1324, Application US/09917800A
; Patent No. US20020119462A1
; GENERAL INFORMATION:
; APPLICANT: Mendlick, Donna

```

```

APPLICANT: Porter, Mark
APPLICANT: Johnson, Kory
APPLICANT: Castle, Arthur
APPLICANT: Elashoff, Michael
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5038-US
CURRENT APPLICATION NUMBER: US/09/917,800A
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/222,040
PRIOR FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: US 60/222,880
PRIOR FILING DATE: 2000-11-02
PRIOR APPLICATION NUMBER: US 60/290,029
PRIOR FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: US 60/290,645
PRIOR FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: US 60/292,336
PRIOR FILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: US 60/295,798
PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: US 60/297,457
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/298,884
PRIOR FILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: US 60/303,459
PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 1740
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1324
LENGTH: 1442
TYPE: DNA
ORGANISM: Rattus norvegicus
FEATURE:
OTHER INFORMATION: Genbank Accession No. US20020119462A1 D00362
US-09-917-800A-1324

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Query Match          4.1%; Score 69.4; DB 10; Length 1442;
Best Local Similarity 53.6%; Pred No. 1e-10;
Matches 217; Conservative 0; Mismatches 176; Indels 12; Gaps 3;

321 TCGGAGATTGCTATACCTGATGTATACCAATGATGTA---TACCAATGACTTGAAACCAAG 377
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
435 TCCGAGAGACTGTCTACTGTAATATTAAGTCTGCTGACTTGACAAAACAGCCG 494
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
378 GCGTCTGTTATGTTTTCATCCATGCGGAGATTTTATTTTCGGGGAAGCAATCGTAA 437
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
495 ATTGCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 554
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
438 CTGTTGGTCCGCACTTATGAGAAACCGTGTCTGTGTAACCGTGCATATTCG 497
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
555 TAG---TGGACTACTCTCTCTGCCCCAGAAACGATGATGATGATGATGATGATG 611
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
498 TTTGGTGTGTTGGTTCTTACCTGAAATGCAATATGTCCTCCCGGCAAGCG 557
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
612 CCTGGATATTTGGGATGTTTACG-----ACCGGTGATGAAACAGCGGGGAACTG 665
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
558 TGGCTCAAGATCAATATGCGCTTGAGATGGGTCAAGAGATATATGCAATTTTCG 617
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
666 GCGTCACTTGGACCAAGCTGCTGCTACTAGCTGGGTCCAGATATGCAATTTTCG 725
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
618 TGGCGATGTAGACAATATATACCGTCTTGGGAAAGTGTGTTGGGCTCAACCCATTA 677
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
726 AGGGAACCGGATTCAGTACCATCTTTGGAGATCAGCAGAGAGTGTAGTGTCTGC 785
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
678 CATGATGATTAACCGAAGACCGGTGTTATTTCCATGATGATGATGATGATGATG 722
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
786 TCTGTCTTATCTCCTGTGGCAAGAACCTCTTCCACAGAGCAT 830
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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RESULT 13
US-09-895-860-3
; Sequence 3, Application US/09895860

```

```
; Patent No. US20020076786A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A. J.
; APPLICANT: Logan, Thomas Joseph
; TITLE OF INVENTION: 25869, A NOVEL HUMAN CARBOXYLESTERASE
; FILE REFERENCE: MNI-167
; CURRENT APPLICATION NUMBER: US/09/895,860
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 60/215,370
; PRIOR FILING DATE: 2000-06-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1641
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1641)
; US-09-895-860-3
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Query Match          4.1%; Score 69.4; DB 10; Length 1641;
Best Local Similarity 53.3%; Pred. No. 1.1e-10;
Matches 220; Conservative 0; Mismatches 181; Indels 12; Gaps 3;
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QY 315 CACAGGTCGAGAGATTGTCTATACCTGAATGTGTATA---CCAAATGACTTGAACCCAGA 371
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 262 CTCCTTTCAAGAGACTGCTGCTCTCAACGCTCTATATAGCCAGCTGAGGTCCCGCAGG 341
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 372 CAAAAGGCGCTCTGTTATGTTTCATTCATGCGGAGATTATTTTGGCGCAACCAA 431
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 342 GTCCGGTAGGCGCGGTCTATGATGGTCCATGAGGCGCTCTATTAACCTGCGCTGCCA 400
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 432 TCGTACTGTTTGTGCTCCCACTATTATGAAGAAACCGTGTGTGTGAACCTGCA 491
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 401 --CCTCTACAGATGATGACCTGCTGCTGCTATGCGGATGCTGCTGTGTTACATCCA 458
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 492 ATATGTTGGGTGTGTTGGTTTCTTACCTGAGCTGAATGCGAAATCTCAATGCTCCCG 551
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 459 GTACCGGCTTGGGCTCTGCTTCTTTCACG-----ACTGGAGATGACCATGCACTGG 512
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 552 CAACGCTGCGCTCAAGGATCAAGTAATGAGCTTGAAGATGGCTGCAAGATATATTCAT 611
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 513 CAACCAAGGCTTCTAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 572
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 612 TTTCGGTGGCGATGTAGCAATATTAACGCTTCCGCGCAAAATGCTGTGGGCGCTCAAC 671
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 573 CTTCGGGGGTGACCTCAACGTGTCTCACTGTCTTGTGTGATGCTGCGGAGGAGCATCAT 632
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 672 CCAATTACATGATGATACCAAGCAAGACCGCTGTTTATTCATCGTGTATCA 724
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 633 CTCTGGCTGTGCTCTCTCCCAAGTGTGCTGCAAGGCGCTGTTCCACAGACCATCA 685
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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RESULT 14
US-09-895-860-1
; Sequence 1, Application US/09895860
; Patent No. US20020076786A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A. J.
; APPLICANT: Logan, Thomas Joseph
; TITLE OF INVENTION: 25869, A NOVEL HUMAN CARBOXYLESTERASE
; FILE REFERENCE: MNI-167
; CURRENT APPLICATION NUMBER: US/09/895,860
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 60/215,370
; PRIOR FILING DATE: 2000-06-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2087
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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (222)...(1862)
; US-09-895-860-1
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Query Match          4.1%; Score 69.4; DB 10; Length 2087;
Best Local Similarity 53.3%; Pred. No. 1.3e-10;
Matches 220; Conservative 0; Mismatches 181; Indels 12; Gaps 3;
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```
QY 315 CACAGGTCGAGAGATTGTCTATACCTGAATGTGTATA---CCAAATGACTTGAACCCAGA 371
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 503 CTCCTTTCAAGAGACTGCTGCTCTCAACGCTCTATATAGCCAGCTGAGGTCCCGCAGG 562
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 372 CAAAAGGCGCTCTGTTATGTTTCATTCATGCGGAGATTATTTTGGCGCAACCAA 431
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 563 GTCCGGTAGGCGCGGTCTATGATGGTCCATGAGGCGCTCTATTAACCTGCGCTGCCA 621
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 432 TCGTACTGTTTGTGCTCCCACTATTATGAAGAAACCGTGTGTGTGAACCTGCA 491
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 622 --CCTCTACAGATGATGACCTGCTGCTGCTATGCGGATGCTGCTGTGTTACATCCA 679
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 492 ATATGTTGGGTGTGTTGGTTTCTTACCTGAGCTGAATGCGAAATCTCAATGCTCCCG 551
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 680 GTACCGGCTTGGGCTCTGCTTCTTTCACG-----ACTGGAGATGACCATGCACTGG 733
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 552 CAACGCTGCGCTCAAGGATCAAGTAATGAGCTTGAAGATGGCTGCAAGATATATTCAT 611
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 734 CAACCAAGGCTTCTAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 793
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 612 TTTCGGTGGCGATGTAGCAATATTAACGCTTCCGCGCAAAATGCTGTGGGCGCTCAAC 671
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 794 CTTCGGGGGTGACCTCAACGTGTCTCACTGTCTTGTGTGATGCTGCGGAGGAGCATCAT 853
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 672 CCAATTACATGATGATACCAAGCAAGACCGCTGTTTATTCATCGTGTATCA 724
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 854 CTCTGGCTGTGCTCTCTCCCAAGTGTGCTGCAAGGCGCTGTTCCACAGACCATCA 906
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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RESULT 15
US-10-036-041-22
; Sequence 22, Application US/10036041
; Publication No. US20020192751A1
; GENERAL INFORMATION:
; APPLICANT: Desnoyers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3030R1C8
; CURRENT APPLICATION NUMBER: US/10/036,041
; CURRENT FILING DATE: 2001-12-26
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/112514
; PRIOR FILING DATE: 1998-12-15
; PRIOR APPLICATION NUMBER: 60/113300
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/113430
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113605
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113621
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/114140
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PRIOR FILING DATE: 1998-12-23  
 PRIOR APPLICATION NUMBER: 60/115552  
 PRIOR FILING DATE: 1999-01-12  
 PRIOR APPLICATION NUMBER: 60/116843  
 PRIOR FILING DATE: 1999-01-22  
 PRIOR APPLICATION NUMBER: 60/125774  
 PRIOR FILING DATE: 1999-03-23  
 PRIOR APPLICATION NUMBER: 60/125778  
 PRIOR FILING DATE: 1999-03-23  
 PRIOR APPLICATION NUMBER: 60/125826  
 PRIOR FILING DATE: 1999-03-24  
 PRIOR APPLICATION NUMBER: 60/127035  
 PRIOR FILING DATE: 1999-03-31  
 PRIOR APPLICATION NUMBER: 60/127706  
 PRIOR FILING DATE: 1999-04-05  
 PRIOR APPLICATION NUMBER: 60/129122  
 PRIOR FILING DATE: 1999-04-13  
 PRIOR APPLICATION NUMBER: 60/130359  
 PRIOR FILING DATE: 1999-04-21  
 PRIOR APPLICATION NUMBER: 60/131270  
 PRIOR FILING DATE: 1999-04-27  
 PRIOR APPLICATION NUMBER: 60/131272  
 PRIOR FILING DATE: 1999-04-27  
 PRIOR APPLICATION NUMBER: 60/131291  
 PRIOR FILING DATE: 1999-04-27  
 PRIOR APPLICATION NUMBER: 60/132371  
 PRIOR FILING DATE: 1999-05-04  
 PRIOR APPLICATION NUMBER: 60/132379  
 PRIOR FILING DATE: 1999-05-04  
 PRIOR APPLICATION NUMBER: 60/132383  
 PRIOR FILING DATE: 1999-05-04  
 PRIOR APPLICATION NUMBER: 60/135750  
 PRIOR FILING DATE: 1999-05-25  
 PRIOR APPLICATION NUMBER: 60/138166  
 PRIOR FILING DATE: 1999-06-08  
 PRIOR APPLICATION NUMBER: 60/144791  
 PRIOR FILING DATE: 1999-07-20  
 PRIOR APPLICATION NUMBER: 60/146970  
 PRIOR FILING DATE: 1999-08-03  
 PRIOR APPLICATION NUMBER: 60/162506  
 PRIOR FILING DATE: 1999-10-29  
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 PRIOR FILING DATE: 2001-05-10  
 PRIOR APPLICATION NUMBER: 09/874503  
 PRIOR FILING DATE: 2001-06-05  
 PRIOR APPLICATION NUMBER: 09/869599  
 PRIOR FILING DATE: 2001-06-29  
 PRIOR APPLICATION NUMBER: 09/908, 827  
 PRIOR FILING DATE: 2001-07-18  
 PRIOR APPLICATION NUMBER: PCT/US99/10733  
 PRIOR FILING DATE: 1999-05-14  
 PRIOR APPLICATION NUMBER: PCT/US99/28551  
 PRIOR FILING DATE: 1999-12-02  
 PRIOR APPLICATION NUMBER: PCT/US99/30720  
 PRIOR FILING DATE: 1999-12-22  
 PRIOR APPLICATION NUMBER: PCT/US00/05601  
 PRIOR FILING DATE: 2000-03-01  
 PRIOR APPLICATION NUMBER: PCT/US00/05841  
 PRIOR FILING DATE: 2000-03-02  
 PRIOR APPLICATION NUMBER: PCT/US00/14042  
 PRIOR FILING DATE: 2000-05-22

PRIOR APPLICATION NUMBER: PCT/US00/15264  
 PRIOR FILING DATE: 2000-06-02  
 PRIOR APPLICATION NUMBER: PCT/US00/23522  
 PRIOR FILING DATE: 2000-08-23  
 PRIOR APPLICATION NUMBER: PCT/US00/23328  
 PRIOR FILING DATE: 2000-08-24  
 PRIOR APPLICATION NUMBER: PCT/US00/32678  
 PRIOR FILING DATE: 2000-12-01  
 PRIOR APPLICATION NUMBER: PCT/US00/34956  
 PRIOR FILING DATE: 2000-12-20  
 PRIOR APPLICATION NUMBER: PCT/US01/06520  
 PRIOR FILING DATE: 2001-02-28  
 PRIOR APPLICATION NUMBER: PCT/US01/17800  
 PRIOR FILING DATE: 2001-06-01  
 PRIOR APPLICATION NUMBER: PCT/US01/19692  
 PRIOR FILING DATE: 2001-06-20  
 PRIOR APPLICATION NUMBER: PCT/US01/21066  
 PRIOR FILING DATE: 2001-06-29  
 PRIOR APPLICATION NUMBER: PCT/US01/21735  
 PRIOR FILING DATE: 2001-07-09  
 NUMBER OF SEQ ID NOS: 80  
 SEQ ID NO 22  
 LENGTH: 3824  
 TYPE: DNA  
 ORGANISM: Homo Sapien  
 US-10-036-041-22

Query Match 4 1%; Score 69.4; DB 9; Length 3824;  
 Best Local Similarity 53.3%; Pred. No. 2e-10; Mismatches 181; Indels 12; Gaps 3;  
 Matches 220; Conservative 0;  
 QY 315 CACAGGTCGAGAGATTGCTATACCTGAATGTATATA--CCAAATGACTTAACCCAGCA 371  
 DB 359 CTCGCTTCAGAGACTGCTGCTCAACGCTATACCCAGCAGAGTCCCGCAGAG 418  
 QY 372 CAAAGGCGTCTGTTATGCTTTTCAATGCGGAGATTTTATTTTGGCGAAGCAAA 431  
 DB 419 GTCGGGTAGGCGCGATCATGATGAGGCGCTGATTAACCTGAGCGCTGCCA- 477  
 QY 432 TCTTAAGTGTGTTGTCGCCGACTACTTTGAAGAAACCGGCTTGTAAACGTGCA 491  
 DB 478 --CCTCCTACAGATGATCACTGCTGCTGCTATGAGGATGTGCTGTTACAGTCA 535  
 QY 492 ATATCGTTGGGTGTGTGGTTTCTTAAGCCTGAATCGAAATCTCAATGTCCCGG 551  
 DB 536 GTACCGGCTTGGGCTCCTTGTCTTTCAGC-----ACTGAGATGACATGCACTGG 589  
 QY 552 CAACGCTGGCTTCAAGGATCAATGAGTGTGAGATGGGTCAAGAGTAATATTCGCA 611  
 DB 590 CAACGAGGCTTCTAGATGTGTAGCTGTTGCGGTGGGTGCAAGAAACATGCGCCC 649  
 QY 612 TTTCGTTGGGATGTAGCAATATTACCGCTTCGCGCAAGTGTGTTGGGCTTCAAC 671  
 DB 650 CTTCGGGGGTGACCTCAACATGTCTCACTGTCTTGGTGAATCTGCGGGTGGAGATCAT 709  
 QY 672 CCAATTACATGATGATTAACGAGACACCGGCTGTTTATTCATCGTGATCA 724  
 DB 710 CTCGCGCTGCTCCTGCTCCCAAGTGGCTGAGGGCTGTTTCCACAGAGCATCA 762

Search completed: April 11, 2003, 13:24:11  
 Job time: 101.362 secs



GenCore version 5.1.4.P5-4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 4, 2003, 09:08:22 ; Search time 15.9846 Seconds  
(without alignments)  
1725.596 Million cell updates/sec

Title: US-09-776-910-15

Perfect score: 1093

Sequence: 1 QTFISGKPRGSEDCLYLVN.....KANPYDLKEPQVLPERN 207

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: /SID2/gcgdata/geneseq/emb1/AA1981.DAT:\*  
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11: /SID2/gcgdata/geneseq/emb1/AA1990.DAT:\*  
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23: /SID2/gcgdata/geneseq/emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1069	97.8	570	18	AAW17767
2	828	75.8	570	18	AAW17766
3	826	75.6	570	18	AAW17768
4	825	75.5	570	16	AAW78142
5	825	75.5	570	18	AAW17765
6	736	67.3	572	22	ABB57850
7	595	54.4	530	22	ABB57857
8	587.5	53.8	567	22	ABB57857
9	582	53.2	554	22	ABB57866
10	573	52.4	565	22	ABB57746

11	563.5	51.6	566	22	ABB61983	Drosophila melanog
12	563	51.5	572	22	ABB57867	Drosophila melanog
13	560	51.2	554	22	ABB59161	Drosophila melanog
14	555	50.8	542	22	ABB57790	Drosophila melanog
15	541.5	49.5	602	23	AAW47598	Drosophila cell cy
16	470	43.0	541	22	ABB57789	Drosophila melanog
17	469	42.9	568	22	ABB57831	Drosophila melanog
18	465	42.5	551	22	ABB57788	Drosophila melanog
19	463.5	42.4	528	22	AAW57863	C. felis esterace,
20	463.5	42.4	528	22	AAW57862	C. felis esterace,
21	463.5	42.4	528	22	AAW57861	C. felis esterace,
22	428	39.2	495	19	AAW57869	C. felis esterace,
23	428	39.2	530	19	AAW57855	C. felis esterace,
24	428	39.2	530	19	AAW57857	C. felis esterace,
25	428	39.2	530	22	AAW57851	C. felis esterace,
26	428	39.2	550	19	AAW57853	C. felis esterace,
27	428	39.2	550	19	AAW57854	C. felis esterace,
28	428	39.2	550	22	AAW57850	C. felis esterace,
29	425	38.9	505	19	AAW57851	C. felis esterace,
30	425	38.9	505	19	AAW57852	C. felis esterace,
31	425	38.9	505	22	AAW57852	C. felis esterace,
32	425	38.9	550	19	AAW57864	C. felis esterace,
33	425	38.9	550	19	AAW57865	C. felis esterace,
34	425	38.9	550	22	AAW57865	C. felis esterace,
35	420.5	38.5	527	22	ABB62333	C. felis esterace,
36	411	37.6	576	22	ABB64915	C. felis esterace,
37	400.5	36.6	562	22	ABB64708	C. felis esterace,
38	397	36.3	530	19	AAW57867	C. felis esterace,
39	397	36.3	530	19	AAW57867	C. felis esterace,
40	375	34.3	570	19	AAW57860	C. felis esterace,
41	375	34.3	570	22	AAW57879	C. felis esterace,
42	375	34.3	570	22	AAW57879	C. felis esterace,
43	375	34.3	595	19	AAW57859	C. felis esterace,
44	375	34.3	595	19	AAW57861	C. felis esterace,
45	375	34.3	595	22	AAW57861	C. felis esterace,

## ALIGNMENTS

RESULT 1	AAW17767	standard; Protein; 570 AA.
ID	AAW17767	
AC	AAW17767	
XX		
DT	08-AUG-1997	(first entry)
XX		
DE	Md-alpha-E7 malathion resistant mutant.	
XX		
KW	Malathion carboxylesterase; organophosphate; insecticide; pesticide; remediation; bioremediation; decontamination.	
XX		
OS	Musca domestica Rutgers strain.	
XX		
FT	Key	Location/Qualifiers
FT	Misc-difference 251	/note="Ser-251 is tryptophan in the susceptible allele expression product"
XX		
PN	W09719176-A1.	
XX		
PD	29-MAY-1997.	
XX		
PE	22-NOV-1996;	96WO-AU00746.
XX		
PR	23-NOV-1995;	95AU-0006751.
XX		
PA	(CSIR ) COMMONWEALTH SCI & IND RES ORG.	
XX		
PI	Boyce T, Brownlie JC, Campbell PM, Claudianos C, Newcomb RD, Oakeshott JG, Robin GC, Russell RJ, Smyth K;	
XX		

Query Match	Best Local Similarity	Score	DB	Length	570:
Matches	202: Conservative	3: Mismatches	2: Indels	0: Gaps	
QY 1	OTPFISGRKPTGSDCLYLVNTNDLNPDKRRPYWFIHGGGFI FGEANRWYCPDYFMKK	60			
Db 97	QDPFISGRKPTGSDCLYLVNTNDLNPDKRRPYWFIHGGGFI FGEANRWYCPDYFMKK	156			
QY 61	PVVLTVTVTRGLVGLFLSLKSENLNPNAGNLKDQVMALRWFNSNIAIFGGVDNTTVFG	120			
Db 157	PVVLTVTVTVTRGLVGLFLSLKSENLNPNAGNLKDQVMALRWFNSNIAIFGGVDNTTVFG	216			
QY 121	ESAGGASTHYMMTTEQTRGLFHRGIMMGSMSMCSSASTECOSRALTMMARKVGYKGGENK	180			
Db 217	ESAGGASTHYMMTTEQTRGLFHRGIMMGSMSMCSSASTECOSRALTMMARKVGYKGGENK	276			
QY 181	DLEFLMKANPYDLIKEEPQVLTPERM	207			
Db 277	DLEFLMKANPYDLIKEEPQVLTPERM	303			
RESULT 2					
AAW17766					
ID	AAW17766 standard; Protein; 570 AA.				
XX AC	AAW17766;				
XX DT	08-AUG-1997 (first entry)				
XX DE	Malathion carboxylesterase.				
XX KW	Malathion carboxylesterase; organophosphate; insecticide;				
XX KW	pesticide; remediation; bioremediation; decontamination; esterase;				
XX OS	Lucilia cuprina.				
XX OS	Synthetic.				
XX FH	Key Location/Qualifiers				
XX FT	Misc-difference 251				
XX FT	/label= 'Leu, Ser, Ala, Ile, Val, Thr, Cys, Met, Gly				
XX FT	/note= "pref. Leu or Ser"				
XX FN	W09719176-A1.				
XX PD	29-MAY-1997.				
XX PF	22-NOV-1996; 96WO-AU00746.				
XX PR	23-NOV-1995; 95AU-0006751.				
XX PA	(CSIR ) COMMONWEALTH SCI & IND RES ORG.				
XX PI	Boyce T, Brownlie JC, Campbell PM, Claudianos C;				
XX PI	Newcomb RD, Oakeshott JG, Robin GC, Russell RJ, Smyth K;				
XX DR	WPI: 1997-298113/27.				

xx	DNA encoding enzyme that degrades organophosphate pesticides -
pt	useful for decontamination of soil, water, food etc
xx	
xx	Claim 1; Fig 1; 52pp; English.
xx	
cc	A malathion carboxylesterase (AAW17766) differs from the esterase
cc	(AAW17765) of a malathion susceptible clone of <i>Lucilia cuprina</i> 251.
cc	a substn. of the tryptophan residue at amino acid position 251.
cc	The enzyme is capable of hydrolysing carboxylester and/or
cc	dimethylloxon organophosphates and can be formulated for use in
cc	bioremediation strategies for treating soil or water.
xx	
xx	Sequence 570 AA;
xx	
xx	Query Match 75.8%; Score 828; DB 18; Length 570;
xx	Best Local Similarity 74.6%; Pred. No. 8,7e-85;
xx	Matches 153; Conservative 25; Mismatches 27; Indels 0; Gaps
Qy	1 QYDFISGKRTGSGEDCLYLVNTDNLDPKRRPVWFHIGGFIFGEANRMWGPDPYMK 60
Db	97 QVDFITGRKCGSEDCILSVYTNLNPETKRPVLVYIHGGSEFIIGENHRDMYGPDIKK 156
Qy	61 PVLVITVQYRLVLGFLSLKSENLVPGNAGLKDQVMAIRFKSNIAIFGSDVDNITVFG 120
Db	157 DVLVLIITQYRLGALGFLSLNSEDNLVPGNAGLKDQVMAIRWIKNNCANFGGPNITVFG 216
Qy	121 ESAGASATHYMMITETGRGLFHRGITMAGSNGSCSASRTECCSRALTMMKRVYKGEENEK 186
Db	217 ESAGASATHYMMITETGRGLFHRGITMAGSNGNAICPAYNTQCHRAFTLAKLAGYGEENDK 276
Qy	181 DLEFLMKRNPYDLIKEPQVLTPE 205
Db	277 DYLEFLMKRKPQDLIKLEKVLTE 301
xx	
xx	RESULT 3
xx	AAW17768
xx	AAW17768 standard; Protein; 570 AA.
xx	
xx	AAW17768:
xx	
xx	08-AUG-1997 (first entry)
xx	
xx	Malathion carboxylesterase RM8con.
xx	
xx	Malathion carboxylesterase; organophosphate; insecticide;
xx	KW pesticide; remediation; bioremediation; decontamination; esterase;
xx	KM <i>Lucilia cuprina</i> .
xx	
xx	<i>Lucilia cuprina</i> .
xx	
xx	WO9719176-A1.
xx	
xx	29-MAY-1997.
xx	
xx	22-NOV-1996; 96WO-AU00746.
xx	
xx	23-NOV-1995; 95AU-0006751.
xx	
xx	(CSIR ) COMMONWEALTH SCI & IND RES ORG.
xx	
xx	Boyce T, Brownlie JC, Campbell PM, Claudianos C;
xx	PI Newcomb RD, Oakeshott JG, Robin GC, Russell RJ, Smyth K;
xx	PI WPI: 1997-298113/27.
xx	
xx	DNA encoding enzyme that degrades organophosphate pesticides -
xx	useful for decontamination of soil, water, food etc
xx	
xx	Claim 6; Fig 1; 52pp; English.
xx	
xx	A malathion carboxylesterase (AAW17768), designated RM-8Con, differs



CC from the esterase (AAW17765) of a malathion susceptible clone of  
CC Lucilia cuprina by a substn. of the tryptophan residue at amino  
CC acid position 251 by a leucine residue. This mutation is situated  
CC at the base of the active site gorge, 6.5 Angstroms from the active  
CC site serine. The RM80on amino acid sequence is a consensus deduced  
CC from the DNA sequences of 3 resistant clones (RM8 A-C) and their  
CC comparison to reference susceptible clone Lc743 (AAT68596) of  
CC Lc-alpha-E7. The enzyme is capable of hydrolysing carboxylester  
CC and/or dimethylloxon organophosphates and can be formulated for use  
CC in bioremediation strategies for treatment of soil or water.

XX Sequence 570 AA;

SO Query Match

Best Local Similarity 74.6%; Score 826; DB 18; Length 570;  
Matches 153; Conservative 25; Mismatches 27; Indels 0; Gaps 0;

QY 1 QTFPIGKPTGSEDCLYLNTYTNLNDLPDKRPVWVFTHGGGFIIGANRNMVGPDYFMK 60  
DB 97 QVDFITGKVCSEDCLYLNTYTNLNDLPDKRPVWVFTHGGGFIIGANRNMVGPDYFMK 156  
QY 61 PVVLTVOYRGLGVGLFSLKSENLNPGNAGLKDQVVALRMFKNIAIFGGDVNTVFG 120  
DB 157 DVVLINQYRLGALGFLSLNSEDLPNPGNAGLKDQVVALRMFKNIAIFGGDVNTVFG 216  
QY 121 ESAGASTHYMMITEQTRGLFHRGIMSGNSMCSASTECOSRALTMAKRVYKGEENEK 180  
DB 217 ESAGASTHYMMITEQTRGLFHRGIMSGNAICPLANTQCOHRAFTLAKIAGYKGEDNDK 276  
QY 181 DLEFLMKANPYDLIKEEPOVLTPE 205  
DB 277 DVLEFLMKAKPDILIKLEEKVLTLE 301

RESULT 4

AAW78142  
ID AAW78142 standard; Protein: 570 AA.

AC AAW78142;

DT 22-DEC-1995 (first entry)

DE OP-sensitive esterase E3.

KW Esterase; E3; bioremediation; organophosphate; carbamate;

KW insecticide; pesticide; water decontamination; meat decontamination.

OS Lucilia cuprina.

PN WO9519440-A1.

PD 20-JUL-1995.

PF 13-JAN-1995; 95WO-AU00016.

PR 13-JAN-1994; 94AU-0003347.

PA (CSIR ) COMMONWEALTH SCI & IND RES ORG.

PI Boyce TM, Campbell PM, Newcomb RD, Oakeshott JG;

PI Parker AG, Robin GC, Russell RJ, Smyth K;

DR WPI: 1995-263870/34.

DR N-PSDB: AAO91561.

PT Pure E3 esterase from Lucilia cuprina and related DNA - used to

PS eliminate residues of organo:phosphate and carbamate pesticides from

CC Example 3; Page 12-17; 38pp; English.

CC cDNA from organophosphate (OP)-sensitive L. cuprina pupa cDNA

CC library was amplified using cluster-specific esterase primers.

CC Isolated clone Lc743, a probable full-length cDNA, was expressed  
CC using a baculovirus vector in insect cells and shown to encode  
CC an OP-susceptible E3 esterase useful in bioremediation.

XX Sequence 570 AA;

SO Query Match

Best Local Similarity 74.6%; Score 825; DB 16; Length 570;  
Matches 153; Conservative 25; Mismatches 27; Indels 0; Gaps 0;

QY 1 QTFPIGKPTGSEDCLYLNTYTNLNDLPDKRPVWVFTHGGGFIIGANRNMVGPDYFMK 60  
DB 97 QVDFITGKVCSEDCLYLNTYTNLNDLPDKRPVWVFTHGGGFIIGANRNMVGPDYFMK 156  
QY 61 PVVLTVOYRGLGVGLFSLKSENLNPGNAGLKDQVVALRMFKNIAIFGGDVNTVFG 120  
DB 157 DVVLINQYRLGALGFLSLNSEDLPNPGNAGLKDQVVALRMFKNIAIFGGDVNTVFG 216  
QY 121 ESAGASTHYMMITEQTRGLFHRGIMSGNSMCSASTECOSRALTMAKRVYKGEENEK 180  
DB 217 ESAGASTHYMMITEQTRGLFHRGIMSGNAICPLANTQCOHRAFTLAKIAGYKGEDNDK 276  
QY 181 DLEFLMKANPYDLIKEEPOVLTPE 205  
DB 277 DVLEFLMKAKPDILIKLEEKVLTLE 301

RESULT 5

AAW17765  
ID AAW17765 standard; Protein: 570 AA.

AC AAW17765;

DT 08-AUG-1997 (first entry)

DE Lc-alpha-E7 malathion susceptible clone Lc743 esterase E3.

KW Malathion carboxylesterase; organophosphate; insecticide;

KW pesticide; remediation; bioremediation; decontamination; esterase.

OS Lucilia cuprina.

PN WO9719176-A1.

PD 29-MAY-1997.

PF 22-NOV-1996; 96WO-AU00746.

PR 23-NOV-1995; 95AU-0006751.

PA (CSIR ) COMMONWEALTH SCI & IND RES ORG.

PI Boyce T, Brownlie JC, Campbell PM, Claudianos C;

PI Newcomb RD, Oakeshott JG, Robin GC, Russell RJ, Smyth K;

DR WPI: 1997-298113/27.

DR N-PSDB: AAT68596.

PT DNA encoding enzyme that degrades organophosphate pesticides -

PS useful for decontamination of soil, water, food etc

XX Disclosure; Fig 1; 52pp; English.

CC Esterase E3 (AAW17765) from a malathion susceptible strain of

CC Lucilia cuprina differs from an esterase enzyme (see also

CC AAW17768) from malathion resistant RM8 strains by a trip for Leu

CC substn. at amino acid position 251, owing to a mutation in the

CC encoding DNA sequence (see also AAT68596). The resistant enzyme,





Seq	Sequence	554 AA;	53.28;	Score 582;	DB 22;	Length 554;
	Query Match		53.28;	Score 582;	DB 22;	Length 554;
	Best Local Similarity		54.68;	Fred. No. 6.4e-57;		
	Matches 112;	Conservative	31;	Mismatches 62;	Indels 0;	Gaps 0;
QY	1 QDTFISGKPTGSEDDLYLVNTYNDINPPDKRPVMEFIHGGFIFGEANNNYGPDIYFMK	60				
Db	81 OKHFVEFEMTDGSEDDLYLVNTYKTNLYPKRPMPVWVIYGGFGFGEASRECSPLYLRE	140				
QY	61 PVLVTQYRGYGLGFLSLKSENLVNPGAGIKDQVMALRWKSNALIFGSDVNDITYG	120				
Db	141 DVVVTSINRFLSPFLCLDDPELDVPGAGIKDQVLAIRWAKNCSRFGGSANTLTIG	200				
QY	121 ESAGASTHYMITEOTRLLFHRGIMSGNSNCSSETECGSRALTMARVYKGEENK	180				
Db	201 DSAGASVHYMITEOTRLLFHKALCMGNTLSPMAVLTQRMVPRYLAQVAGYAGENNTR	260				
QY	181 DILEFLMKANPYDLKKEPQVLTPE	205				
Db	261 DWMEFLKNAKGSIIIRKANGELCID	285				

XX	RESULT 10
XX	ABBS57746
XX	ID ABBS57746 standard; Protein: 565 AA.
XX	AC
XX	ABBS57746;
XX	DT 26-MAR-2002 (first entry)
XX	DE Drosophila melanogaster polypeptide SEQ ID NO 30.
XX	KW Drosophila; developmental biology; cell signalling; insecticide;
XX	KW pharmaceutical.
XX	OS Drosophila melanogaster.
XX	PN WO200171042-A2.
XX	PD 27-SEP-2001.
XX	PF 23-MAR-2001; 2001WO-US09231.
XX	PR 23-MAR-2000; 2000US-191637P.
XX	PR 11-JUL-2000; 2000US-0614150.
XX	PA (PEKE ) PE CORP NY.
XX	PI Venter JC, Adams M, Li PWD, Myers EW;
XX	DR WPI: 2001-6556860/75.
XX	DR N-PSDB; ABL01849.
XX	PT New isolated nucleic acid detection reagent for detecting 1000 or more
XX	PT genes from Drosophila and for elucidating cell signalling and cell-cell
XX	PT interactions -
XX	PS Disclosure; SEQ ID NO 30; 21pp + Sequence Listing; English.
XX	CC The invention relates to an isolated nucleic acid detection reagent
XX	CC capable of detecting 1000 or more genes from Drosophila. The invention is
XX	CC useful in developmental biology and in elucidating cell signalling and
XX	CC cell-cell interactions in higher eukaryotes for the development of
XX	CC insecticides, therapeutics and pharmaceutical drugs. The invention
XX	CC discloses genomic DNA sequences (AB116176-AB130511), expressed DNA
XX	CC sequences (ABBS7737-ABBS72072).
XX	CC The sequence data for this patent did not form part of the printed
XX	CC specification, but was obtained in electronic format directly from WIPO
XX	CC at ftp.wipo.int/pub/published_pct_sequences.
XX	Sequence 565 AA;

Query Match	52.4%	Score 573	DB 22	Length 565
Best Local Similarity	58.7%	Pred. No. 6.9e-56		
Matches 111	Conservative 23	Mismatches 55	Indels 0	Gaps 0

Qy	1	QDTFSGRPTSGSEDDLYLVNTYNDINPDKKRPVWFIHGGGFI	ESGASASTHYMMIT	EQTKGLFHRI	GMSSGNSKCSAST	ECOSRAL	TMARVGYK	GBENENK	180
				:		:		:	
Db	98	QKHFFSLIYEGSEDDLYLVNYSKRLRSDKPLPLVIWIIYGGGF	ESGAGHDEFS	PDYFMQ	157				
				:		:		:	
Qy	61	PVLVLTVOYRLGLVLEFLSLKSENLVNPGNAGLKDQVMALRM	WFESKNI	AI	GGVDNIT	YVG	120		
				:		:		:	
Db	158	DVYVVTENTRVVAGLFLSLADRDLDVPGNAGLKDQVMALRM	LSQNI	ADNGSP	QUNIT	YVG	217		
				:		:		:	
Qy	121	ESAGASASTHYMMIT	EQTKGLFHRI	GMSSGNSKCSAST	ECOSRAL	TMARVGYK	GBENENK	180	
				:		:		:	
Db	218	ESAGASASTHYMMIT	EQTKGLFHRI	KAIMOGSSMPC	EWANEP	SGFWAYRL	ACQLGYG	SEENENK	277
				:		:		:	
Qy	181	DILEFLMKA	189						
	:::								
Db	278	EVFRILQKA	286						

RESULT 11  
 ABB61983  
 ID ABB61983 standard; Protein: 566 AA.  
 XX  
 AC ABB61983;  
 XX  
 DT 26-MAR-2002 (first entry)  
 XX  
 DE Drosophila melanogaster polypeptide SEQ ID NO 12741.  
 XX  
 KW Drosophila; developmental biology; cell signalling; insecticide;  
 KW pharmaceutical.  
 XX  
 OS Drosophila melanogaster.  
 XX  
 PN WO200171042-A2.  
 XX  
 PD 27-SEP-2001.  
 XX  
 PF 23-MAR-2001; 2001WO-US09231.  
 XX  
 PR 23-MAR-2000; 2000US-191637P.  
 PR 11-JUL-2000; 2000US-0614150.  
 XX  
 PA (PEKE ) PE CORP NY.  
 XX  
 PI Venter JC, Adams M, Li PWD, Myers EW;  
 DR N-PSDB; ABL06086.  
 XX  
 PT New isolated nucleic acid detection reagent for detecting 1000 or more  
 PT genes from Drosophila and for elucidating cell signalling and cell-cell  
 PT interactions -  
 PT  
 PT  
 XX  
 PS Disclosure: SEQ ID NO 12741; 21pp + Sequence Listing; English.  
 XX  
 CC The invention relates to an isolated nucleic acid detection reagent  
 CC capable of detecting 1000 or more genes from Drosophila. The invention is  
 CC useful in developmental biology and in elucidating cell signalling and  
 CC cell-cell interactions in higher eukaryotes for the development of  
 CC insecticides, therapeutics and pharmaceutical drugs. The invention  
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
 CC sequences (ABL01840-ABL16175) and the encoded proteins  
 CC (ABB57737-ABB72022).  
 CC  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 SQ Sequence 566 AA;

[illegible]

The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from *Drosophila*. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmacological drugs. The invention discloses genomic DNA sequences (AB116175-AB130511), expressed DNA sequences (AB101840-AB116175) and the encoded proteins (AB57737-AB172072).

The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published\\_pct\\_sequences](http://ftp.wipo.int/pub/published_pct_sequences).

51.58; Score 563; DB 22; Length 572.

Query Match	51.2%;	Score 560;	DB 22;	Length 554
Best Local Similarity	58.0%;	Pred. No. 2e-54;		



```

QY 1 QTFISGKPTGSEDCLYLNVYTNNDLNPDKKRPVWVFIHGSGFIFGEANRNMWGPDYFMK 60
Db 143 QTHMFERKRYAGSEDCLYLNVYVKDLQDPDKLRPVWVWITGGYGEASR---GLD----- 194
QY 61 PVVLYTVQYRGLGVYGLSLSENINVPGNAGLKDQVNALMWEKSNIAIFSGDVNDITVFG 120
Db 195 -VVIVTVAYRIGALGPLSLDDPOLNVPGNAGLKDQVNALMWEKSNIAIFSGDSNNTITLFG 253
QY 121 ESAGGASTHYWMITEOTRGLEFHGIMMGSNGSMSSASTECOSRALTMKRVGYKEENEK 180
Db 254 ESAGGASTHFLATSPOTBGLHKAIWMSGVYLCPTQPPRNNWYRLAQKIGYTGDNKDK 313
QY 181 DLEFLMKANPYDLIKEEPOVLT 203
Db 314 AIFELRSMMSGGEIVKATATVLS 336

```

Search completed: April 4, 2003, 09:13:04  
 Job time : 18.9846 secs





GenCore version 5.1.4-p5\_4578  
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OM protein - protein search, using sw model

Run on: April 4, 2003, 09:10:33; Search time 6.92664 Seconds  
(without alignments) 2872.940 Million cell updates/sec

Title: US-09-776-910-15

Perfect score: 1093  
Sequence: 1 QTFDISGKPTGSEDLILNV.....KANPYDLKEEPVLTPERM 207

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

1: PIR73:\*  
2: PIR1:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	458	41.9	540	2	S53370 carboxylesterase (
2	454	41.5	540	2	A35986 esterase B1 - sout
3	447	40.9	503	2	S53372 carboxylesterase (
4	446	40.8	540	2	S53371 carboxylesterase (
5	359	32.8	564	2	A34325 juvenile-hormone e
6	354	32.4	578	2	F89068 protein T28C12.4b
7	354	32.4	658	2	T32053 hypothetical prote
8	345	31.6	564	1	S36787 carboxylesterase (
9	344.5	31.5	603	2	S70849 cholinesterase (EC
10	344	31.5	548	2	T32907 hypothetical prote
11	343.5	31.4	596	1	ACRYE acetylcholinestera
12	341	31.2	614	2	JH0314 acetylcholinestera
13	340	31.1	489	2	B69680 para-nitrobenzyl e
14	340	31.1	614	2	JH0811 acetylcholinestera
15	338	30.9	552	2	S36786 carboxylesterase (
16	337	30.8	583	2	S10712 acetylcholinestera
17	337	30.8	583	2	S10712 hypothetical prote
18	336	30.7	602	1	ACHU cholinesterase (EC
19	335.5	30.7	581	2	C39768 cholinesterase (EC
20	335	30.6	614	2	A39256 acetylcholinestera
21	334.5	30.6	547	2	S55233 juvenile hormone e
22	334.5	30.6	599	1	A38868 acetylcholinestera
23	334.5	30.6	767	2	S47639 acetylcholinestera
24	334	30.6	565	2	S10367 carboxylesterase (
25	333	30.5	612	2	A34967 sterol esterase (E
26	331	30.3	567	1	A41010 carboxylesterase (
27	331	30.3	599	2	A57701 sterol esterase (E
28	329.5	30.1	561	2	S71597 carboxylesterase (
29	329	30.1	597	2	A33668 sterol esterase (E

30	328.5	30.1	584	2	S48724 acetylcholinestera
31	326	29.8	561	2	JC2447 carboxylesterase (
32	325.5	29.8	561	2	S62788 carboxylesterase (
33	324.5	29.7	956	2	A56920 glutactin precurs
34	324	29.6	593	1	S25062 triacylglycerol 11
35	324	29.6	561	2	S47655 carboxylesterase (
36	321	29.4	745	2	S13586 triacylglycerol 11
37	320	29.3	554	2	S34607 carboxylesterase (
38	318	29.1	549	2	JX0054 carboxylesterase (
39	316	28.9	562	2	A55281 carboxylesterase (
40	315.5	28.9	545	2	S58980 carboxylesterase (
41	315.5	28.9	559	1	JC5408 carboxylesterase (
42	315	28.8	554	2	A39060 carboxylesterase (
43	314.5	28.8	602	2	A54413 acetylcholinestera
44	314	28.7	520	2	A60666 probable esterase
45	314	28.7	566	2	S19307 carboxylesterase (

#### ALIGNMENTS

##### RESULT 1

S53370 carboxylesterase (EC 3.1.1.1) B2 - southern house mosquito

C:Species: Culex pipiens quinquefasciatus (southern house mosquito)

C:Date: 15-Jul-1995 #sequence\_revision 08-Sep-1995 #text\_change 21-Jul-2000

C:Accession: S53370; S44211

R:Vaughan, A.; Rodriguez, M.; Hemingway, J.

Biochem. J. 305, 651-658, 1995

A:Title: The independent gene amplification of electrophoretically indistinguishable

A:Reference number: S53370; M01D:95134253; PMID:7530448

A:Accession: S53370

A:Molecule type: mRNA

A:Residues: 1-540 <VAD>

A:Cross-references: EMBL:Z32694; NID:g475067; PIDN:CA83643.1; PID:g475068

A:Experimental source: strain PeIR

A:Superfamily: cholinesterase; cholinesterase homology

C:Keywords: carboxylic ester hydrolase

Query Match 41.9%; Score 458; DB 2; Length 540;  
Best Local Similarity 44.0%; Pred. No. 8.9e-36;  
Matches 88; Conservative 40; Mismatches 72; Indels 0; Gaps 0;

QY	8	KPTGSEDCLYLVNTDLPDKRPVWFIHGGGFTFGANRWGPDVFMKKPVITVY	67
DB	77	KIVGCEDSIKINFAKEINPSKPLPVMLEYGGFTGSELVGPDPVLVKDVLVSF	136
QY	68	QYRLVGLFSLKSENUNPGNAGLDQYVALRFKSNIAIFGQVDNITTFGESAGAS	127
DB	137	NYRIGALGFICQSEDDGVPGNGLKDQNLAIWVLENTAIFGQDKRTLYGHSAGAS	196
QY	128	THVMITTEOTRGLEHFGIMWSGMSASSTECOSRALTMARVGYKGEENEKDIIEFLM	187
DB	197	VQHLHISDASKDLFORAIWSSGTSYNSWLSLRQNMVETLAKRIGMDGGGSGALRFK	256
QY	188	KANPYDLKEEPVLTPERM	207
DB	257	AAKPEDIVANOEKLTDDDM	276

##### RESULT 2

A35986 esterase B1 - southern house mosquito

C:Species: Culex pipiens quinquefasciatus (southern house mosquito)

C:Date: 16-Nov-1990 #sequence\_revision 13-Jan-1993 #text\_change 21-Jul-2000

C:Accession: A35986

R:Muches, C.; Papuljin, Y.; Agarwal, M.; Lemieux, L.; Herzog, M.; Abadon, M.; Beyssat

Proc. Natl. Acad. Sci. U.S.A. 87, 2574-2578, 1990

A:Title: Characterization of amplification core and esterase B1 gene responsible for

A:Reference number: A35986; M01D:90207238; PMID:2320576

A:Accession: A35986

A>Status: preliminary

A:Molecule type: DNA





A:Residues: 1-603 <TAY>  
 A:Cross-references: EMBL:M99492; NID:9191579; PIDN:AAA37328.1; PID:9191580  
 R:Rachinsky, T.L.; Camp, S.; Li, Y.; Ekstrom, T.J.; Newton, M.; Taylor, P.  
 Neuron 5, 317-327, 1990  
 A:Title: Molecular cloning of mouse acetylcholinesterase: tissue distribution of alternat  
 A:Reference number: J00314; MUID:90380429; PMID:2400605  
 A:Accession: S15680  
 A:Status: nucleic acid sequence not shown  
 A:Molecule type: nucleic acid  
 A:Residues: 30-128, 'P', 130-603 <RAC>  
 A:Cross-references: EMBL:M99492  
 R:Arpagaus, M.; Chalmers, A.; Masson, P.; Newton, M.; Vaughan, T.A.; Bartels, C.F.; Nog  
 J. Biol. Chem. 266, 6966-6974, 1991  
 A:Title: Use of the polymerase chain reaction for homology probing of butyrylcholinester  
 A:Reference number: A39768; MUID:91201348; PMID:2016308  
 A:Accession: A39768  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 97-128, 'P', 130-237 <ARP>  
 C:Superfamily: cholinesterase; cholinesterase homology  
 C:Keywords: carboxylic ester hydrolase; glycoprotein  
 F:57-557/Domain: cholinesterase homology <CHE>

Query Match 31.5%; Score 344.5; DB 2; Length 603;  
 Best Local Similarity 41.5%; Pred. No. 7, 5e-25;  
 Matches 81; Conservative 39; Mismatches 68; Indels 7; Gaps 5;

OY 12 SEDCLYLVNVDLPDKRPVVFHGGGFISEANRMVGPDEYMK-RPVYLVTVQYR 70  
 Db 118 SEDCLYLVNVDLPDKRPVVFHGGGFISEANRMVGPDEYMK-RPVYLVTVQYR 176  
 OY 71 LGVGFSLKSENVNPGNGKLVNPKVNFHGGGFISEANRMVGPDEYMK-RPVYLVTVQYR 130  
 Db 177 VGAGGFSLKSENVNPGNGKLVNPKVNFHGGGFISEANRMVGPDEYMK-RPVYLVTVQYR 235  
 OY 131 MITEQTRGLFHRCIMNSGMSA---STECOSRALTVAKRYGGENEDIEFLM 187  
 Db 236 HLLCPQSYPLFTRALLESSSNAPWAKHPEANRRLTLAKFTGC-SKENEEMIKCLR 294  
 OY 188 KANYDYDIKEPOVL 202  
 Db 295 SKDQELIRNERFVL 309

## RESULT 10

hypotheical protein F56C11.6 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 31-Jan-2000  
 C:Accession: T32907  
 R:Lin-Wollam, A.; Wohldmann, P.; Morris, M.  
 submitted to the EMBL Data Library, January 1998  
 A:Description: The sequence of C. elegans cosmid F56C11.  
 A:Reference number: Z21244  
 A:Accession: T32907  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-548 <TIN>  
 A:Cross-references: EMBL:AF043697; PIDN:AMB97558.1; GSPB:GN00019; CESP:F56C11.6  
 C:Experimental source: strain Bristol N2; clone F56C11  
 C:Genetics:  
 A:Gene: CESP:F56C11.6  
 A:Map position: 1  
 A:Introns: 29/3; 264/1; 340/1; 398/3; 447/1; 490/2  
 C:Superfamily: cholinesterase; cholinesterase homology

Query Match 31.5%; Score 344; DB 2; Length 548;  
 Best Local Similarity 40.2%; Pred. No. 7, 4e-25;  
 Matches 84; Conservative 34; Mismatches 65; Indels 26; Gaps 8;

OY 4 FTSGKPTGSECLYLVNVDLPDKRPVVFHGGGFISEANRMVGPDEYMK 59  
 Db 85 FNVYTKSEHCLSNVFLPKHSEWEPD-GFVWVFHGGGFSEVSSN--YGCASIR 141

OY 60 ----KPVYLVTVQYRGLVGLSLKSENVNPGNGKLVNPKVNFHGGGFISEANRMVGPDEYMK 115  
 Db 142 NCTKDDVVVTVNTRVGLVGLSLKSENVNPGNGKLVNPKVNFHGGGFISEANRMVGPDEYMK 199  
 OY 116 ITVFGESAGASTHYMITEQTRGLFHRCIMNSGMSA---STECOSRALTVAKRYGGENEDIEFLM 172  
 Db 200 VTFICQSGAGASVDLCLSPHSGRLNRAIPMAGNCECPAMRTSQQLSREFARYLG 259  
 OY 173 YKGEENE-KDLEFL-----MKANP 191  
 Db 260 WEGDDNSEDLLQFDQPLKYMGINP 288

## RESULT 11

ACRYE  
 acetylcholinesterase (EC 3.1.1.7) precursor, 11s form [validated] - Pacific electric  
 N:Alternate names: acetylcholinesterase, asymmetric form  
 C:Species: Torpedo californica (Pacific electric ray)  
 C:Date: 17-Mar-1987 #sequence\_revision 08-Nov-1996 #text\_change 15-Sep-2000  
 C:Accession: A00773; A08020; A31962; B31962; A23902; B41117; S15677  
 R:Schumacher, M.; Camp, S.; Maulet, Y.; Newton, M.; Macphée-Quigley, K.; Taylor, S.S.  
 Nature 319, 407-409, 1986  
 A:Title: Primary structure of Torpedo californica acetylcholinesterase deduced from 1  
 A:Reference number: A00773; MUID:86118676; PMID:3753747  
 A:Accession: A00773  
 A:Molecule type: mRNA  
 A:Residues: 'NS', 11-596 <SCH>  
 A:Cross-references: GB:X03439; NID:964389  
 A:Experimental source: electric organ  
 A:Note: Parts of this sequence, including the amino and carboxyl ends of the mature p  
 R:Schumacher, M.; Camp, S.; Maulet, Y.; Newton, M.; Macphée-Quigley, K.; Taylor, S.S.  
 Fed. Proc. 45, 2976-2981, 1986  
 A:Title: Primary structure of acetylcholinesterase: implications for regulation and f  
 A:Reference number: A08020; MUID:87054662; PMID:3536598  
 A:Accession: A08020  
 A:Status: nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 22-596 <SC2>  
 R:Schumacher, M.; Maulet, Y.; Camp, S.; Taylor, P.  
 J. Biol. Chem. 263, 18979-18987, 1988  
 A:Title: Multiple messenger RNA species give rise to the structural diversity in acet  
 A:Reference number: A2701; MUID:89066695; PMID:3198606  
 A:Accession: A31962  
 A:Molecule type: mRNA  
 A:Residues: 1-23 <SC3>  
 A:Cross-references: EMBL:X03439; NID:964389  
 A:Experimental source: clones AChE-11 and AChE-18  
 A:Note: revision to sequence A00773  
 A:Accession: B31962  
 A:Molecule type: DNA; mRNA  
 A:Residues: 499-565 <SC4>  
 A:Cross-references: GB:X03439; NID:964389  
 R:Macphée-Quigley, K.; Taylor, P.; Taylor, S.  
 J. Biol. Chem. 260, 12185-12189, 1985  
 A:Title: Primary structures of the catalytic subunits from two molecular forms of ace  
 A:Reference number: A23902; MUID:86008285; PMID:3900071  
 A:Accession: A23902  
 A:Molecule type: protein  
 A:Residues: 22, 'B', 24-45; 214-237 <MAC>  
 A:Note: active site Ser identification  
 R:Kreienkamp, H.J.; Weise, C.; Rada, R.; Aaviksaar, A.; Hucho, F.  
 Proc. Natl. Acad. Sci. U.S.A. 88, 6117-6121, 1991  
 A:Title: Anticodon subunits of the catalytic center of acetylcholinesterase from Torped  
 A:Reference number: A41117; MUID:91296772; PMID:2068091  
 A:Accession: B41117  
 A:Molecule type: protein  
 A:Residues: 100-108 <KRE>  
 A:Note: substrate binding site  
 R:Maulet, Y.; Camp, S.; Gbney, G.; Rachinsky, T.L.; Ekstrom, T.J.; Taylor, P.  
 Neuron 4, 289-301, 1990  
 A:Title: Single gene encodes glycopospholipid-anchored and asymmetric acetylcholines



C:Keywords: carboxylic ester hydrolase  
F:24-478/Domain: cholinesterase homology <CHE>

Query Match 31.1%; Score 340; DB 2; Length 489;  
Best Local Similarity 41.2%; Pred. No. 1.5e-24;  
Matches 82; Conservative 26; Mismatches 83; Indels 8; Gaps 5;

Qy 9 PTGSEDCILYNTYNDLPDKRPVWFTHGGGFIHGGEANRMWY-GPDYEMKRPVLTVT 67  
Db PROSEDCILYNTYNDLPDKRPVWFTHGGGFIHGGEANRMWY-GPDYEMKRPVLTVT 134  
Qy 68 QYRLGVGFLSKSENLNVPENAGLKQVVALRMFKSNIAIFGSDVDNITVFGESAGAS 127  
Db NYRLGPEFELHSSFNENAYSDNLDLDOAALWKVRENISAFGGDPNVITVFGESAGAS 194  
Qy 128 THYMITETQTRGLFHRGIMSGNSMCSASTECOSRALTMARKRYGKGEENKDIIEFLM 187  
Db IVALAMPAAKGLFOKALIMESGASR-TWTKEQANSTSAFLQVLT---NEGO-LDKLH 248  
Qy 188 KANPYDLKEEPOVLTPE 206  
Db TVSAEDILKADQLRIAEK 267

## RESULT 14

JH0811  
acetylcholinesterase (EC 3.1.1.7) catalytic chain precursor - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 03-Feb-1994 #sequence-revision 03-Feb-1994 #text-change 18-Jun-1999  
C:Accession: JH0811  
R:Legay, C.; Bon, S.; Vernier, P.; Coussem, F.; Massoulié, J.  
J. Neurochem. 60, 337-346, 1993  
A:Title: Cloning and expression of a rat acetylcholinesterase subunit: generation of mu  
A:Reference number: JH0811; MUID:93107932; PMID:8417155  
A:Accession: JH0811  
A:Molecule type: mRNA  
A:Residues: 1-614 <LEG>  
A:Cross-references: GB:S50879; NID:9262092; PIDN:AA24566.1; PID:9262093  
A:Experimental source: Striatum  
C:Comment: This protein is responsible for hydrolysis of acetylcholine at cholinergic sy  
C:Superfamily: cholinesterase; cholinesterase homology  
C:Keywords: carboxylic ester hydrolase; glycoprotein; membrane protein; muscle; nerve; r  
F:1-31/Domain: signal sequence #status predicted <SIG>  
F:32-614/Product: acetylcholinesterase catalytic chain #status predicted <CAT>  
F:63-569/Domain: cholinesterase homology <CHE>  
F:100-127-288-303,440-560/Disulfide bonds: #status predicted  
F:234,365,478/Active site: Ser, Glu, His #status predicted  
F:296,381,495/Binding site: carbonyl (Asn) (covalent) #status predicted

Query Match 31.1%; Score 340; DB 2; Length 614;  
Best Local Similarity 39.3%; Pred. No. 2.1e-24;  
Matches 79; Conservative 37; Mismatches 77; Indels 8; Gaps 5;

Qy 12 SECDCLYNTYNDLPDKRPVWFTHGGGFIHGGEANRMWYGPDYFMK-KPVLTLYOYR 70  
Db SECDCLYNTYNDLPDKRPVWFTHGGGFIHGGEANRMWYGPDYFMK-KPVLTLYOYR 183  
Qy 71 LGVIGFLSKSENLNVPENAGLKQVVALRMFKSNIAIFGSDVDNITVFGESAGASTHY 130  
Db LGVIGFLSKSENLNVPENAGLKQVVALRMFKSNIAIFGSDVDNITVFGESAGASTHY 242  
Qy 131 KMITEQTRGLFHRGIMSG--NSMCSAST-ECOSRALTMARKRYGK--GEENKDIIE 184  
Db HILSLPSRSLFHRAYLQSTGTPGNMAYVAGARRATILALVCGPFGAGGNDTELIS 302  
Qy 185 FLKANPYDLKEEPOVLTPE 205  
Db 303 CLTRPADLVDEHWHVLPQE 323

RESULT 15  
S36786  
carboxylesterase (EC 3.1.1.1) E4 - green peach aphid

C:Species: Myzus persicae (green peach aphid)  
C:Date: 09-Jun-1994 #sequence-revision 01-Dec-1995 #text-change 18-Jun-1999  
C:Accession: S36786  
R:Field, L.M.; Williamson, M.S.; Moores, G.D.; Devonshire, A.L.  
Biochem. J. 294, 569-574, 1993  
A:Title: Cloning and analysis of the esterase genes conferring insecticide resistance  
A:Reference number: S36786; MUID:93384534; PMID:8373371  
A:Accession: S36786  
A:Status: Preliminary  
A:Molecule type: mRNA  
A:Residues: 1-552 <FIE>  
A:Cross-references: EMBL:X74554; NID:9397510; PIDN:CA452648.1; PID:9397511  
C:Superfamily: cholinesterase; cholinesterase homology  
C:Keywords: carboxylic ester hydrolase  
F:52-552/Domain: cholinesterase homology <CHE>

Query Match 30.9%; Score 338; DB 2; Length 552;  
Best Local Similarity 41.3%; Pred. No. 2.8e-24;  
Matches 81; Conservative 30; Mismatches 63; Indels 22; Gaps 7;

Qy 3 DFLSG-KPTGSEDCILYNTYNDLPDK---RPVWFTHGGGFIHGGEANRMWYGPDYF 57  
Db EFGSGSKIIIGDCLFLNVTPEKLPQENSAGDLMNVIHIGGGYFEGG--ILYGPYL 150  
Qy 58 M-KRPVLTLYOYRIGVGLFLSKSENLNVPENAGLKQVVALRMFKSNIAIFGSDVDNI 116  
Db LNNDFVYVYVIRGLVGLFASFGVLT--GNMLKQVVALKWIQNIYAFGSDPVS 208  
Qy 117 TVFGESAGASTHYMITEQTRGLFHRGIMSGNSMCSASTECOSRALTMARKRYGKGE 176  
Db TITGMSAGASVHNHILISPMKGLFNRAIIQSGAFCHWSTAE-----NVAQTKYIAN 262  
Qy 177 -----ENKDIIEFL 186  
Db 263 IMGCPNNSVETVECL 278

Search completed: April 4, 2003, 09:17:20  
Job time: 8.92664 secs

GenCore version 5.1.4.P5-4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 4, 2003, 09:09:07 ; Search time 3.86293 Seconds  
(without alignments)  
2222.559 Million cell updates/sec

Title: us-09-776-910-15

Perfect score: 1093  
Sequence: 1 QTFDTSKRTGSEDCLYLV.....KANPYDLKEPQVLTBERM 207

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 112892 segs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database: SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	454	41.5	540	EST1_CULPI	P16854 culex pipie
2	359	32.8	564	EST1_HELVI	P12992 heliothis v
3	357.5	32.7	574	CHLE_HORSE	P11908 equus caball
4	348	31.6	613	ACES_BOVIN	P23795 bos taurus
5	344.5	31.5	564	ESTF_MYZPE	P35502 myzus persi
6	343.5	31.4	586	CHLE_MOUSE	P04058 torpedo cal
7	343.5	31.4	586	ACES_TORCA	P04058 torpedo cal
8	342	31.3	611	ACES_FELCA	P02763 felis silve
9	341	31.2	581	ACES_BUNFA	P09203 bungarus fa
10	341	31.2	614	ACES_MOUSE	P21836 mus musculu
11	340	31.1	614	ACES_RABIT	P37136 rattus norv
12	339	31.0	584	ACES_RABIT	P02949 oryctolagus
13	338	30.9	552	ESTF_MYZPE	P35502 myzus persi
14	336	30.7	602	CHLE_HUMAN	P35501 myzus persi
15	335.5	30.7	581	CHLE_RABIT	P06276 homo sapien
16	335	30.6	565	ES10_RAT	P13927 oryctolagus
17	335	30.6	614	ACES_HUMAN	P22303 homo sapien
18	334.5	30.6	590	ACES_TORMA	P07692 torpedo mar
19	334.5	30.6	767	ACES_CHICK	P36196 gallus gall
20	333	30.5	489	PNEA_BACSU	P37967 bacillus su
21	333	30.5	612	BAL_RAT	P07882 rattus norv
22	331.5	30.3	357	CHLI_BRALA	P09500 branchiost
23	331	30.3	567	EST1_HUMAN	P23141 homo sapien
24	331	30.3	599	BAL_MOUSE	P06485 mus musculu
25	330.5	30.2	561	EST5_RAT	P03010 rattus norv
26	329	30.1	597	BAL_BOVIN	P30122 bos taurus
27	329	30.1	634	ACES_BRARE	P063108 rattus norv
28	326	29.8	561	EST3_RAT	P063108 rattus norv
29	325.5	29.7	561	EST4_RAT	P063108 rattus norv
30	324.5	29.4	561	ACES_ELEEL	P042275 electrophor
31	321	29.4	561	EST1_MESAU	P064419 mesocricetu
32	321	29.4	742	BAL_HUMAN	P19835 homo sapien
33	320	29.3	554	ESTM_MOUSE	P063880 mus musculu

Result ID	Score	Query Match	Length	ID	Description
34	318	29.1	549	EST1_RAT	P10959 rattus norv
35	316	28.9	562	EST2_MOUSE	P064176 mus musculu
36	315	28.8	554	ESTN_MOUSE	P23953 mus musculu
37	314.5	28.8	620	ACEL_CABER	P27459 caenorhabdi
38	314.5	28.8	620	ACEL_CABER	P27459 caenorhabdi
39	314	28.7	566	EST1_PIG	P29550 sus scrofa
40	310.5	28.4	629	ACES_LEPDE	P27677 leptotars
41	310	28.4	532	EST2_RABIT	P14943 oryctolagus
42	310	28.4	545	ESTC_DROPS	P25725 drosophila
43	309.5	28.3	545	ESTB_DROPS	P25726 drosophila
44	308.5	28.2	542	EST6_DROMA	P47982 drosophila
45	308.5	28.2	547	ESTA_DROPS	P25727 drosophila

## ALIGNMENTS

Result ID	Score	Query Match	Length	ID	Description
EST1_CULPI	1093	41.5	540	EST1_CULPI	P16854 culex pipie
AC	16854	41.5	540	EST1_CULPI	P16854 culex pipie
DT	01-AUG-1990 (Rel. 15, Created)				
DT	01-AUG-1990 (Rel. 15, Last sequence update)				
DT	01-FEB-1994 (Rel. 28, Last annotation update)				
DE	Esterase B1 precursor (EC 3.1.1.1).				
GN	B1.				
OS	Culex pipiens (House mosquito).				
OC	Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;				
OC	Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;				
OC	Culicoidae; Culex.				
OX	NCBI_TaxID=7175;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=TEM-R;				
RX	MEDLINE=90207238; PubMed=2320576;				
RA	Mouches C., Pauplin Y., Agarwal M., Lemieux L., Herzog M.,				
RA	Abadon M., Baysat-Arnaout V., Hyrien O., de Saint Vincent B.R.,				
RA	Georgiou G.P., Pasteur N.;				
RT	"Characterization of amplification core and esterase B1 gene				
RT	responsible for insecticide resistance in Culex ";				
RL	Proc. Natl. Acad. Sci. U.S.A. 87:2574-2578(1990)				
CC	- FUNCTION: OVERPRODUCTION OF NONSPECIFIC ESTERASES IS A COMMON				
CC	MECHANISM OF RESISTANCE TO ORGANOPHOSPHATE INSECTICIDES.				
CC	- CARBOXYLIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a				
CC	carboxylic anion.				
CC	- MISCELLANEOUS: THERE ARE TWO SUCH ESTERASES: A AND B. ALLELES OF				
CC	BOTH A AND B ARE KNOWN.				
CC	- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
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CC	the European Bioinformatics Institute. There are no restrictions on its				
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CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>				
CC	or send an email to <a href="mailto:license@sib-sib.ch">license@sib-sib.ch</a> ).				
CC	-----				
DR	EMBL: M3328: AAA28289.1: -				
DR	PIR: A35986; A35986.				
DR	HSP: P21836; IMAA.				
DR	InterPro: IPR002018; Carboxylesterase.				
DR	InterPro: IPR000379; Ser_estrs_site.				
DR	Pfam: PF00135; Coesterase; 1.				
DR	PROSITE: PS00122; CARBOXYLESTERASE_B.2; FALSE_NEG.				
DR	PROSITE: PS00941; CARBOXYLESTERASE_B.2; FALSE_NEG.				
DR	Hydroxylase; Serine esterase; Glycoprotein; Multigene family; Signal.				
KW	SIGNAL				
FT	CHAIN	1	540		
FT	ACT_SITE	191	191		
FT	ACT_SITE	442	442		
FT	DISULFID	68	81		
FT	CARBOHD	452	452		
FT	SEQUENCE	540 AA:	60806 MW:		

Query Match 41.5%; Score 454; DB 1; Length 540;  
 Best Local Similarity 43.5%; Pred. No. 6,2e-35;  
 Matches 87; Conservative 41; Mismatches 72; Indels 0; Gaps 0;

OY 8 KPTGSDCLYNTYNDLNPCKRPVWVFHGGGFTFGANRWYGPDPYMKRPVLYVY 67  
 DB 77 KIVGDEDLKTNVAKELNPSPLVYLYYGGFTGFTGTELYGPDFLVQKDIYVSR 136  
 OY 68 QYRLGVLEFLSKSENLNPGNAGLKQVVALRFRKFNIAIEGGDVNITVGEASGAS 127  
 DB 137 NYRIGALGFLCCQSGDEGVGNAGLKQVVALRFRKFNIAIEGGDVNITVGEASGAS 196  
 OY 128 THYMMITEQTLGFLRHMISGNSGSSASTECOSRALTMKRVGKGENEDILEFIM 187  
 DB 197 VQYHLISDASKDLFQRRIVMSGSYSSWILTRNNVEXLAKAIGMDGGGSGALRFLR 256  
 OY 188 KANFYDLKEEPOVLPFERM 207  
 DB 257 RAKPEDIVAHQEKILTDQM 276

## RESULT 2

ESTD\_HELVI STANDARD; PRT; 564 AA.

AC P12992;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DE Juvenile hormone esterase precursor (EC 3.1.1.59) (JH esterase).  
 OS Heliothis virescens (Noctuid moth) (Owllet moth).  
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
 OC Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata;  
 OC Diptera; Noctuoidea; Noctuidae; Heliothinae; Heliothis.  
 OX NCBI\_Taxid=7102;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 20-54.  
 RA MEDLINE=89308671; PubMed=2745451;  
 RA Hanzlik T.N., Yehia A.I.A.-A., Harsman L.G., Hammock B.D.;  
 RT "Isolation and sequencing of cDNA clones coding for juvenile hormone  
 RT esterase from *Heliothis virescens*. Evidence for a catalytic mechanism  
 RT for the serine carboxylesterases different from that of the serine  
 RT proteases.";  
 RT J. Biol. Chem. 264:12419-12425(1989).  
 RL [2]  
 RN REVISIONS.  
 RA Hanzlik T.N.;  
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: JH ESTERASE PLAYS A CRUCIAL ROLE IN THE DECREASE OF  
 CC JH ACTIVITY IN LEPIDOPTERAN INSECTS, BY HYDROLYZING THE METHYL  
 CC ESTER OF JH. IT IS ALSO INVOLVED IN THE TRANSPORT OF JH.  
 CC -1- CATALYTIC ACTIVITY: Methyl (2E,6E)-(10R,11S)-10,11-epoxy-3,7,11-  
 CC trimethyltrideca-2,6-dienoate + H(2)O = (2E,6E)-(10R,11S)-10,11-  
 CC epoxy-3,7,11-trimethyltrideca-2,6-dienoate + methanol.  
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.  
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 CC EMBL: J04955; AAB88629.1. -  
 DR HSSP: A34325; A34325.  
 DR HSSP: P37967; 10E3.  
 DR InterPro: IPR002018; Carbesteraseb.  
 DR InterPro: IPR000379; Ser\_estr\_site.  
 DR Pfam: PF00135; Coesterase; 1.  
 DR PROSITE: PS00122; CARBOXYLESTERASE\_B\_1; 1.  
 DR PROSITE: PS00941; CARBOXYLESTERASE\_B\_2; FALSE\_NEG.  
 DR Hydrolase; Serine esterase; Glycoprotein; Signal.  
 KW

FT SIGNAL 1 19  
 FT CHAIN 20 564 JUVENILE HORMONE ESTERASE.  
 FT ACT\_SITE 220 220 BY SIMILARITY.  
 FT ACT\_SITE 351 351 BY SIMILARITY.  
 FT ACT\_SITE 465 465 BY SIMILARITY.  
 FT DISULFID 89 109 BY SIMILARITY.  
 FT CARBOHYD 81 81 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 180 180 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 402 402 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 515 515 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT VARIANT 29 29 V->L.  
 FT VARIANT 52 52 F->P.  
 SO SEQUENCE 564 AA; 62614 MW; D1405DD91914E8D CRC64;

Query Match 32.8%; Score 359; DB 1; Length 564;  
 Best Local Similarity 42.5%; Pred. No. 5.1e-26;  
 Matches 71; Conservative 30; Mismatches 44; Indels 22; Gaps 4;

OY 1 QTFPISKPTG-----SDCLYLVNY-----TNDLNDPKRPVWVFHGGGFTFG 45  
 DB 91 QTVLYGRILMAASEMSEACIVANIHVPMQSLPRVGTPL-----RLVYIHGGGFAFG 145  
 OY 46 EANRNNYGPDPYMKRPVLYVQYRLGVLEFLSKSENLNPGNAGLKQVVALRFRKSN 105  
 DB 146 SCHEDLHCPYLYTKVYITFNRYLVNFGELSNMT--TKIPNAGLGRDQVTLRLWQRN 203  
 OY 106 IALFGSDVNITVGEASGASTHYMMITEQTLGFLRHMISGNSGNSM 152  
 DB 204 AKNFGDPSDITLACQSGASNAHLTLTSKATEGLFRKAILMSGTGM 250

## RESULT 3

CHIE\_HORSE STANDARD; PRT; 574 AA.

ID CHIE\_HORSE  
 AC P81908;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DE 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Cholinesterase (EC 3.1.1.8) (Acetylcholine acylhydrolase) (Choline  
 DE esterase II) (Butyrylcholine esterase) (Pseudocholinesterase) (Bg-  
 DE BChE).  
 GN BChE.  
 OS Equus caballus (Horse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
 OX NCBI\_Taxid=9796;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Plasma;  
 RA Moorad D.R., Luo C., Garcia G.E., Doctor B.P.;  
 RT "Amino acid sequence of horse serum butyrylcholinesterase.";  
 RT (In) Doctor B.P., Taylor P., Quinn D.M., Rotundo R.L., Gentry M.K.  
 RT (eds.);  
 RL Structure and function of cholinesterases and related proteins,  
 RL pp.145-146, Plenum Press, New York and London (1998).  
 CC -1- CATALYTIC ACTIVITY: An acylcholine + H(2)O = choline + a  
 CC carboxylic acid anion.  
 CC -1- SUBUNIT: HOMOTETRAMER. THE TETRAMER IS COMPOSED OF TWO DIMERS. THE  
 CC TWO SUBUNITS IN A DIMER ARE LINKED BY A DISULFIDE BOND.  
 CC -1- TISSUE SPECIFICITY: PRESENT IN MOST CELLS EXCEPT ERYTHROCYTES.  
 CC -1- MISCELLANEOUS: CHOLINESTERASE IS HIGHLY REACTIVE WITH  
 CC ORGANOPHOSPHATE ESTERS.  
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.  
 DR HSSP: P21836; 1MA.  
 DR InterPro: IPR002018; Carbesteraseb.  
 DR InterPro: IPR000997; Cholinesterase.  
 DR InterPro: IPR000379; Ser\_estr\_site.  
 DR Pfam: PF00135; Coesterase; 1.  
 DR PRINTS: PR00878; CHOLINESTRASE.  
 DR PROSITE: PS00122; CARBOXYLESTERASE\_B\_1; 1.  
 DR PROSITE: PS00941; CARBOXYLESTERASE\_B\_2; 1.  
 DR Hydrolase; Serine esterase; Glycoprotein.  
 KW ACT\_SITE 198 198 BY SIMILARITY.



MONOMERS AND DIMERS TO COLLAGEN-TAILED AND HYDROPHOBIC-TAILED FORMS, IN WHICH CATALYTIC TETRAMERS ARE ASSOCIATED WITH ANCHORING PROTEINS THAT ATTACH THEM TO THE BASAL LAMINA OR TO CELL MEMBRANES. IN THE COLLAGEN-TAILED FORMS, ISOCORM T SUBUNITS ARE ASSOCIATED WITH A SPECIFIC COLLAGEN, COLO, WHICH TRIGGERS THE FORMATION OF ISOCORM T TETRAMERS, FROM MONOMERS AND DIMERS.

-1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; H AND T (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.

-1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.

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CC      EMBL, AF061815; AAC64270.1; . JOINED.
CC      EMBL, AF061813; AAC64270.1; JOINED.
CC      EMBL, AF061814; AAC64270.1; JOINED.
CC      PIR: S10712; S10712.
CC      HSSP: P22303; ZCLJ.
CC      GlycoSuiteDB: P23795; .
DR      InterPro: IPR002018; Carboxylesterase.
DR      InterPro: IPR000097; Cholinesterase.
DR      InterPro: IPR000379; Ser_ests_site.
DR      Pfam: PF00135; Coesterase; 1.
DR      PRINTS: PR00878; CHOLINESTRASE.
DR      PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
DR      PROSITE: PS00941; CARBOXYLESTERASE_A_2; 1.
KW      Hydrolase; Serine esterase; Synapse; Membrane; Nerve; Muscle; Signal;
KW      Neurotransmitter degradation; Glycoprotein; Alternative splicing.
FT      SIGNAL          1       30
FT      CHAIN           1       613
FT      ACT_SITE        233      233
FT      ACT_SITE        364      364
FT      ACT_SITE        477      477
FT      ACT_SITE        99       126
FT      DISULFID        287      302
FT      DISULFID        439      559
FT      DISULFID        610      610
FT      DISULFID        91       91
FT      CARBOHYD         295      295
FT      CARBOHYD         380      380
FT      CARBOHYD         484      494
FT      CARBOHYD         574      613
FT      VARSPLIC
FT      FT              46       46
FT      CONFLICT        169      169
FT      CONFLICT        212      212
FT      CONFLICT        323      323
FT      CONFLICT        352      352
FT      CONFLICT        424      424
FT      CONFLICT        524      524
FT      CONFLICT        549      554
FT      CONFLICT        571      571
SQ      SEQUENCE        613 AA;  67663 MW;  698DAFD0F8624B12 CRC64;

Query Match      31.8%; Score 348; DB 1; Length 613;
Best Local Similarity 40.2%; Pred. No. 6e-25;
Matches 82; Conservative 37; Mismatches 71; Indels 14; Gaps 7;

OY      12 SEDCLVLYNVTVNDLNLDKRRPVWVFTHGGGFTEGEANNNMYGPDIYFMK-KPYVLVYYQYR 70
Db      123 SEDCLVLYNVTVTPVRSPSPYLVWVIYGGGGFGSGASISVDYDGREFLLVQAGTYLVSMNTR 182

OY      71 LGVIGFLSKSENLNPQANAELKDOWMALRWKSNIAITAFEGGDVNINIVFECSAGASTHY 130
Db      183 VGAGGFLALPGSR-EAPGVNGLLDQLATLQWQENVAAFGDDPPHSVTILLFGSSAAABAVGM 241

OY      131 MTITEOTRGIFLRHGIMMSG--NSMCSAST-ECOSRALTMARKRYGYK-----GENEKDI 182
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PROSITE; PS00122; CARBOXYLESTERASE\_B\_1; 1.



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DR Pfam: PF00135; Coesterase: 1.  
DR PRINTS: PR00878; CHOLINESTERASE.  
DR PROSITE: PS00122; CARBOXYLESTERASE_B_1: 1.  
DR PROSITE: PS00941; CARBOXYLESTERASE_B_2: 1.  
KW Hydrolase; Serine esterase; Synapse; Membrane; Nerve; Muscle; Signal;  
KW Neurotransmitter degradation; Glycoprotein; GPI-anchor; 3D-structure;  
KW Alternative splicing.  
FT SIGNAL 1 21  
FT CHAIN 22 564  
FT PROPSEP 565 586  
FT ACT_SITE 221 221  
FT ACT_SITE 348 348  
FT ACT_SITE 461 461  
FT DISULFID 88 115  
FT DISULFID 275 286  
FT DISULFID 423 542  
FT DISULFID 558 558  
FT CARBOHYD 80 80  
FT CARBOHYD 437 437  
FT CARBOHYD 478 478  
FT CARBOHYD 554 554  
FT LIPID 564 564  
FT VARSPIC 557 586  
  
INTERCHAIN.  
N-LINKED (GLCNAC. . .) (POTENTIAL).  
N-LINKED (GLCNAC. . .) (POTENTIAL).  
N-LINKED (GLCNAC. . .) (POTENTIAL).  
GPI-ANCHOR.  
ADGGELSSCTSSSGKIFVYLFILYLIF -> ETIDAE  
RQKTEFFHRSSTMMHKQDFHSRHESCAEL (IN ISOFORM T').  
  
Query Match 31.4%; Score 343.5; DB 1; Length 586;  
Best Local Similarity 41.0%; Pred. No. 1.5e-24;  
Matches 80; Conservative 31; Mismatches 77; Indels 7; Gaps 5.  
  
QY 12 SEDCLLVNTNDLNDPKRPVWVFHHGGFIPEGANRWGYDDYF-MKKPVLYTVQYR 70  
DB 112 SEDCLVLNVWDSPRP-KETIVWWVIYGGGFSGSTLDVYNGKYLAAYEEVVLVSLSYR 170  
QY 71 LGVLGLSLKSSENLANVPGNAGLKDVMAIRFKSNIAIGCGVDNIITVGESAGASATHY 130  
DB 171 VGAFGLALHGSG-EAPGVVGLDDRMALQWHDNIQFFGGDPKVTTIFGSAGASAVGM 229  
QY 131 MMITQDTRELFRHGTMSGNSMCSASS--TFCGRALTMAKRVGKEENKEKTLIEFLM 187  
DB 230 HLLSGSRDLFRRLLOSSEPCNPWASVVAEGRRRAVELGNLCNLINSD-ELIHCLR 288  
QY 188 KANPYDLKEEPQVL 202  
DB : |::| |::| |:  
DB 289 EKKPELIDVENVVL 303  
  
RESULT 8  
ACES_FELCA STANDARD; PRT; 611 AA.  
AC ACES_FELCA O62763; O62762;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Acetylcholinesterase precursor (EC 3.1.1.7) (AcHe).  
GN ACHE.  
OS Felis silvestris catus (Cat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheraia; Carnivora; Fissipedia; Felidae; Felis.  
OX NCBI_TaxId=9685;  
RN [1]  
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
RX MEDLINE=20334351; PubMed=10874122;  
RA Bartels C.F., Xie W., Miller-Lindholm A.K., Schopfer L.M., Lockridge O.;  
RT "Determination of the DNA sequences of acetylcholinesterase and butyrylcholinesterase from cat and demonstration of the existence of both in cat plasma.";  
RL Biochem. Pharmacol. 60:479-487(2000).  
CC -1- FUNCTION: RAPIDLY HYDROLYZES CHOLINE RELEASED INTO THE SYNAPSE (BY SIMILIARITY).  
CC -1- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.  
CC -1- SUBUNIT: ISOPORM H GENERATES GPI-ANCHORED DIMERS; DISULFIDE
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QY 185 FLKMANPYDLKEEPOVLTPE 205  
 DB 303 CLRTRPADLVDEHWHVLPQE 323

RESULT 11  
 ACES\_RAT STANDARD; PRT; 614 AA.

AC P37136;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DE 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Acetylcholinesterase precursor (EC 3.1.1.7) (AChE);  
 GN AChE.  
 OS Rattus norvegicus (Rat).  
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM T).  
 RA MEDLINE=93107932; PubMed=8417155;  
 RA Legay C., Bon S., Vernier P., Coussen F., Massoulie J.;  
 RT "Cloning and expression of a rat acetylcholinesterase subunit:  
 RT generation of multiple molecular forms and complementarity with a  
 RT Torpedo collagenic subunit";  
 RT J. Neurochem. 60:337-346(1993).  
 RL [2]  
 RN SEQUENCE FROM N.A. (ISOFORMS H AND R).  
 RX MEDLINE=93114454; PubMed=8417973;  
 RA Legay C., Bon S., Massoulie J.;  
 RT "Expression of a cDNA encoding the glycolipid-anchored form of rat  
 RT acetylcholinesterase";  
 RL FEBS Lett. 315:163-166(1993).  
 CC -1- FUNCTION: RAPIDLY HYDROLYZES CHOLINE RELEASED INTO THE SYNAPSE.  
 CC -1- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.  
 CC -1- SUBUNIT: OLIGOMER COMPOSED OF DISULFIDE-LINKED HOMODIMERS  
 CC CATALYTIC FORMS H (GPI-ANCHOR DIMER) AND T (ASYMMETRIC COLLAGEN-  
 CC TAILED), WHICH DIFFER IN THEIR C-TERMINUS, ACCOUNT FOR ALL TYPES  
 CC OF KNOWN AChE FORMS.  
 CC -1- ALTERNATIVE PRODUCTS: 3 isoforms; T (shown here), H and R; are  
 CC produced by alternative splicing. It is not known whether isoform  
 CC R is functional.  
 CC -1- TISSUE SPECIFICITY: HAS BEEN FOUND IN CENTRAL NERVOUS SYSTEM AND  
 CC MUSCLE. FOUND IN EMBRYONIC LIVER AND SPLEEN BUT NOT IN ADULT  
 CC LIVER.  
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLSTERASE/LIPASE FAMILY.  
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 CC -----  
 CC EMBL; S50879; AAB24586.1; -;  
 CC EMBL; X70140; CAA49717.1; -;  
 CC EMBL; X70141; CAA49718.1; -;  
 CC PIR; JH0811; JH0811.  
 CC HSSP; P21836; IMAA.  
 CC InterPro; IPR002018; CarbesteraseB.  
 CC InterPro; IPR000997; Cholinesterase.  
 CC InterPro; IPR000379; Ser\_estrs-site.  
 CC Pfam; PF00135; Coesterase; 1.  
 CC PRINTS; PR00878; CHOLNSTRASE.  
 CC PROSITE; PS00122; CARBOXYLSTERASE.  
 CC PROSITE; PS00941; CARBOXYLSTERASE\_B\_2; 1.  
 CC Hydrolase; Serine esterase; Synapse; Membrane; Nerve; Muscle; Signal;  
 CC Neurotransmitter degradation; Glycoprotein; Alternative splicing.  
 FT SIGNAL 1 31  
 FT CHAIN 32 614  
 FT ACT\_SITE 234 365  
 FT ACT\_SITE 365 365  
 FT BY SIMILARITY.  
 FT BY SIMILARITY.

FT ACT\_SITE 478 478 BY SIMILARITY.  
 FT DISULFID 100 127 BY SIMILARITY.  
 FT DISULFID 288 303 BY SIMILARITY.  
 FT DISULFID 440 560 BY SIMILARITY.  
 FT DISULFID 611 611 INTERCHAIN (BY SIMILARITY).  
 FT CARBOHYD 296 296 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 381 381 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 495 495 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT VARSPIC 575 614 DTLEAEKRMKAEFFHFWSSYVWKNQDPHYSKORCSDL  
 FT VARSPIC 575 614 -> GRRGVKGQGHKARPAVGRIGERGKGRHM (IN  
 FT ISOFORM R).  
 FT VARSPIC 575 614 LKWL (IN ISOFORM H).  
 FT VARSPIC 575 614 DTLEAEKRMKAEFFHFWSSYVWKNQDPHYSKORCSDL  
 FT VARSPIC 575 614 -> GRRGVKGQGHKARPAVGRIGERGKGRHM (IN  
 FT ISOFORM R).  
 SO SEQUENCE 614 AA; 68196 MW; 2EDAFF746282E7C0 CR664;  
 Query Match 31.1%; Score 340; DB 1; Length 614;  
 Best Local Similarity 39.3%; Pred. No. 3,4e-24;  
 Matches 79; Conservative 37; Mismatches 77; Indels 8; Gaps 5;

QY 12 SEDCLYLVNTDNLNPKRPVWVFTHGGFIFGEANRMWGPDPFMK-KPVLYTVQYR 70  
 DB 124 SEDCLYLVNTDNLNPKRPVWVFTHGGFIFGEANRMWGPDPFMK-KPVLYTVQYR 183  
 QY 71 LGVLGLSLKSENLNPNAGLADQYVALRFRKSNIAIFGDVNTITVGEASGASTHY 130  
 DB 184 VGFEGFLALPGSR-EAPGNVGLDQRLAQWQENIAAFGQDPMSTYTLRCEASGASVGM 242  
 QY 131 MMTTEQRLGFLHFGIMMSG--NSMCSAST-EGOSRALTMAKVGK---GEENENDILE 184  
 DB 243 HILSLPFSRLFHRVAVLQSGTPNGPMATVSGAEARRRATLLARLVGCPGAGGNDTELIS 302

QY 185 FLKMANPYDLKEEPOVLTPE 205  
 DB 303 CLRTRPADLVDEHWHVLPQE 323

RESULT 12  
 ACES\_RABBIT STANDARD; PRT; 584 AA.

AC Q29499;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Acetylcholinesterase precursor (EC 3.1.1.7) (AChE) (Fragment).  
 GN AChE.  
 OS Oryctolagus cuniculus (Rabbit).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Muscle;  
 RX MEDLINE=95010096; PubMed=7925428;  
 RA Djillo O., Thermitte Y., Toulant J., Chatonnet A.;  
 RT "Acetylcholinesterase and butyrylcholinesterase expression in adult  
 RT rabbit tissues and during development.";  
 RL Eur. J. Biochem. 225:115-124(1994).  
 CC -1- FUNCTION: RAPIDLY HYDROLYZES CHOLINE RELEASED INTO THE SYNAPSE.  
 CC -1- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.  
 CC -1- SUBUNIT: OLIGOMER COMPOSED OF DISULFIDE-LINKED HOMODIMERS.  
 CC -1- MISCELLANEOUS: SYNAPSES USUALLY CONTAIN ASYMMETRIC MOLECULES OF  
 CC CHOLINSTERASE, WITH A COLLAGEN-LIKE PART DISULFIDE-BONDED TO THE  
 CC CATALYTIC PART. A DIFFERENT, GLOBULAR TYPE OF CHOLINSTERASE  
 CC OCCURS ON THE OUTER SURFACES OF CELL MEMBRANES, INCLUDING THOSE OF  
 CC ERYTHROCYTES.  
 CC -1- MISCELLANEOUS: THIS IS THE CATALYTIC SUBUNIT OF AN ASYMMETRIC OR  
 CC SOLUBLE FORM OF AChE.  
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLSTERASE/LIPASE FAMILY.  
 CC -----  
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DR EMBL: U05036; AAA5335.1; -  
 DR HSSP: P22303; 2CLJ.  
 DR InterPro: IPR002018; Carboxylesterase.  
 DR InterPro: IPR000379; Ser-esterase.  
 DR Pfam: PF00135; Coesterase; 1.  
 DR PROSITE: PS00122; CARBOXYLESTERASE\_B\_1; 1.  
 DR PROSITE: PS00941; CARBOXYLESTERASE\_B\_2; 1.  
 DR Hydrolyase, Serine esterase; Synapse; Membrane; Nerve; Muscle; Signal;  
 KW Neurotransmitter degradation; Glycoprotein.  
 FT NON\_TER 1  
 FT SIGNAL 1  
 FT CHAIN 1  
 FT ACT\_SITE 2 584  
 FT ACT\_SITE 204 204  
 FT ACT\_SITE 335 335  
 FT ACT\_SITE 448 448  
 FT DISULFID 70 97  
 FT DISULFID 258 273  
 FT DISULFID 410 530  
 FT DISULFID 581 581  
 FT CARBOHYD 266 266  
 FT CARBOHYD 351 351  
 FT CARBOHYD 465 465  
 SEQUENCE 584 AA; 64630 MW; 2AE157F3063649FE CRC64;

Query Match 31.0%; Score 339; DB 1; Length 584;  
 Best Local Similarity 39.4%; Pred. No. 4e-24; Mismatches 76; Indels 12; Gaps 6;  
 Matches 80; Conservative 35;

OY 12 SEDCLYLVNTYNDLMDPKRPVWFIHGSGFTFGEANRN-WGPDYEMKKPVLVVOYR 70  
 DB 94 SEDCLYLVNTYNDLMDPKRPVWFIHGSGFTFGEANRN-WGPDYEMKKPVLVVOYR 153  
 OY 71 LGVLGFLSKSENLVPGNAGLKDQVMAIWRKSNIAIFGQVDNITVEGSSAGASTHY 130  
 DB 154 VGAFGFTCLPGSR-EAPGNVGLDRLALQVQENVAAGFQDPASVTLGESSAGASVGL 212  
 OY 131 WMTETGRLFLHRGIMSG--NSMSSAST-ECQSALTMARKV-----GYGEEHEKDI 182  
 DB 213 HLLSPSRRLGFRAVLQSGAPNGPVAIVGVEARRRATILARLVCCPGAGG--NDTEL 270  
 OY 183 LEFLKAMPYDLIKEPQVLTPE 205  
 DB 271 VACLTRPAQDLVDHEWRVLPGE 293

RESULT 13  
 ESTE\_MYZPE STANDARD; PRT; 552 AA.  
 AC P35501:  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 01-OCT-1994 (Rel. 30, Last annotation update)  
 DE Esterase B4 precursor (EC 3.1.1.1) (Carboxylic-ester hydrolase).  
 OS Myzus persicae (peach-potato aphid).  
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
 OC Insecta; Pterygota; Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha;  
 OC Aphidiformes; Aphidoidea; Aphididae; Macrosiphini; Myzus.  
 NCBI\_TaxID=13164;  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 24-63.  
 RC STRAIN=R3 / isolate 794J;  
 RA MEDLINE=93384534; PubMed=8373371;  
 RA Field L.M., Williamson M.S., Moores G.D., Devonshire A.L.;  
 RT "Cloning and analysis of the esterase genes conferring insecticide  
 RT resistance in the peach-potato aphid, Myzus persicae (Sulzer).";  
 RL Biochem. J. 294:569-574(1993).  
 CC -1- FUNCTION: OVERPRODUCTION OF NONSPECIFIC ESTERASES IS A COMMON  
 CC MECHANISM OF RESISTANCE TO ORGANOPHOSPHATE INSECTICIDES.

CC -1- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a  
 CC carboxylic anion.  
 CC -1- MISCELLANEOUS: THIS ESTERASE CONFERS INSECTICIDE RESISTANCE.  
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.

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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).

DR EMBL: X74524; CAA52648.1; -  
 DR PIR: S36786; S36786.  
 DR HSSP: P21836; 1MAA.  
 DR InterPro: IPR002018; Carboxylesterase.  
 DR InterPro: IPR000379; Ser-esterase.  
 DR Pfam: PF00135; Coesterase; 1.  
 DR PROSITE: PS00122; CARBOXYLESTERASE\_B\_1; 1.  
 DR PROSITE: PS00941; CARBOXYLESTERASE\_B\_2; FALSE\_NEG.  
 KW Hydrolyase, Serine esterase; Glycoprotein; Signal.  
 FT SIGNAL 1  
 FT CHAIN 24 552  
 FT ACT\_SITE 214 214  
 FT ACT\_SITE 339 339  
 FT ACT\_SITE 463 463  
 FT DISULFID 89 106  
 FT DISULFID 266 277  
 FT CARBOHYD 81 81  
 FT CARBOHYD 269 269  
 FT CARBOHYD 371 371  
 FT CARBOHYD 404 404  
 FT CARBOHYD 443 443  
 SEQUENCE 552 AA; 61348 MW; B97B67272DFF7209 CRC64;

Query Match 30.9%; Score 338; DB 1; Length 552;  
 Best Local Similarity 41.3%; Pred. No. 4.6e-24; Mismatches 63; Indels 22; Gaps 7;  
 Matches 81; Conservative 30;

OY 3 DFISG-KPTGSEDCYLVNTYNDLMDPKR---RPVWFIHGSGFTFGEANRNWGPDYF 57  
 DB 93 EFGSGSKITIGEDCLFLNNTYTRKLPQENSGADLMNVIHHGGYGFSG--ILVGPRL 150  
 OY 58 M-KRPVLTVOYRIGVLGFLSKSENLVPGNAGLKDQVMAIWRKSNIAIFGQVDNI 116  
 DB 151 LDNDPFFVYVSYNIRGLVLFASFGDGLT--GNNGIKDQVMAIWRKSNIAIFGQVNSV 208  
 OY 117 TVFGESAGASTHYMMITQETGLFLHRGIMSGNSMSSASTFQCSALTMARKVYKGE 176  
 DB 209 TTGMSAGASVYHNNLILSPMSKGLFRKATIQSSAFCHWSTAF-----NVAQRTYIAN 262  
 OY 177 -----ENEKDLLEFL 186  
 DB 263 IMGCPPTNSVEIPECL 278

RESULT 14  
 CHEL\_HUMAN STANDARD; PRT; 602 AA.  
 AC P06276:  
 DT 01-JAN-1988 (Rel. 06, Created)  
 DT 01-AUG-1988 (Rel. 08, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Cholinesterase precursor (EC 3.1.1.8) (Acetylcholine acylhydrolase)  
 DE (Pseudocholesterase II) (Butyrylcholine esterase)  
 DE BCHE OR CHE1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 NCBI\_TaxID=9606;  
 RN [1]





QY 12 SEDCLYLVNVTNDLNDPKRRVWVFHGGGFIPEGANRMWGPDPYMK-KPVVLVTVQYR 70  
 |||||  
 Db 117 SEDCLYLVNWTIPAPKP-KNATVLMIVYGGGFGTGTSLHYDGKFLRVRYVWSMNR 175  
 QY 71 LGVIGFELSKSENLNVPNGAGLKQDVALLRMFKSNIAIFGGDVNITVFEESAGASTHY 130  
 :|||||  
 Db 176 VGALGFLLPG-NPEAPGNMGLFPODLALQWQKNIAAFGNGPKSVTLFEGESAGASVSL 234  
 QY 131 MITEQRTGLFHRGIMSGNSMCSAST---ECOSRALTMARKVGYGGENEKDILEFLM 187  
 :|||  
 Db 235 HLLSGSHLFTRALILQSGSNAPWATSLYEARNRKLTLAKLGC-SRENETEIIKCLR 293  
 QY 188 KANPYDLIKEPOVL---TP 204  
 :|||  
 Db 294 NKDQETILNEAFVVPYGT 313

## RESULT 15

CHLE\_RABIT STANDARD; PRT; 581 AA.  
 ID CHLE\_RABIT  
 AC P21927;  
 DT 01-MAY-1991 (Rel. 18, Created)  
 DT 01-MAY-1991 (Rel. 18, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Cholinesterase precursor (EC 3.1.1.8) (Acylcholine acylhydrolase)  
 DE (Choline esterase II) (Butyrylcholine esterase)  
 DE (Pseudochoolinesterase)  
 GN BCHE.

OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID:9986;  
 RN 11

RP SEQUENCE FROM N.A.  
 RC STRAIN-New Zealand;  
 RC MEDLINE-90326526; PubMed-2374720;  
 RA Jbilo O., Roudani S., Chatonnet A.;  
 RT "Complete sequence of rabbit butyrylcholinesterase.";  
 RL Nucleic Acids Res. 18:3990-3990(1990).  
 RN 12

RP SEQUENCE OF 75-215 FROM N.A.

RC TISSUE-Liver;  
 RC MEDLINE-91201348; PubMed-2016308;  
 RA Arpagus M., Chatonnet A., Masson P., Newton M., Vaughan T.A.,  
 RA Bartels C.F., Nogueira C.P., La Du B.N., Lockridge O.;  
 RT "Use of the polymerase chain reaction for homology probing of  
 RT butyrylcholinesterase from several vertebrates.";  
 RL J. Biol. Chem. 266:6966-6974(1991).  
 CC 1- CATALYTIC ACTIVITY: An acylcholine + H(2)O = choline + a  
 CC carboxylic acid anion.

CC 1- SUBUNIT: HOMOTETRAMER. THE TETRAMER IS COMPOSED OF TWO DIMERS. THE  
 CC TWO SUBUNITS IN A DIMER ARE LINKED BY A DISULFIDE BOND.  
 CC 1- TISSUE SPECIFICITY: PRESENT IN MOST CELLS EXCEPT ERYTHROCYTES.  
 CC 1- MISCELLANEOUS: CHOLINESTERASE IS HIGHLY REACTIVE WITH  
 CC ORGANOPHOSPHATE ESTERS.

CC 1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYL ESTERASE/LIPASE FAMILY.

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DR EMBL: X52090; CAA36308.1;  
 DR EMBL: X52091; CAA36308.1; JOINED.  
 DR EMBL: X52092; CAA36308.1; JOINED.  
 DR EMBL: M62779; AAA31169.1;  
 DR PIR: S10255; S10255.  
 DR PIR: C39768; C39768.  
 DR HSSP: P21836; IMAA.

DR InterPro: IPR002018; CarbesteraseB.  
 DR InterPro: IPR000997; Cholinesterase.  
 DR InterPro: IPR000379; Ser\_estrs\_site.  
 DR Pfam: PF00135; Coesterase\_1.  
 DR PRINTS: PR00878; CHOLINESTERASE.  
 DR PROSITE: PS00122; CARBOXYL ESTERASE\_B.1; 1.  
 DR PROSITE: PS00941; CARBOXYL ESTERASE\_B.2; 1.  
 KW Hydrolyase; Serine esterase; Glycoprotein; Signal.  
 FT SIGNAL 1  
 FT CHAIN 8  
 FT ACT\_SITE 205  
 FT ACT\_SITE 205  
 FT ACT\_SITE 332  
 FT ACT\_SITE 445  
 FT DISULFID 72  
 FT DISULFID 259  
 FT DISULFID 407  
 FT DISULFID 526  
 FT DISULFID 578  
 FT CARBOHYD 64  
 FT CARBOHYD 113  
 FT CARBOHYD 113  
 FT CARBOHYD 248  
 FT CARBOHYD 263  
 FT CARBOHYD 263  
 FT CARBOHYD 348  
 FT CARBOHYD 462  
 FT CARBOHYD 488  
 FT CARBOHYD 492  
 FT CARBOHYD 493  
 FT CARBOHYD 493  
 SQ SEQUENCE 581 AA; 66156 MW; FE8B199E7B32EB0A CRC64;

Query Match 30.7%; Score 335.5; DB 1; Length 581;  
 Best Local Similarity 40.3%; Pred. No. 8.4e-24;  
 Matches 77; Conservative 40; Mismatches 67; Indels 7; Gaps 5;

QY 12 SEDCLYLVNVTNDLNDPKRRVWVFHGGGFIPEGANRMWGPDPYMK-KPVVLVTVQYR 70  
 |||||  
 Db 96 SEDCLYLVNWTIPAPKP-KNATVLMIVYGGGFGTGTSLHYDGKFLRVRYVWSMNR 154  
 QY 71 LGVIGFELSKSENLNVPNGAGLKQDVALLRMFKSNIAIFGGDVNITVFEESAGASTHY 130  
 :|||||  
 Db 155 VGALGFLLPG-NPEAPGNMGLFPODLALQWQKNIAAFGNGPKSVTLFEGESAGASVSL 213  
 QY 131 MITEQRTGLFHRGIMSGNSMCSAST---SASTECOSRALTMARKVGYGGENEKDILEFLM 187  
 :|||  
 Db 214 HLLSGSHLFTRALILQSGSNAPWATSLYEARNRKLTLAKLGC-SRENETEIIKCLR 272  
 QY 188 KANPYDLIKEE 198  
 :|||  
 Db 273 NKDQETILNE 283

Search completed: April 4, 2003, 09:13:40  
 Job time: 6.86293 secs

GenCore version 5.1.4\_p5\_4578  
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OM protein - protein search, using sw model

Run on: April 4, 2003, 09:09:58 ; Search time 20.6467 Seconds  
(without alignments)  
2065.788 Million cell updates/sec

Title: US-09-776-910-15

Perfect score: 1093  
Sequence: 1 QTFDFISGKPTGSEDCILYLVN.....KANPYDLIKEPOVLTPEKM 207

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL.21:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_prodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1053	96.3	570	5	09XZ70 musca domes
2	840	76.9	570	5	09Y409 haemaphys
3	825	75.5	570	5	025252 lucilia cup
4	736	67.3	556	5	024201 dirosophila
5	736	67.3	572	5	09Y1B5 dirosophila
6	735.5	67.3	345	5	09N153 dirosophila
7	595	54.4	530	5	0917L5 dirosophila
8	595	54.4	549	5	024204 dirosophila
9	593	54.3	565	5	09N159 dirosophila
10	587.5	53.8	567	5	09Y1B3 dirosophila
11	586.5	53.7	558	5	024202 dirosophila
12	585	53.5	297	5	09N151 dirosophila
13	582	53.2	554	5	09Y1B0 dirosophila
14	579	53.0	286	5	09N152 dirosophila
15	573	52.4	553	5	024194 dirosophila
16	573	52.4	565	5	09Y1C3 dirosophila

17	568	52.0	572	5	024203 dirosophila
18	567	51.9	401	5	09N160 dirosophila
19	563.5	51.6	566	5	09W243 dirosophila
20	563	51.5	572	5	09Y1B1 dirosophila
21	560	51.2	554	5	09Y1C2 dirosophila
22	560	51.2	566	5	09N160 dirosophila
23	559	51.1	564	5	09N161 dirosophila
24	556	50.9	554	5	024195 dirosophila
25	555	50.8	555	5	095U30 dirosophila
26	555	50.8	542	5	024198 dirosophila
27	555	50.8	542	5	09Y1B9 dirosophila
28	542	49.6	446	5	09N155 dirosophila
29	504.5	46.2	532	5	061726 anisopterom
30	503.5	46.1	532	5	061727 culix pipie
31	481	44.0	467	5	091597 culix pipie
32	480	43.9	540	5	08W089 culix pipie
33	478	43.7	540	5	09G095 culix pipie
34	478	43.7	540	5	08W088 culix pipie
35	475	43.5	360	5	09U9R1 dirosophila
36	475	43.5	467	5	091596 culix pipie
37	475	43.5	467	5	091598 culix pipie
38	475	43.5	540	5	023733 culix quing
39	475	43.5	540	5	092025 culix quing
40	470	43.0	541	5	024197 dirosophila
41	470	43.0	541	5	09Y1C0 dirosophila
42	469	42.9	568	5	09Y1B6 dirosophila
43	468.5	42.9	435	5	09N154 dirosophila
44	466.5	42.7	526	5	076177 aphs gossy
45	466	42.6	540	5	091920 culix tarsa

## ALIGNMENTS

## RESULT 1

ID	Q9XZ70	PRELIMINARY;	PRT;	570 AA.
AC	Q9XZ70;			
DT	01-NOV-1999 (TREMBLrel. 12, Created)			
DT	01-NOV-1999 (TREMBLrel. 12, Last sequence update)			
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)			
DE	Carboxylesterase MdaE7 (EC 3.1.1.1).			
GN	MdaE7.			
OS	Musca domestica (House fly).			
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;			
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;			
OC	Muscoidea; Muscidae; Musca.			
OX	NCBI_TaxID=7370;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=ROTTERS DIAZINON-R.			
RX	MEDLINE=9381228; PubMed=10451921;			
RA	Claudianos C., Russell J.R., Oakeshott J.G.;			
RT	"The same amino acid substitution in orthologous esterases confers organophosphate resistance on the house fly and a blowfly.";			
RT	Insect Biochem. Mol. Biol. 29:675-686(1999).			
RL	-1 SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.			
CC	EMBL; AF13341; AAD29685.1; -			
DR	HSSP; P37967; 10E3.			
DR	InterPro: IPR002018; Carboxylesterase.			
DR	InterPro: IPR000379; Ser estersite.			
DR	Pfam; PF00135; Coesterase; 1.			
DR	PROSITE; PS00122; CARBOXYLESTERASE_B.1; 1.			
KW	Hydrolase.			
SC	SEQUENCE 570 AA; 65421 MW; 08AFEBEF284003BB CRC64;			

Query Match 96.3%; Score 1053; DB 5; Length 570;  
Best Local Similarity 96.6%; Pred. No. 2.5e-91;  
Matches 200; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 QTFDFISGKPTGSEDCILYLVNNDINPDKKRPVWVFTHGGFTTGEANRWNYGDPYFKK 60  
|||||  
DB 97 QTFDFISGKPTGSEDCILYLVNNDINPDKKRPVWVFTHGGFTTGEANRWNYGDPYFKK 156

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QY 61 PVLVTVOYRLGVLGFLSLKSENLNVPNGAGLKDQVVALRMFKSNIAIFGGDVNITVVG 120
DB 157 PVLVTVOYRLGVLGFLSLKSENLNVPNGAGLKDQVVALRMFKSNIAIFGGDVNITVVG 216
QY 121 ESAGGASTHYMTTEQTRGLFHRGIMSGNSMCSASTCQSBALTMARVYKGEENK 180
DB 217 ESAGGASTHYMTTEQTRGLFHRGIMSGNSMCSASTCQSBALTMARVYKGEENK 276
QY 181 DLEFLMKANPYDLIKEEPOVLTPERM 207
DB 277 DLEFLMKANPYDLIKEEPOVLTPERM 303

RESULT 2
ID Q90409 PRELIMINARY; PRT; 570 AA.
AC Q90409;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
OS Alpha E7 esterase.
GN AE7.
OC Haemolysis irritans irritans.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Muscidae; Muscidae; Haemolysis.
OX NCBI_Taxid=75445;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CAMP COOLEY 4/97;
RX MEDLINE=20445807; PubMed=10989298;
RA Guerrero F.D.;
RT "Cloning of a horn fly cDNA, HialphaE7, encoding an esterase whose
transcript concentration is elevated in diazinon-resistant flies."
RL Insect Biochem. Mol. Biol. 30:1107-1115(2000).
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL: AF139082; AAF14517.1;
DR HSSP: P37967; 1OE3.
DR InterPro: IPR002018; CarbesteraseB.
DR InterPro: IPR000379; Ser_estrs_site.
DR Pfam: PF00135; Coesterase; 1.
DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
KW Hydrolase.
SQ SEQUENCE 570 AA; 65613 MW; 18DA0A9A94AB970D CRC64;

Query Match 76.9%; Score 840; DB 5; Length 570;
Best Local Similarity 75.4%; Pred. No. 4e-71;
Matches 156; Conservative 20; Mismatches 31; Indels 0; Gaps 0;

```

```

DE 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DB Alpha esterase (LCAE7) (carboxylesterase).
GN LCAE7.
OS Lucilia cuprina (Greenbottle fly) (Australian sheep blowfly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Oestroidae; Calliphoridae; Lucilia.
OX NCBI_Taxid=7375;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LS2;
RA Newcomb R.D., East P.D., Russell R.J., Oakeshott J.G.;
RL Insect Mol. Biol. 5:0-0(0).
RN [2]
RP SEQUENCE OF 70-181 FROM N.A.
RC STRAIN=LS2;
RA Newcomb R.D., East P.D., Russell R.J., Oakeshott J.G.;
RL Insect Mol. Biol. 0:0-0(0).
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL: U56636; AAB6728.1;
DR EMBL: U49421; AAA92012.1;
DR HSSP: P37967; 1OE3.
DR InterPro: IPR002018; CarbesteraseB.
DR InterPro: IPR000379; Ser_estrs_site.
DR Pfam: PF00135; Coesterase; 1.
DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
KW Hydrolase.
SQ SEQUENCE 570 AA; 65416 MW; 399D7283A0F338FD CRC64;

Query Match 75.5%; Score 825; DB 5; Length 570;
Best Local Similarity 74.6%; Pred. No. 1.1e-69;
Matches 153; Conservative 25; Mismatches 27; Indels 0; Gaps 0;

```

DR InterPro: IPR000379; Ser\_estrs\_site.  
 DR Pfam: PF00135; Coesterase; 1.  
 DR PROSITE: PS00122; CARBOXYLESTERASE\_B\_1; 1.  
 KW Hydrolase.  
 FT NON\_TER 1 1  
 FT NON\_TER 556 556  
 SQ SEQUENCE 556 AA; 63397 MW; AF0F80A1D3C34425 CRC64;  
 Query Match 67.3%; Score 736; DB 5; Length 556;  
 Best Local Similarity 67.5%; Pred. No. 2.8e-61;  
 Matches 141; Conservative 25; Mismatches 41; Indels 2; Gaps 2;

OY 1 QPDIISGKPGSEDCILYNTNDLNPDKRPVNFHGGGFIIGEANRMYGPDYFMKK 60  
 DB 81 QVQFVFDKVEGSEDCILYNTNDLNPDKRPVNFHGGGFIIGEANRMYGPDYFMKK 140  
 OY 61 PVLVTVQYRLGLVGLFLSKSENLNVPNGNGLKQVMALEWFKSNIAIFGSDVDNITYFG 120  
 DB 141 DVLVTVIQRGLGALGFMGSLKSPELNVPNGNGLKQVLALEWFKSNIAIFGSDVDNITYFG 200  
 OY 121 ESAGASTHYMMITTEOTRGLFHRGIMSGNSMCSA-STECOSRALTMARVGYGGEENE 179  
 DB 201 ESAGASTHYMMITTEOTRGLFHRGIMSGNSMCSA-STECOSRALTMARVGYGGEENE 260  
 OY 180 KDLEFLMKANPYDLKEEPOVLT-PERM 207  
 DB 261 KDLEFLMKANPYDLKEEPOVLT-PERM 289

RESULT 5  
 OYVIB5 PRELIMINARY; PRT; 572 AA.  
 ID 09VIB5:  
 AC 09VIB5:  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
 DE ALPHA-EST7 OR CG112.  
 GN ALPHA-EST7 OR CG112.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OC NCBI\_TaxID=7227;  
 OX [1]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN-BERKELEY;  
 RC MEDLINE-20196006; PubMed-10731132;  
 RX Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 Amaratilake P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 Sulton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 Brandon R.C., Rogers Y.H.C., Blazer R.G., Chame M., Pfeiffer B.D.,  
 Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 April J.F., Agbayani A., An H.-J., Andrews-Plattner C., Baldwin D.,  
 Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 Beeson K.V., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 Borokova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,  
 Burkova D., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,  
 de Pallos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houch J.,  
 Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegami C.,  
 Jalali M.E., Kalush F., Karpen G.H., Ke Z., Kemison J.A., Ketchum K.A.,  
 Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 Liu X., Mettel B., McIntosh T.C., McLeod M.P., McPherson D.,  
 Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pauley J.M.,

Palazzo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 Shier B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 Sytkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,  
 Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 Ye J., Yen R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 GIBBS R.A., Myers E.W., Rubin G.M., Venter J.C.,  
 "The genome sequence of Drosophila melanogaster."  
 Science 287:2185-2195(2000).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BERKELEY;  
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,  
 Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,  
 Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,  
 Nuno J., Pauley J., Paragay V., Park S., Phuanavong S., Wan K.,  
 Yu C., Lewis S.E., Rubin G.M., Celniker S.,  
 Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.  
 RL -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.  
 CC EMBL: AE003671; AF54010.1; -;  
 DR EMBL: AY051473; AA92897.1; -;  
 DR HSSP: P21836; IMAA.  
 DR FLYBASE: FBgn0015575; alpha-Est7.  
 DR InterPro: IPR002018; Carboxylesterase.  
 DR InterPro: IPR000379; Ser\_estrs\_site.  
 DR Pfam: PF00135; Coesterase; 1.  
 DR PROSITE: PS00122; CARBOXYLESTERASE\_B\_1; 1.  
 DR KW Hydrolase.  
 SQ SEQUENCE 572 AA; 65435 MW; 693D9360DA18AE27 CRC64;  
 Query Match 67.3%; Score 736; DB 5; Length 572;  
 Best Local Similarity 67.5%; Pred. No. 2.9e-61;  
 Matches 141; Conservative 25; Mismatches 41; Indels 2; Gaps 2;

OY 1 QPDIISGKPGSEDCILYNTNDLNPDKRPVNFHGGGFIIGEANRMYGPDYFMKK 60  
 DB 97 QVQFVFDKVEGSEDCILYNTNDLNPDKRPVNFHGGGFIIGEANRMYGPDYFMKK 156  
 OY 61 PVLVTVQYRLGLVGLFLSKSENLNVPNGNGLKQVMALEWFKSNIAIFGSDVDNITYFG 120  
 DB 157 DVLVTVIQRGLGALGFMGSLKSPELNVPNGNGLKQVLALEWFKSNIAIFGSDVDNITYFG 216  
 OY 121 ESAGASTHYMMITTEOTRGLFHRGIMSGNSMCSA-STECOSRALTMARVGYGGEENE 179  
 DB 217 ESAGASTHYMMITTEOTRGLFHRGIMSGNSMCSA-STECOSRALTMARVGYGGEENE 276  
 OY 180 KDLEFLMKANPYDLKEEPOVLT-PERM 207  
 DB 277 KDLEFLMKANPYDLKEEPOVLT-PERM 305

RESULT 6  
 OYVIB5 PRELIMINARY; PRT; 345 AA.  
 ID 09VIB5:  
 AC 09VIB5:  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
 DE Alpha-esterase 7 (Fragment).  
 GN AEA7 OR AEA7.  
 OS Drosophila buzzatii (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OC NCBI\_TaxID=7264;  
 OX [1]  
 RN SEQUENCE FROM N.A.  
 RP Robin C., Claudianos C., Russell R.J., Oakeshott J.G.,  
 "The alpha-esterase cluster of Drosophila buzzatii."  
 Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.  
 DR EMBL: AF216215; AAF26729.1; .  
 DR HSP; P21836; IMAA.  
 DR FlyBase: FBgn0029447; DbnvAae7A.  
 DR InterPro: IPR002018; CarboxylesteraseB.  
 DR InterPro: IPR000379; Ser-estrs-site.  
 DR Pfam: PF00135; Coesterase\_1.  
 DR PROSITE: PS00122; CARBOXYLESTERASE\_B\_1; 1.  
 DR Hydrolyase.  
 KM NON\_TER 1  
 FT TER 345  
 SQ SEQUENCE 345 AA; 38472 MW; C08564A34E8C97A CRC64;  
 Query Match 67.3%; Score 735.5; DB 5; Length 345;  
 Best Local Similarity 68.0%; Pred. No. 1.6e-61;  
 Matches 140; Conservative 27; Mismatches 38; Indels 1; Gaps 1;  
 QY 1 QDTFISGKPTGSEDCLYNTYNDLNDKRRPVMVFHGGGFTFGANRMVGPDPYMK 60  
 Db 28 QVHFVPEBRESSECLLYNTYNNLSAPKRPVWVHGGGFTFGANRMVGPDPYMK 87  
 QY 61 PVLVTVQVRLGVLFGLSLKSENLPVGNAGLKDQVVALRPFKSNIAIFGVDNITVFG 120  
 Db 88 DVVTVTVQVRLGVLFGLSLKSENLPVGNAGLKDQVVALRPFKSNIAIFGVDNITVFG 147  
 QY 121 ESAGASTHYMIMTEQTRGLFHRGIMSGNSMCSA-STECOSRALFMKRVGYGGEENE 179  
 Db 148 ESAGASTHYMIMTEQTRGLFHRGIMSGNSMCSA-STECOSRALFMKRVGYGGEENE 179  
 QY 180 KDLEFLMKANPYDLIKEPQVLTPE 205  
 Db 208 KDVLQFLQTVRARDLIRVEQVLTPE 233  
 RESULT 7  
 Q91715 PRELIMINARY; PRT; 530 AA.  
 AC Q91715;  
 DT 01-MAR-2001 (Tremblrel. 16, Created)  
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)  
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)  
 DE Alpha-Est10 protein.  
 GN ALPHA-EST10 OR CG1131.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BERKELEY;  
 RX MEDLINE-20196006; PubMed-10731132;  
 RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner R.A., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Landell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,  
 RA Burlingame K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Paulis B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey J., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwa C.,  
 RA Jalali M., Kalish F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshireli A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusser D.R., Paclet J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spler E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svrlaks R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yen R.-E., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhou S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RL "The genome sequence of Drosophila melanogaster.";  
 CC Science 287:2185-2195(2000)  
 -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.  
 DR EMBL: AEO03671; AAC22202.1; .  
 DR HSP; P37967; I0E3.  
 DR FlyBase: FBgn0015569; alpha-Est10.  
 DR InterPro: IPR002018; CarboxylesteraseB.  
 DR InterPro: IPR000997; Cholinesterase.  
 DR InterPro: IPR000379; Ser-estrs-site.  
 DR Pfam: PF00135; Coesterase\_1.  
 DR PRINTS: PR00878; CHOLINESTRASE.  
 DR PROSITE: PS00122; CARBOXYLESTERASE\_B\_1; 1.  
 KM Hydrolyase.  
 SQ SEQUENCE 530 AA; 59739 MW; F9011F52DEAD07F1 CRC64;  
 Query Match 54.4%; Score 595; DB 5; Length 530;  
 Best Local Similarity 55.7%; Pred. No. 6.2e-46;  
 Matches 113; Conservative 31; Mismatches 59; Indels 0; Gaps 0;  
 QY 1 QDTFISGKPTGSEDCLYNTYNDLNDKRRPVMVFHGGGFTFGANRMVGPDPYMK 60  
 Db 62 QTHMFEKRYAGSEDCLYNTYNNLSAPKRPVWVHGGGFTFGANRMVGPDPYMK 121  
 QY 61 PVLVTVQVRLGVLFGLSLKSENLPVGNAGLKDQVVALRPFKSNIAIFGVDNITVFG 120  
 Db 122 DVVTVTVQVRLGVLFGLSLKSENLPVGNAGLKDQVVALRPFKSNIAIFGVDNITVFG 181  
 QY 121 ESAGASTHYMIMTEQTRGLFHRGIMSGNSMCSA-STECOSRALFMKRVGYGGEENE 180  
 Db 182 ESAGASTHYMIMTEQTRGLFHRGIMSGNSMCSA-STECOSRALFMKRVGYGGEENE 180  
 QY 181 DLEFLMKANPYDLIKEPQVLT 203  
 Db 242 AIFELRSMGSEIVKATVLS 264  
 RESULT 8  
 Q24204 PRELIMINARY; PRT; 549 AA.  
 AC Q24204;  
 DT 01-NOV-1996 (Tremblrel. 01, Created)  
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)  
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)  
 DE Alpha-esterase (Fragment).  
 GN ALPHA-EST10 OR AE10 OR CG1131.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC Roblin C., Medveczky K.M., Russell R.J., Oakeshott J.G.;  
 RA J. Mol. Evol. 0:0-0(0).  
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.  
 DR EMBL: U51054; AAB01153.1; .  
 DR HSP; P21836; IMAA.  
 DR FlyBase: FBgn0015569; alpha-Est10.



KW Hydrolase.  
SQ SEQUENCE 567 AA; 64831 MW; 07D6ACC72786F14A CRC64;

Query Match 53.8%; Score 587.5; DB 5; Length 567;  
Best Local Similarity 54.9%; Pred. No. 3.5e-47;  
Matches 112; Conservative 32; Mismatches 60; Indels 1; Gaps 1;

QY 1 QDIFISGKPTGSEDCILYLVNTNDLPDKRPVWFHIGGFGFGEARNNMGDPYFVK 60  
DB 90 QNVIVLKVOGSEDCILYLVNTRELPHRPLVLTWITGGGFQMGESRDLYSPDYIME 149  
QY 61 PVLVTVQYRLGVLFSLIKSENLVNPGNAGLKDOVALLRWFKSNIAIFGGDVNITVFG 120  
DB 150 HVLVVISIRLGLFSLADELDVPGNAGLKDOVALLRWVKNRCQFFGGDPDNITVFG 209  
QY 121 ESAGASTHYMMITTEOTRGLEFRGIMSGNSMCSASTECQ-SRALLMARKVYKGEENE 179  
DB 210 ESAGASTHYMMITDOAGLGFHKTIVMSGSALAPMAQTPHTINWPYRLAQTGYTDAND 269  
QY 180 KDLEFLMKANPYDLKEEPOVLTPE 205  
DB 270 RDIFFALKKCKKASSMLKVAEDITIME 295

## RESULT 11

Q24202 PRELIMINARY; PRT; 558 AA.

AC Q24202.  
DT 01-NOV-1996 (Tremblrel. 01, Created)  
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)  
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)  
DE Alpha esterase (Fragment).  
GN ALPHA-EST8 OR CG1121.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Robin C., Medveczky K.M., Russell R.J., Oakeshott J.G.;  
RL J. Mol. Evol. 0:0-0(0).  
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.  
DR EMBL: U51052; AAB01151.1; -.  
DR HSSP: P37967; IQE3.  
DR Flybase: FBgn0015576; alpha-Est8.  
DR InterPro: IPR002018; Carboxylesterase.  
DR Pfam: PF00135; Coesterase\_1.  
DR PROSITE: PS00122; CARBOXYLESTERASE\_B\_1; 1.  
KW Hydrolase.  
FT NON\_TER  
SQ SEQUENCE 558 AA; 63916 MW; BFF62C8FF212720 CRC64;

Query Match 53.7%; Score 586.5; DB 5; Length 558;  
Best Local Similarity 54.4%; Pred. No. 4.2e-47;  
Matches 112; Conservative 33; Mismatches 60; Indels 1; Gaps 1;

QY 1 QDIFISGKPTGSEDCILYLVNTNDLPDKRPVWFHIGGFGFGEARNNMGDPYFVK 60  
DB 81 QNVIVLKVOGSEDCILYLVNTRELPHRPLVLTWITGGGFQMGESRDLYSPDYIME 140  
QY 61 PVLVTVQYRLGVLFSLIKSENLVNPGNAGLKDOVALLRWFKSNIAIFGGDVNITVFG 120  
DB 141 HVLVVISIRLGLFSLADELDVPGNAGLKDOVALLRWVKNRCQFFGGDPDNITVFG 200  
QY 121 ESAGASTHYMMITTEOTRGLEFRGIMSGNSMCSASTECQ-SRALLMARKVYKGEENE 179  
DB 201 ESAGASTHYMMITDOAGLGFHKTIVMSGSALAPMAQTPHTINWPYRLAQTGYTDAND 260  
QY 180 KDLEFLMKANPYDLKEEPOVLTPE 205

DB 261 RDIFFALKKCKKASSMLKVAEDITIME 286

## RESULT 12

Q9N151 PRELIMINARY; PRT; 297 AA.

AC Q9N151.  
DT 01-OCT-2000 (Tremblrel. 15, Created)  
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)  
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)  
DE Alpha-esterase 9 (Fragment).  
GN AE9A OR AE9.  
OS Drosophila buzzatii (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7264;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Robin C., Claudianos C., Russell R.J., Oakeshott J.G.;  
RT "The alpha-esterase cluster of Drosophila buzzatii."  
RL Submitted (DEC-1999) to the EMBL/GenBank/DBD databases.  
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.  
DR EMBL: AF216217; AAF26731.1; -.  
DR HSSP: P37967; IQE3.  
DR Flybase: FBgn0029445; DbuzAE9A.  
DR InterPro: IPR002018; Carboxylesterase.  
DR Pfam: PF00135; Coesterase\_1.  
DR PROSITE: PS00122; CARBOXYLESTERASE\_B\_1; 1.  
KW Hydrolase.  
FT NON\_TER  
SQ SEQUENCE 297 AA; 33635 MW; 89CF7761871B362D CRC64;

Query Match 53.5%; Score 585; DB 5; Length 297;  
Best Local Similarity 54.6%; Pred. No. 2.5e-47;  
Matches 112; Conservative 33; Mismatches 60; Indels 0; Gaps 0;

QY 1 QDIFISGKPTGSEDCILYLVNTNDLPDKRPVWFHIGGFGFGEARNNMGDPYFVK 60  
DB 81 QKHVFEMTGGSEDCILYLVNTKNLYPVKPMVWITGGGFQFEASRECYSPDYLTRE 140  
QY 61 PVLVTVQYRLGVLFSLIKSENLVNPGNAGLKDOVALLRWFKSNIAIFGGDVNITVFG 120  
DB 141 DVVVISINRYRLGLFSLADELDVPGNAGLKDOVALLRWVKNRCQFFGGDPDNITVFG 200  
QY 121 ESAGASTHYMMITTEOTRGLEFRGIMSGNSMCSASTECQSRALLMARKVYKGEENE 180  
DB 201 DSAGSASTHYMMITTEOTRGLEFRGIMSGNSMCSASTECQSRALLMARKVYKGEENE 260  
QY 181 DLEFLMKANPYDLKEEPOVLTPE 205  
DB 261 EWWEFLKNAKGSIDIKANGELCTIXE 285

## RESULT 13

Q9VIB0 PRELIMINARY; PRT; 554 AA.

AC Q9VIB0.  
DT 01-MAY-2000 (Tremblrel. 13, Created)  
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)  
DE Alpha-EST9 protein.  
GN ALPHA-EST9 OR CG1128.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA STRAIN-BERKELEY.  
RX MEDLINE=20196006; PubMed=10731132;



RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Ananides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers J.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Mikos G.L.G.,  
 RA April J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,  
 RA Borokova D., Botchan M.R., Bouck J., Brockstein P., Brotler P.,  
 RA Burlingame K., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrelia S., Fleischmann W.,  
 RA Fodor C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegawa C.,  
 RA Jaitani M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Mekulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclik J.M.,  
 RA Palazzolo R., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Sytkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhan Q., Zhao Q., Zheng L.,  
 RA Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,  
 RT "The genome sequence of Drosophila melanogaster".  
 RL Science 287:2185-2195(2000).  
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.  
 DR EMBL: AE003671; AAF54014.1; -.  
 DR HSSP: P37967; 10E3.  
 DR FlyBase: FBgn0015577; alpha-Est9.  
 DR InterPro: IPR002018; Carboxylesterase.  
 DR InterPro: IPR000997; Carboxylesterase.  
 DR InterPro: IPR000379; Ser-estrs-site.  
 DR Pfam: PF00135; Coesterase; 1.  
 DR PRINTS: PR00878; CHOLNESTRASE.  
 DR PROSITE: PS00122; CARBOXYLESTERASE\_B\_1; 1.  
 KW Hydroxylase.  
 SQ SEQUENCE 554 AA; 63670 MW; 0A72368389DFPC2B CRC64;

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 Best Local Similarity 54.6%; Pred. No. 1, le-46;  
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 DB 81 OHKFEFEMTGDSEDCILYNTDNLNPKRRPVVFHGGGTFEGANRMWGPDPYFMKK 140  
 QY 61 PVLVTVVYRGLVGLFSLKSENINVPNAGLKDQVMAIRFMSNTAIFGGVDNITVFG 120  
 DB 141 DVVVISINIRGLPLGLCLDDELVDVPGNAGLKDQVMAIRFMSNTAIFGGVDNITVFG 200  
 QY 121 ESAGGASTHYMMITEQTRGLFHGIMSGNSKSSASTECOSALIMAKRVYKGEENEK 180  
 DB 201 DSAGASVHYMMITEQTRGLFHGIMSGNSKSSASTECOSALIMAKRVYKGEENEK 260  
 QY 181 DLEFLMKANPYDLIKEEPOVLTPPE 205  
 DB 261 DWMEFLKNAKGEIIRKANGELCID 285  
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 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)  
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)  
 DE Alpha-esterase 8 (Fragment).  
 GN AEA8 OR AEB.  
 OS Drosophila buzzatii (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OC NCB1\_Taxid=7264;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Robin C., Claudianos C., Russell R.J., Oakeshott J.G.;  
 RT "The alpha-esterase cluster of Drosophila buzzatii".  
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.  
 DR EMBL: AF216216; AAF26730.1; -.  
 DR HSSP: P21836; 1MAA.  
 DR FlyBase: FBgn0029446; DbuzaaE8a.  
 DR InterPro: IPR002018; Carboxylesterase.  
 DR InterPro: IPR000379; Ser-estrs-site.  
 DR Pfam: PF00135; Coesterase; 1.  
 DR PROSITE: PS00122; CARBOXYLESTERASE\_B\_1; 1.  
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 FT NON\_TER  
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 QY 61 PVLVTVVYRGLVGLFSLKSENINVPNAGLKDQVMAIRFMSNTAIFGGVDNITVFG 120  
 DB 88 HVLVTVVYRGLVGLFSLKSENINVPNAGLKDQVMAIRFMSNTAIFGGVDNITVFG 147  
 QY 121 ESAGGASTHYMMITEQTRGLFHGIMSGNSKSSASTECOSALIMAKRVYKGEENEK 180  
 DB 148 ESAGGASTHYMMITEQTRGLFHGIMSGNSKSSASTECOSALIMAKRVYKGEENEK 207  
 QY 181 DLEFLMKANPYDLIKEEPOVLTPPE 205  
 DB 208 EIFKHLOCCAKSSMLRMAEGIVIME 232  
 RESULT 15

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 AC 024194;  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)  
 DE Alpha-esterase E1.  
 GN ALPHA-EST1 OR AEL OR CG1031.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OC NCB1\_Taxid=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CANTON S;  
 RX MEDLINE=97056255; PubMed=8900595;  
 RA Russell R.J., Robin C., Kostakov P., Newcomb R.D., Boyce T.M.,  
 Medveczky K.M., Oakeshott J.G.;

RT "Molecular cloning of an alpha-esterase gene cluster on chromosome 3R  
RT of *Drosophila melanogaster*.".  
RL Insect Biochem. Mol. Biol. 26:235-247(1996).  
CC -1. SIMILARITY: BELONGS TO THE TYPE-B CARBOXYL-ESTERASE/LIPASE FAMILY.  
DR EMBL; U51043; AB01142.1; -.  
DR HSSP; P21836; 1MAH.  
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DR InterPro; IPR002018; CarboxylesteraseB.  
DR InterPro; IPR000379; Ser\_ests\_site.  
DR Pfam; PF00135; Coesterase; 1.  
KW Hydrolase.  
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GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using sw model

Run on: April 4, 2003, 09:10:57 ; Search time 5.7278 Seconds  
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Title: US-09-776-910-15

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Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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- 3: /cgn2.6/ptodata/1/1aa/6A.COMB.pep.\*
- 4: /cgn2.6/ptodata/1/1aa/6B.COMB.pep.\*
- 5: /cgn2.6/ptodata/1/1aa/PCITUS.COMB.pep.\*
- 6: /cgn2.6/ptodata/1/1aa/Backfilest.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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5	826	75.6	570	4	US-09-068-960-4
6	826	75.6	570	4	US-09-068-960-6
7	826	75.6	570	4	US-09-068-960-10
8	825	75.5	570	2	US-08-669-524-3
9	825	75.5	570	4	US-09-068-960-8
10	811	74.2	570	2	US-08-669-524-4
11	736	67.3	572	2	US-08-669-524-8
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17	428	39.2	550	3	US-09-005-051-19
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31	348.5	31.9	575	1	US-08-348-920-1	Sequence 1, Appl
32	342.5	31.3	498	4	US-09-058-260-16	Sequence 16, Appl
33	342.5	31.3	503	2	US-08-781-802-2	Sequence 2, Appl
34	342.5	31.3	503	2	US-08-781-802-10	Sequence 10, Appl
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36	342.5	31.3	503	4	US-08-694-078-2	Sequence 2, Appl
37	342.5	31.3	503	4	US-08-694-078-2	Sequence 2, Appl
38	342.5	31.3	503	4	US-09-058-260-12	Sequence 12, Appl
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43	339.5	31.1	503	4	US-08-348-920-2	Sequence 2, Appl
44	336	30.7	573	6	US-09-058-260-26	Sequence 26, Appl
45	336	30.7	602	3	US-08-446-100-1	Sequence 1, Appl

## ALIGNMENTS

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US-09-068-960-15  
Sequence 15, Application US/09068960A  
Patent No. 6235515  
GENERAL INFORMATION:  
APPLICANT: Commonwealth Scientific and Industrial Rsrch. Org.  
TITLE OF INVENTION: MALATHION CARBOXYLESTERASE  
FILE REFERENCE: Attorney Docket No. 6235515 50179-051  
CURRENT FILING DATE: 1998-05-20  
EARLIER FILING DATE: 1996-11-22  
EARLIER APPLICATION NUMBER: PCT/AU96/00746  
EARLIER FILING DATE: 1996-11-22  
EARLIER APPLICATION NUMBER: AU 6751  
NUMBER OF SEQ ID NOS: 43  
SOFTWARE: Patentln Ver. 2.0  
SEQ ID NO 15  
LENGTH: 207  
TYPE: PRT  
ORGANISM: Musca domestica  
US-09-068-960-15

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Patent No. 6235515  
GENERAL INFORMATION:  
APPLICANT: Commonwealth Scientific and Industrial Rsrch. Org.  
TITLE OF INVENTION: MALATHION CARBOXYLESTERASE





VERSION AI109901.1 GI:3478225  
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 SOURCE fruit fly.  
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 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
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 Ephydroidea; Drosophilidae; *Drosophila*.  
 1 (bases 1 to 646)  
 REFERENCE Harvey D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G.,  
 Lewis, S. and Rubin, G.M.  
 BDGP/HHMI *Drosophila* EST Project  
 JOURNAL Unpublished (2001)  
 COMMENT Contact: Stapleton, M.  
 BDGP  
 Lawrence Berkeley National Lab  
 One Cyclotron Rd, Berkeley, CA 94720, USA  
 Fax: 510 486 6798  
 Email: <http://www.fruitfly.org/EST>, [est@fruitfly.berkeley.edu](mailto:est@fruitfly.berkeley.edu)  
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 Ephydroidea; Drosophilidae; *Drosophila*.  
 1 (bases 1 to 646)  
 REFERENCE Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G.,  
 Lewis, S. and Rubin, G.M.  
 BDGP/HHMI *Drosophila* EST Project  
 JOURNAL Unpublished (2001)  
 COMMENT Contact: Stapleton, M.  
 BDGP  
 Lawrence Berkeley National Lab  
 One Cyclotron Rd, Berkeley, CA 94720, USA  
 Fax: 510 486 6798  
 Email: <http://www.fruitfly.org/EST>, [est@fruitfly.berkeley.edu](mailto:est@fruitfly.berkeley.edu)  
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 ligated into pot2. Plasmid cDNA library."  
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 Best Local Similarity 64.8%; Pred. No. 1.6e-55;  
 Matches 361; Conservative 0; Mismatches 196; Indels 0; Gaps 0;  
 Db 1 ATGATTTCAACGTTAGTTGATGAGAAATTAATAAGAGATTAATGATGAAT 60  
 89 ATGATTAAGAAACCTCGCTTTGTGTGAGCGCTTGCGGCTGACCAACATCAGCAT 148  
 Qy 61 AAGTTTAACTATCGTTTAACTACCAATGAACGCTGTGAGTGAATGATATGCG 120  
 149 AAGATCCAGCATATCGCGACGACCAATGAACATGATGTCGACACGAGTACGGC 208  
 Db 121 AAAGTGAAGCGCTTAACGTTAATCTGTACGATGATTCCTACTACAGTTTGAGGT 180  
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 Qy 181 ATACGTCAGCCCAACGCCAGTGGGTGAGCTGAGATTTAAAGACCCAGGACCA 240  
 269 ATCCGTCAGCCCAACGCCAGTGGGTGAGCTGAGATTTAAAGCCCTCAGAGGCCAT 328  
 Db 241 CCTGGAGTGTGTGCTGATGTTTGAATCAATAAAGATAGTCAAGTCAAGTATTT 300







GenCore version 5.1.4\_p5-4578  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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6	1703.4	99.4	1713	4	US-08-669-524-2
7	1678.2	98.0	1713	2	US-08-669-524-14
8	1678.2	98.0	1713	2	US-08-669-524-15
9	1678.2	98.0	1713	2	US-08-669-524-16
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32	138.6	8.1	2144	3	US-08-747-221B-59	Sequence 59, Appl
33	138.6	8.1	2144	4	US-09-005-051-57	Sequence 57, Appl
34	138.6	8.1	2144	4	US-09-005-051-59	Sequence 59, Appl
35	138.6	8.1	1515	3	US-08-747-221B-16	Sequence 16, Appl
36	138.6	8.1	1515	3	US-08-747-221B-17	Sequence 17, Appl
37	138.6	8.1	1515	4	US-09-005-051-16	Sequence 16, Appl
38	138.6	8.1	1515	4	US-09-005-051-17	Sequence 17, Appl
39	138.6	8.1	1982	3	US-08-747-221B-13	Sequence 13, Appl
40	138.6	8.1	1982	3	US-08-747-221B-15	Sequence 15, Appl
41	138.6	8.1	1982	4	US-09-005-051-13	Sequence 13, Appl
42	138.6	8.1	1982	4	US-09-005-051-15	Sequence 15, Appl
43	138.6	8.1	1694	3	US-09-136-421-11	Sequence 11, Appl
44	138.6	8.1	2989	1	US-07-927-851-1	Sequence 1, Appl
45	138.6	8.1	2989	1	US-08-453-323-1	Sequence 1, Appl

#### ALIGNMENTS

RESULT 1  
US-09-068-960-9  
; Sequence 9, Application US/09068960A  
; Patent No. 6235515  
; GENERAL INFORMATION:  
; APPLICANT: Commonwealth Scientific and Industrial Rsrch. Org.  
; TITLE OF INVENTION: MALATHION CARBOXYESTERASE  
; FILE REFERENCE: Attorney Docket No. 6235515 50179-051  
; CURRENT APPLICATION NUMBER: US/09/068,960A  
; EARLIER FILING DATE: 1998-05-20  
; EARLIER APPLICATION NUMBER: PCT/AU96/00746  
; EARLIER FILING DATE: 1996-11-22  
; EARLIER APPLICATION NUMBER: AU 6751  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: Patentlin Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 1713  
; TYPE: DNA  
; ORGANISM: Lucilia cuprina  
; US-09-068-960-9

Query Match 100.0%; Score 1713; DB 4; Length 1713;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1713; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ATGATTTTCAACGTTAGTTGATGAGAAATTTAAATGAAGTTAAATGATTTGAAT	60
DB	1	ATGATTTTCAACGTTAGTTGATGAGAAATTTAAATGAAGTTAAATGATTTGAAT	60
QY	61	AAAGTTTAAACCTATCTTAACTACCAATGAACGTTAGTGAATGATTTGAT	120
DB	61	AAAGTTTAAACCTATCTTAACTACCAATGAACGTTAGTGAATGATTTGAT	120
QY	121	AAAGTTTAAACGTTAAACGTTAACTAGTGTAGATTTTAAAGACCCGACGAC	180
DB	121	AAAGTTTAAACGTTAAACGTTAACTAGTGTAGATTTTAAAGACCCGACGAC	180
QY	181	ATACCGTAGCGCCCAACGCGAGTGGTGTAGATTTTAAAGACCCGACGAC	240
DB	181	ATACCGTAGCGCCCAACGCGAGTGGTGTAGATTTTAAAGACCCGACGAC	240
QY	241	CCCTGGATGCTGTGCTGATTTTGAATCATTAAGATTAAGTCAAGTGTAT	300
DB	241	CCCTGGATGCTGTGCTGATTTTGAATCATTAAGATTAAGTCAAGTGTAT	300
QY	301	ATAAGGCGCAAGTGTGTGCTGATTTTGAATCATTAAGTCAAGTGTAT	360
DB	301	ATAAGGCGCAAGTGTGTGCTGATTTTGAATCATTAAGTCAAGTGTAT	360

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Db      1441  AATCAATTTGGCCAAACGATATGCTCTAAAGAAATCCGGGTAAATACAAACAAATTGAACGTATG 1500
|||
QY      1501  ACTGCTATATGATACATTTGGCCACACACTGGTAACTCTATACCAATGAAATGAGAGT 1560
|||
Db      1501  ACTGCTATATGATACATTTGGCCACACACTGGTAACTCTATACCAATGAAATGAGAGT 1560
|||
QY      1561  ATGGAAGAAATGTTTCTGGGATCCCAATTAAAGAAATCCGATGAAGTATCAAGTGTTGAAT 1620
|||
Db      1561  ATGGAAGAAATGTTTCTGGGATCCCAATTAAAGAAATCCGATGAAGTATCAAGTGTTGAAT 1620
|||
QY      1621  ATTATGATGATGATGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
|||
Db      1621  ATTATGATGATGATGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
|||
QY      1681  TCGATGTTTGAAGAAACATAGAGATTTATTTTAA 1713
|||
Db      1681  TCGATGTTTGAAGAAACATAGAGATTTATTTTAA 1713
|||

RESULT 2
US-09-068-960-1
; Sequence 1, Application US/09068960A
; Patent No. 6235515
; GENERAL INFORMATION:
; APPLICANT: Commonwealth Scientific and Industrial Rsrch. Org.
; TITLE OF INVENTION: MALATHION CARBOXYLESTERASE
; FILE REFERENCE: Attorney Docket No. 6235515 50179-051
; CURRENT APPLICATION NUMBER: US/09/068,960A
; EARLIER FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: PCT/US96/00746
; EARLIER FILING DATE: 1996-11-22
; EARLIER APPLICATION NUMBER: AU 6751
; EARLIER FILING DATE: 1995-11-23
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1713
; TYPE: DNA
; ORGANISM: Lucilia cuprina
US-09-068-960-1

Query Match          99.9%; Score 1711.4; DB 4; Length 1713;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1712; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  ATGAATTTCAAGCTTAGTTGATGGAGAAATTAATGGAAGATTAATATGATGGAAT 60
|||
Db      1  ATGAATTTCAAGCTTAGTTGATGGAGAAATTAATGGAAGATTAATATGATGGAAT 60
|||
QY      61  AAGTTTTTAACTATCGTTTAACTACCAATGAACGGTGTAGCGTGAACACTGAATATGCG 120
|||
Db      61  AAGTTTTTAACTATCGTTTAACTACCAATGAACGGTGTAGCGTGAACACTGAATATGCG 120
|||
QY      121  AAGTGAAGAAAGCGGTTAAAGCTTAACTACGTGTACGATGATTCCTACTACAGTTTGAAGGT 180
|||
Db      121  AAGTGAAGAAAGCGGTTAAAGCTTAACTACGTGTACGATGATTCCTACTACAGTTTGAAGGT 180
|||
QY      181  ATACCGTACGCCCAACCGCCAGTCAGTGTAGAGTGAATTTAAAGCAACCCAGCGACCAACA 240
|||
Db      181  ATACCGTACGCCCAACCGCCAGTCAGTGTAGAGTGAATTTAAAGCAACCCAGCGACCAACA 240
|||
QY      241  CCCTGGGATGGTGTGCGGTGATTTGTCATCATTAAGAATAGTCAGTCAAGTTGATTTT 300
|||
Db      241  CCCTGGGATGGTGTGCGGTGATTTGTCATCATTAAGAATAGTCAGTCAAGTTGATTTT 300
|||
QY      301  ATTAAGGGGCAAAAGTGTGGGCTCAGAGGATTTGCTATACCTAAAGTCTATACGATATAT 360
|||
Db      301  ATTAAGGGGCAAAAGTGTGGGCTCAGAGGATTTGCTATACCTAAAGTCTATACGATATAT 360
|||
QY      361  CTAAATCCCGAAACTAAACGTCGCCGTTTATATACATACATACATGCTGTGTATATATATC 420
|||
Db      361  CTAAATCCCGAAACTAAACGTCGCCGTTTATATACATACATACATGCTGTGTATATATATC 420
|||

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QY 181 ATACCGTAGCCCAACGCCAGTGGGTGAGCTGATTTAAAGACCCACGCCACA 240
DB 181 ATACCGTAGCCCAACGCCAGTGGGTGAGCTGATTTAAAGACCCACGCCACA 240
QY 241 CCTGGGATGTGTGGGTGATTTGGCAATCAATAAGATGACGAGTGTATTT 300
DB 241 CCTGGGATGTGTGGGTGATTTGGCAATCAATAAGATGACGAGTGTATTT 300
QY 301 ATACGGGCAAAAGTGTGTGCTAGAGAGTGTCTATACCTAAGTGTCTATAC 360
DB 301 ATACGGGCAAAAGTGTGTGCTAGAGAGTGTCTATACCTAAGTGTCTATAC 360
QY 361 CTAAATCCCAAACTAAACGCTCCGTTTATATACATACATGAGTGTATATC 420
DB 361 CTAAATCCCAAACTAAACGCTCCGTTTATATACATACATGAGTGTATATC 420
QY 421 GGTGAAATCATGTGTATGTATGTCTGATTTATTTCAATTTAAAGATGTG 480
DB 421 GGTGAAATCATGTGTATGTATGTCTGATTTATTTCAATTTAAAGATGTG 480
QY 481 ATTAACCTAATATCTGTTGGAGCTCTAGTCTTCTAAGTTAAATTCAGACCT 540
DB 481 ATTAACCTAATATCTGTTGGAGCTCTAGTCTTCTAAGTTAAATTCAGACCT 540
QY 541 AATGCGCCGTAATGCGGCTTAAGATCAAGTCATGCGCTTGGATTAAAT 600
DB 541 AATGCGCCGTAATGCGGCTTAAGATCAAGTCATGCGCTTGGATTAAAT 600
QY 601 AATGCGCCGTAATGCGGCTTAAGATCAAGTCATGCGCTTGGATTAAAT 660
DB 601 AATGCGCCGTAATGCGGCTTAAGATCAAGTCATGCGCTTGGATTAAAT 660
QY 661 GGTGCTCTACCCCACTAGTATGTATTAACGAAACCAATCGCGTCTTTCAT 720
DB 661 GGTGCTCTACCCCACTAGTATGTATTAACGAAACCAATCGCGTCTTTCAT 720
QY 721 ATACTAATGTCGGGTATGCTATTTGCTATGCTAATACCAATGTCATGTC 780
DB 721 ATACTAATGTCGGGTATGCTATTTGCTATGCTAATACCAATGTCATGTC 780
QY 781 TTTCACCTTACCAATGTCGGGTATGCTAATGCTAATGTCATGTCATGTC 840
DB 781 TTTCACCTTACCAATGTCGGGTATGCTAATGCTAATGTCATGTCATGTC 840
QY 841 TTTCACCTTACCAATGTCGGGTATGCTAATGCTAATGTCATGTCATGTC 900
DB 841 TTTCACCTTACCAATGTCGGGTATGCTAATGCTAATGTCATGTCATGTC 900
QY 901 GAAGAGCGTACAAATTAAGTGTATGCTTGTGCTCCACTGTTGAGCCATFAC 960
DB 901 GAAGAGCGTACAAATTAAGTGTATGCTTGTGCTCCACTGTTGAGCCATFAC 960
QY 961 GGTGATTTGCTTACCAAACTCTCGGAATGTTAAACCTGTTGGGTAATTC 1020
DB 961 GGTGATTTGCTTACCAAACTCTCGGAATGTTAAACCTGTTGGGTAATTC 1020
QY 1021 ATACCACTATGATGGGTAACCTTCAATGAGGCTATTTTCACTTCAATCTTA 1080
DB 1021 ATACCACTATGATGGGTAACCTTCAATGAGGCTATTTTCACTTCAATCTTA 1080
QY 1081 CAATGCGCTATGCTTAAAGAAATGGAATCTGTCAATTTTGTCCAAAGTAAT 1140
DB 1081 CAATGCGCTATGCTTAAAGAAATGGAATCTGTCAATTTTGTCCAAAGTAAT 1140
QY 1141 GGTGATGCTGAGACGCGCCGAGAGACCTTGAATGGTGTCTAAATTAAGGCT 1200
DB 1141 GGTGATGCTGAGACGCGCCGAGAGACCTTGAATGGTGTCTAAATTAAGGCT 1200
QY 1201 CATGTTACAGAGAAACACCAAGAGTGTATTTATGATCTTGTCTACATCTAT 1260
DB 1201 CATGTTACAGAGAAACACCAAGAGTGTATTTATGATCTTGTCTACATCTAT 1260

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QY 1261 TTCTGTTCCCATGATCGTTTGTTCATTAAGCTTTCATACACACCTCCGATACCC 1320
DB 1261 TTCTGTTCCCATGATCGTTTGTTCATTAAGCTTTCATACACACCTCCGATACCC 1320
QY 1321 GTTACTTTGATGCTTTCGACTTCGATTTGGGAAGATCTTATCAATCCCTATGATATG 1380
DB 1321 GTTACTTTGATGCTTTCGACTTCGATTTGGGAAGATCTTATTAATCCCTATGATATG 1380
QY 1381 CGTATGAGCTGTGTAAAGGCTGTAGTATGCTATGATGATTAATTAATCTTCTTCG 1440
DB 1381 CGTATGAGCTGTGTAAAGGCTGTAGTATGCTATGATGATTAATTAATCTTCTTCG 1440
QY 1441 AATCAATTTGGCCAAACGATATGCTTAAAGATGCGCTGAATTCAAACATTTGAACGATG 1500
DB 1441 AATCAATTTGGCCAAACGATATGCTTAAAGATGCGCTGAATTCAAACATTTGAACGATG 1500
QY 1501 ACTGATATGATGATACATTTTCCACAGCTGATGCTTATACATGAAATGAGGT 1560
DB 1501 ACTGATATGATGATACATTTTCCACAGCTGATGCTTATACATGAAATGAGGT 1560
QY 1561 ATGGAATGTTTCTGATCCATTAAGAAATCCGATGAGTATACAGTGTGAT 1620
DB 1561 ATGGAATGTTTCTGATCCATTAAGAAATCCGATGAGTATACAGTGTGAT 1620
QY 1621 ATTAATGATGATTAATTAAGATGATGCTTAAATGCTTAAATTAATTAAGATGAGGAG 1680
DB 1621 ATTAATGATGATTAATTAAGATGATGCTTAAATGCTTAAATTAATTAAGATGAGGAG 1680
QY 1681 TCGATGTTTGAAGAAACATAGATTTATTTAG 1713
DB 1681 TCGATGTTTGAAGAAACATAGATTTATTTAG 1713

RESULT 6
US-09-960-7
: Sequence 7, Application US/09068960A
: Patent No. 6235515
: GENERAL INFORMATION:
: APPLICANT: Commonwealth Scientific and Industrial Rsrch. Org.
: TITLE OF INVENTION: MALATHION CARBOXYLESTERASE
: FILE REFERENCE: Attorney Docket No. 6235515 50179-051
: CURRENT APPLICATION NUMBER: US/09/068, 960A
: EARLIER FILING DATE: 1998-05-20
: EARLIER APPLICATION NUMBER: PCT/AU96/00746
: EARLIER FILING DATE: 1996-11-22
: EARLIER APPLICATION NUMBER: AU 6751
: NUMBER OF SEQ ID NOS: 43
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 7
: LENGTH: 1713
: TYPE: DNA
: ORGANISM: Lucilia cuprina
US-09-960-7

Query Match 99.4%; Score 1703.4; DB 4; Length 1713;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1707; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 ATGATTTCAACGTTAGTTGATGAGAAATTAATAATGGAATTAATGATGAAAT 60
DB 1 ATGATTTCAACGTTAGTTGATGAGAAATTAATAATGGAATTAATGATGAAAT 60
QY 61 AAGTTTAAACCTATGCTTAACTACCAATGAACCGGTGATGCTGAACCTGAATATGCG 120
DB 61 AAGTTTAAACCTATGCTTAACTACCAATGAACCGGTGATGCTGAACCTGAATATGCG 120
QY 121 AAAGTGAAGCGCTTAAACGTTTAACTGTGTACGATGATTTCTACTACAGTTTGAGGCT 180
DB 121 AAAGTGAAGCGCTTAAACGTTTAACTGTGTACGATGATTTCTACTACAGTTTGAGGCT 180
QY 181 ATACCGTAGCCCAACGCCAGTGGGTGAGCTGATTTAAAGACCCACGCCACA 240
DB 181 ATACCGTAGCCCAACGCCAGTGGGTGAGCTGATTTAAAGACCCACGCCACA 240

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TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-669-524-2

Query Match 98.0%; Score 1678.2; DB 2; Length 1713;  
Best Local Similarity 98.1%; Pred. No. 0;  
Matches 1680; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 1 ATGAATTTCAACGTTAGTTGATGAGAAATTAATAAGAGATTAATGATGAAAT 60  
DB 1 ATGAATTTCAACGTTAGTTGATGAGAAATTAATAAGAGATTAATGATGAAAT 60  
QY 61 AAGTTTTAACTATCGTTTAACTACCAATGAACGGGTGAGCTGAATGATGCT 120  
DB 61 AAGTTTTAACTATCGTTTAACTACCAATGAACGGGTGAGCTGAATGATGCT 120  
QY 121 AAGTGAAGGCGTTAAACGTTTAACTAGTGTAGATGCTTCTCTCTCTCTCT 180  
DB 121 AAGTGAAGGCGTTAAACGTTTAACTAGTGTAGATGCTTCTCTCTCTCTCT 180  
QY 181 ATACCGTACGCCAACCGCCAGTGGTGAGCTGAGATTTAAAGCACCACGACACA 240  
DB 181 ATACCGTACGCCAACCGCCAGTGGTGAGCTGAGATTTAAAGCACCACGACACA 240  
QY 241 CCCCTGGATGGTGGCGGATGTTGTCATATCAATGATGATGATGATGATGAT 300  
DB 241 CCCCTGGATGGTGGCGGATGTTGTCATATCAATGATGATGATGATGATGAT 300  
QY 301 ATACGCGCAAGTGTGGCTCAGAGATGCTATACCTAAGTGTCTATACCAATAT 360  
DB 301 ATACGCGCAAGTGTGGCTCAGAGATGCTATACCTAAGTGTCTATACCAATAT 360  
QY 361 CTAATATCCGCAAACTAAACGTCCTTTAGTATACATACATGCTGGTGGTATAT 420  
DB 361 CTAATATCCGCAAACTAAACGTCCTTTAGTATACATACATGCTGGTGGTATAT 420  
QY 421 GGTGAATATCTCGTATATATGATGCTGATGCTGATGCTGATGCTGATGCTG 480  
DB 421 GGTGAATATCTCGTATATATGATGCTGATGCTGATGCTGATGCTGATGCTG 480  
QY 481 ATTAACATACATATGCTGGAGCTGTAGGTTTCTAAGTTTAAATGAGAAGCTT 540  
DB 481 ATTAACATACATATGCTGGAGCTGTAGGTTTCTAAGTTTAAATGAGAAGCTT 540  
QY 541 AATGTCGGGTAATGCGGCTTAAAGATCACTGATGCTGCTGATGATGATGAT 600  
DB 541 AATGTCGGGTAATGCGGCTTAAAGATCACTGATGCTGCTGATGATGATGAT 600  
QY 601 AATGTCGGGTAATGCGGCTTAAAGATCACTGATGCTGCTGATGATGATGAT 660  
DB 601 AATGTCGGGTAATGCGGCTTAAAGATCACTGATGCTGCTGATGATGATGAT 660  
QY 661 GCTGCTCTACCACTACATGATGTTAAACGCAAACTGCGGCTCTTTCCATCGTGT 720  
DB 661 GCTGCTCTACCACTACATGATGTTAAACGCAAACTGCGGCTCTTTCCATCGTGT 720  
QY 721 ATACTAATGTCGGTAAATGCTATTTGTCATGCTGCTAATACCAATGCTCAAT 780  
DB 721 ATACTAATGTCGGTAAATGCTATTTGTCATGCTGCTAATACCAATGCTCAAT 780  
QY 781 TTGACCTTAGCAATGTCGGGCTATTAAGGTAAGATGATGATGATGATGATGAT 840  
DB 781 TTGACCTTAGCAATGTCGGGCTATTAAGGTAAGATGATGATGATGATGATGAT 840  
QY 841 TTCTTTATGAAGCAAGCAAGCAAGATTTAATAAATGAGAAAGATTTAACTCTA 900  
DB 841 TTCTTTATGAAGCAAGCAAGCAAGATTTAATAAATGAGAAAGATTTAACTCTA 900  
QY 901 GAAGAGCGTAAATTAAGTATGCTCTTTGGTCCACTGTTGAGCATATCAGACC 960  
DB 901 GAAGAGCGTAAATTAAGTATGCTCTTTGGTCCACTGTTGAGCATATCAGACC 960  
QY 961 GCTGATTTGCTCTTACCCAAACATCCTCGGGAATGCTTAAACTGCTGGGTAATTCG 1020

DB 961 GCTGATTTGCTCTTACCCAAACATCCTCGGGAATGCTTAAANNCTGGGGTAATTCG 1020  
QY 1021 ATACCCATATGATGGGTAAACCTTCATATGAGGGCTTTTTCATCTCAATTTTAG 1080  
DB 1021 ATACCCATATGATGGGTAAACCTTCATATGAGGGCTTTTTCATCTCAATTTTAG 1080  
QY 1081 CAATGCTATGCTTTTAAAGAAATTTGAACCTTGTCTCAATTTTGTGCAAGTAATG 1140  
DB 1081 CAATGCTATGCTTTTAAAGAAATTTGAACCTTGTCTCAATTTTGTGCAAGTAATG 1140  
QY 1141 GCTGATGCTGAACGACCGCCGACAGACCTTGAATGAGTGTCTTAAATTTAAAGCT 1200  
DB 1141 GCTGATGCTGAACGACCGCCGACAGACCTTGAATGAGTGTCTTAAATTTAAAGCT 1200  
QY 1201 CATGTTACAGAGAAACACCAACAGCTGATTAATTTTATGATGATGATGATGAT 1260  
DB 1201 CATGTTACAGAGAAACACCAACAGCTGATTAATTTTATGATGATGATGATGAT 1260  
QY 1261 TTCTGTTCCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320  
DB 1261 TTCTGTTCCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320  
QY 1321 GCTGATGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380  
DB 1321 GCTGATGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380  
QY 1381 CGTAGTGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440  
DB 1381 CGTAGTGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440  
QY 1441 AATCAATTTGGCCAAACGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500  
DB 1441 AATCAATTTGGCCAAACGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500  
QY 1501 ACTGATATGATGATTAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560  
DB 1501 ACTGATATGATGATTAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560  
QY 1561 ATGGAATATGTTTCCGCGGATCNAATTAAGAAATGCGAAGATTTACAGTGTGAT 1620  
DB 1561 ATGGAATATGTTTCCGCGGATCNAATTAAGAAATGCGAAGATTTACAGTGTGAT 1620  
QY 1621 ATTAGTGAATGATGAAATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680  
DB 1621 ATTAGGANGAATTTGAATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680  
QY 1681 TCGATGTTGAAAACATAGATTTATTTTAG 1713  
DB 1681 TCGATGTTGAAAACATAGATTTATTTTAG 1713

RESULT 8  
US-09-068-960-14  
Sequence 14, Application US/09068960A  
Patent No. 623515  
GENERAL INFORMATION:  
APPLICANT: Commonwealth Scientific and Industrial Rsrch. Org.  
TITLE OF INVENTION: MALATHION CARBOXYL ESTERASE  
FILE REFERENCE: Attorney Docket No. 623515 50179-051  
CURRENT APPLICATION NUMBER: US/09/068,960A  
EARLIER FILING DATE: 1998-05-20  
EARLIER APPLICATION NUMBER: PCT/AU96/00746  
EARLIER FILING DATE: 1996-11-22  
EARLIER APPLICATION NUMBER: AU 6751  
NUMBER OF SEQ ID NOS: 43  
SOFTWARE: Patentl Ver. 2.0  
SEQ ID NO 14  
LENGTH: 1710  
TYPE: DNA  
ORGANISM: Musca domestica  
US-09-068-960-14



Query Match 55.8%; Score 956.6; DB 4; Length 1710;  
 Best Local Similarity 73.48; Pred. No. 1e-267;  
 Matches 123; Conservative 0; Mismatches 444; Indels 0; Gaps 0;

44 TTTAAATGATGAAATTAAGTTTAACTATGCTTTAACTAACAATGAAACGGTGTAG 103  
 44 TTTAAATGATGCTAATTAATACAAACCTACCGTGTGATGAAATGAAACCAATTA 103  
 104 CTGAATGATTAATGCAAGTAAAGGCTTAAAGCTTAAGCTGCTGATGATTCCT 163  
 104 TCGATGATGATTAATGCAAGTAAAGGCTTAAAGCTGCTGATGATTCCT 163  
 164 ACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 223  
 164 ACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 223  
 224 CACCCGACGACCAACCCCTGGAGTGTGCTGATGATGATGATGATGATGATGATG 283  
 224 CACCCGACGACGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 283  
 284 CAGTGAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 343  
 344 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 403  
 344 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 403  
 404 GTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 463  
 404 GGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 463  
 464 AAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 523  
 464 AAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 523  
 524 TAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 583  
 524 TAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 583  
 584 TCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 643  
 584 TCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 643  
 644 TCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 703  
 644 TCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 703  
 704 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 763  
 704 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 763  
 764 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 823  
 764 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 823  
 824 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 883  
 824 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 883  
 884 AAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 943  
 884 AAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 943  
 944 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1003  
 944 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1003  
 944 TAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1063  
 1004 CTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1063  
 1004 GCGCTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1063

1064 TCACTTCAATTCCTTAAAGCAATGCTTAAAGCAATGCTTAAAGCAATGCTTAAAGCAAT 1123  
 1064 CCAATCAATTCCTTAAAGCAATGCTTAAAGCAATGCTTAAAGCAATGCTTAAAGCAAT 1123  
 1124 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1183  
 1124 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1183  
 1184 CTAAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1243  
 1184 CCAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1243  
 1244 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1303  
 1244 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1303  
 1304 ACACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1363  
 1304 ACACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1363  
 1364 ATCCCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1423  
 1364 ACCCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1423  
 1424 TAACCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1483  
 1424 TAACCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1483  
 1484 AAACATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1543  
 1484 AAACATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1543  
 1544 GCAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1603  
 1544 GCAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1603  
 1604 TATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1663  
 1604 TATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1663  
 1664 AATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1710  
 1664 AATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1710

RESULT 9  
 US-08-747-221B-51  
 : Sequence 51, Application US/08747221B  
 : Patent No. 6063610  
 : GENERAL INFORMATION:  
 : APPLICANT: Silver, Gary W.  
 : APPLICANT: Wisniewski, Nancy  
 : TITLE OF INVENTION: No. 6063610e1 Carboxylesterase Nucleic Acid  
 : TITLE OF INVENTION: Molecules, Proteins and Uses Thereof  
 : NUMBER OF SEQUENCES: 66  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: Carol Talkington Verser, Ph.D.  
 : ADDRESSEE: Hesk Corporation  
 : STREET: 1825 Sharp Point Drive  
 : CITY: Fort Collins  
 : STATE: Colorado  
 : COUNTRY: USA  
 : ZIP: 80525  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : OPERATING SYSTEM: Windows 95  
 : SOFTWARE: WordPerfect for Windows, Version 7.0  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/747,221B  
 : FILING DATE: No. 6063610e1 December 12, 1996  
 : CLASSIFICATION: 435  
 : ATTORNEY/AGENT INFORMATION:

NAME: Verser, Carol Talkington  
 REGISTRATION NUMBER: 37,459  
 REFERENCE/DOCKET NUMBER: FC-1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 970/493-7272  
 TELEFAX: 970/484-9505  
 INFORMATION FOR SEQ ID NO: 51:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1584 nucleotides  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 1..1584  
 US-08-747-221B-51

Query Match 10.5%; Score 179.6; DB 3; Length 1584;  
 Best Local Similarity 56.2%; Pred. No. 2.5e-42;  
 Matches 360; Conservative 0; Mismatches 274; Indels 6; Gaps 1;

QY 116 ATGGCAAGTGAAGGCGTTAAAGTGTACGATGATTCCTACAGTTTG 175  
 Db 29 AAGTACTTAAAGGAAAGCAATAGTAAAGAAATGTTCCATAGTATT 88  
 QY 176 AGGTATACCGTACGCCCAACCCGAGTGGTGTAGCTGAATTTAAAGCCCGCAGCAG 235  
 Db 89 CTGGAATTCATATGCCAAACCTCTGTAGGTGATCTAGATTAAAGCAGCTCAACCTG 148  
 QY 236 CAACACCTGGGATGGTGTGCGGATGTTGCAATCATTAAGTAAAGTGAAGTGTG 295  
 Db 149 CAGACCTTGGTCAAGTGTCTTGTGATGATGATGATGATGATGATGATGATGATGATG 208  
 QY 296 ATTTTAAACGGGCAAGTGTGCTCAGAGGATGTTCTATACCTAAGTGTCTATACGA 355  
 Db 209 ATTTTAAATTAATAAGTAGAGGCTGAGAGTTGTTTATACCTCATGTATGTAC 268  
 QY 356 ATATCTAATATCCGAAATTAAGCCGCTTTAGTATACATACATGATGATGATGATGATG 415  
 Db 269 CAAATACATCAGAAATACATCTTCCAGTATGATGATGATGATGATGATGATGATGATG 328  
 QY 416 TATCGGTAAATATCATGCTGATGATGATGATGATGATGATGATGATGATGATGATG 475  
 Db 329 TATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 388  
 QY 476 TGTGATTAACATACATATGCTTGGGAGCTGATGATGATGATGATGATGATGATGATG 535  
 Db 389 TTTGTTTCTTCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 448  
 QY 536 ACCTTAATGTGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 595  
 Db 449 AA-----GCGCTGGCAATGTGGTTGATGAGCAGAGTGAAGCTCTAATAATGGTTAA 502  
 QY 596 AAAATATTTGGGCAACTTTGGTGGCAATCCGCAATATATTAAGCTTTGGTGAAGTGG 655  
 Db 503 AAAAATAATTTGATCTTTTGGTGGTGAAGCCCAATGATGATGATGATGATGATGATGATG 562  
 QY 656 CCGGTGCTGCTTACCCATCATGATGATGATGATGATGATGATGATGATGATGATGATG 715  
 Db 563 CAGGTGCTGCAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 715  
 QY 716 GTGTATATCTATGCTGGGATGATGATGATGATGATGATGATGATGATGATGATGATG 755  
 Db 623 AAGGATCTCACAAGTAGAGTGTCTTTTATCTCTGGG 662

RESULT 10  
 US-08-747-221B-52/c  
 Sequence 52; Application US/08/747221B  
 Patent No. 6063610  
 GENERAL INFORMATION:  
 APPLICANT: Silver, Gary W.

APPLICANT: Wisniewski, Nancy  
 TITLE OF INVENTION: No. 6063610e1 Carboxylesterase Nucleic Acid  
 TITLE OF INVENTION: Molecules, Proteins and Uses Thereof  
 NUMBER OF SEQUENCES: 66  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Carol Talkington Verser, Ph.D.  
 ADDRESS: Hesk Corporation  
 STREET: 1825 Sharp Point Drive  
 CITY: Fort Collins  
 STATE: Colorado  
 COUNTRY: USA  
 ZIP: 80525  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: Windows 95  
 SOFTWARE: Wordperfect for Windows, Version 7.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/747,221B  
 FILING DATE: No. 6063610e1ember 12, 1996  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Verser, Carol Talkington  
 REGISTRATION NUMBER: 37,459  
 REFERENCE/DOCKET NUMBER: FC-1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 970/493-7272  
 TELEFAX: 970/484-9505  
 INFORMATION FOR SEQ ID NO: 52:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1584 nucleotides  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 US-08-747-221B-52

Query Match 10.5%; Score 179.6; DB 3; Length 1584;  
 Best Local Similarity 56.2%; Pred. No. 2.5e-42;  
 Matches 360; Conservative 0; Mismatches 274; Indels 6; Gaps 1;

QY 116 ATGGCAAGTGAAGGCGTTAAAGTGTACGATGATTCCTACAGTTTG 175  
 Db 1556 AAGTACTTAAAGGAAAGCAATAGTAAAGAAATGTTCCATAGTATT 1497  
 QY 176 AGGTATACCGTACGCCCAACCCGAGTGGTGTAGCTGAATTTAAAGCCCGCAGCAG 235  
 Db 1496 CTGGAATTCATATGCCAAACCTCTGTAGTATGATGATGATGATGATGATGATGATG 1437  
 QY 236 CAACACCTGGGATGGTGTGCGGATGTTGCAATCATTAAGTAAAGTGAAGTGTG 295  
 Db 1436 CAGAACCTTGGTCAAGTGTGCTTGTATGATGATGATGATGATGATGATGATGATGATG 1377  
 QY 296 ATTTTAAACGGGCAAGTGTGCTCAGAGATGTTCTATACCTAAGTGTCTATACGA 355  
 Db 1376 ATTTTAAATTAATAAGTAGAGGCTGAAGTGTGTTATATCCCAATGCTCTATGTAC 1317  
 QY 356 ATATCTAATATCCGAAACTAAGCTGCTTTTATGATGATGATGATGATGATGATGATGATG 415  
 Db 1316 CAAATACATCAGAAATATCACTTCTTCCAGTATGATGATGATGATGATGATGATGATG 1257  
 QY 416 TTATCGGTAAATATCATGCTGATGATGATGATGATGATGATGATGATGATGATGATG 475  
 Db 1256 TCAAGGATCTGGAATAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1197  
 QY 476 TGTGATTAACATACATATGCTTGGGAGCTGATGATGATGATGATGATGATGATGATGATG 535  
 Db 1196 TTTGTTTCTTCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1137  
 QY 536 ACCTTAATGTGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 595  
 Db 1136 AA-----GCGCTGGCAATGTGGTTGATGATGATGATGATGATGATGATGATGATGATG 1063

QY	596	AAATTAATTGGCCCAACTTTTGGTGCCCAATGCCGATATAATTACAGCTTTGGTGAAGTG	655
Dd	1082	AAAAACAATATTGCATCCTTTGGTGTCGACCACCAACATGTACATATTTTTGGAGAATCAG	102
QY	656	CGGGTGGCGCCTCACCCACATACATCATGATGTTAACCGAACAACGCGCGTCTTTCCATC	715
Dd	1022	CAGGGGGGCAAGTGTTCATATTATTGATGATGTTATCAGATCTTTCCAAGGACTTTTTCATA	963
QY	716	GTTGATATCTAATGTGGGTAATGCTATTTGTCCATTGGC	755
Dd	962	AAGCATCTCACAAGTAGTGAGTGTCTTTATCCTTGGGC	923

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?      TELEPHONE: 970/493-7272
?      TELEFAX: 970/484-9505
?      INFORMATION FOR SEQ ID NO: 52
?      SEQUENCE CHARACTERISTICS:
?      LENGTH: 1584 nucleotides
?      TYPE: nucleic acid
?      STRANDEDNESS: single
?      TOPOLOGY: linear
?      MOLECULE TYPE: cDNA
?
US-09-005-051-52

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Query Match	10.5%	Score 179,6;	DB 4;	Length 1584;
Best Local Similarity	56.2%;	Pred. No. 2.5e-42;		
Matches 360;	Conservative	0;	Mismatches 274;	Indels 6;
				Gaps 1

OY	116	ATGGCAAACTGAAGAAGCCGTTAAAGCTTAAACGTGTCAGATGATCTCTACTACAGTTTG	175
Db	1556	AAGGTAACCTTTAAAAGAGAAAAAGACAATTACGTGAAAAAAGAAATGTCCTCATAAGTTAT	149
OY	176	AAGGTAATACCGTAGACGCCACCACCGCAGTGGGTGAGCTGAGATTTTAAAGCACCCAGGCAC	235
Db	1496	CTGGAAATTCATATTCSCCAAACCTCCTGTAGGTATCTAAGATTAAAGCCACCTCAACCTG	143
OY	236	CAGAACCCCTGGATGSGTGGTGCATTTCTTCATCATATAAGATTAAGTCACTGACAGTTG	295
Db	1436	CAGAACCTTGGTCAAGTCTCTTGAATGCTATAAAGAGGAAATGTTAGATCAAGTAC	137
OY	296	ATTTTATACGGGCAAGATGTGTGGCTCAGAGATTTCTATACCTPAAGTGTCTATACGA	355
Db	1376	ATTTTATTTAAAAAATTTAAATAGGGGCGTGAAGTCTTTTATACCTCAATGTCTATGTAC	131
OY	356	ATAATCTAAATCCGAAACCTAAAGCTCCCGTTTACATATCATACATAGTGTGTGTTTTA	415
Db	1316	CAAAACACTCAGAGAACTACTCTTCCAGTAATGATGTGAATACATAGGAGGCGCTCT	125
OY	416	TTCATCGTGAATAATCATCGTGATATGTATGGTCCCTGATTTTCATTTAAAGAGATGTG	475
Db	1256	TCATCGGAGATCTGAAATATGATATGATGTATGTCTCTGAATTTTGATGATGATTAAGAA	119
OY	476	TGTTGATTAACATCATATTCGTTTGGGAGACTCTAGSTTTTCTAAGTTTAAATTCGAAG	535
Db	1196	TTTCGTTACTTTCAATTATTCGATTAGGTCTTTTGGATTTTGAACCTGGGAATGAAAG	113
OY	536	ACCTTAATGTGCCCGGTAAATCCGCGCTTAAAGATCAAGTCATGCGCTTGCGTTGATTA	595
Db	1136	AA-----GCCCCCTGGCAATGTTGGTTTGANAGCACGTTGAAGCTTAAATATGGTAA	108
OY	596	AAAATATTTGGCGCAACTTTTGGTGGCAATCCCATATATTAACAGCTTTGGTGAAGTG	655
Db	1082	AAAACAATATTTGCATCTCTTTGGTGGTGAACCCCAACAATAGCATTTATTTGGGAATCAG	1022
OY	656	CCGCTGCTGCTCTACCCACTACATGATGTTTAAACGCAAAACTCGCGCTCTTTCCATTC	715
Db	1022	CAGGTGTGCAAGTGTTCATTATTTGATGTATTCACAGTCTTTCCAAGAGACTTTTCATA	963
OY	716	GTTGATACTAATATGTCCGTTAATAGTCATTTGTCCATTTGCG	755
Db	962	AAGCATCTCACAAGTAGGAAGTCTTTAATCCTTGCGC	923
 RESULT 13 US-08-747-221B-36 Sequence 36, Application US/08747221B Patent No. 6063610  GENERAL INFORMATION: APPLICANT: Silver, Gary W. APPLICANT: Wisniewski, Nancy TITLE OF INVENTION: No. 6063610el Carboxylesterase Nucleic Acid TITLE OF INVENTION: Molecules, Proteins and Uses Thereof NUMBER OF SEQUENCES: 66 CORRESPONDENCE ADDRESS: ADDRESSEE: Carol Talkington Verser, Ph.D. ADDRESSEE: Heska Corporation			

```

/ STREET: 1825 Sharp Point Drive
/ CITY: Fort Collins
/ STATE: Colorado
/ COUNTRY: USA
/ ZIP: 80525
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: Windows 95
/ SOFTWARE: Wordperfect for Windows, Version 7.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/74/221B
/ FILING DATE: No. 6063610ember 12, 1996
/ CLASSIFICATION: 435
/
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Verser, Carol Talkington
/ REGISTRATION NUMBER: 37,459
/ REFERENCE/DOCKET NUMBER: PC-1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 970/493-7272
/ TELEFAX: 970/484-9505
/
/ INFORMATION FOR SEQ ID NO: 36:
/
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 2007 nucleotides
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/
/ MOLECULE TYPE: cDNA
/ FEATURE:
/
/ NAME/KEY: CDS
/ LOCATION: 11..1594
/
/ US-08-747-221B-36
/
Query Match 10.5%; Score 179.6; DB 3; Length 2007;
Best Local Similarity 56.2%; Pred.No.2.8e-42;
Matches 360; Conservative 0; Mismatches 274; Indels 6; Gaps 1.
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OY 116 ATGCGAAGTGAAGGCGCTTAAACGTTTACGTTGTACGATGATTCCTACTACAGTTTG 175
Db 39 AAGGTACTTTAAAGGAAAGAAAGCAATATTAGTAAAGAAATGTCCTCATAGTTATT 98
OY 176 AGGTATACCGTGTGCGCCCAACGCGCAGGCGGTGACTCATGATTTAAAGCACCCAGCGAC 235
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OY 236 CAACCCCTGGAGTGTGCTGATGTTGTGCATCATTAAGATTAAGTCAAGTCAAGTTG 295
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OY 296 ATTTATTAAGGCGCAAGTGTGTGCTCAGAGGATGTCTACTAAGTCTATACGA 355
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Db 279 CAAAAACATCAGAGAAATCACTTTCTCCAGTAATGATGATGATACATGAGAGCGCTTCT 338
OY 416 TTATGCGTGAATAATCATCTGCTATATGATATGCTGCTGATATTTCATTAAAAAGATGCG 475
Db 339 TCATGGGATCTGGAATTAAGTATGATGATGATGCTGCTGATATTGATGATTAATGGAATTG 398
OY 476 TGTGATTAAACATACATATGCTTTGGGAGCTCAGATTTTCAAGTTTAAATTCAGAG 535
Db 399 TTTGCTTACTTTCATTATGATTAATGATTAAGTGTGTTTGGGATTTTGAACCTGGGAATAGAAG 458
OY 536 ACCTTATATGCCCCGATATGCGCGCTTAAAGATCAAGTCATGATGCGCTTGCCTGGATTA 595
Db 459 AA-----GCGCTCTGGCAATGTGTGTTGATGAGCCAGGTGAAGCTCAAAATGGGTAA 512
OY 596 AAAATATTGGCCCAACTTGTGTGGCATCCCGGATATATTACAGTCTTGGTGAAGAG 655
Db 513 AAAACATTTTTCATCCTTTGTGTGTGATACCCCAACATATGTACTATTTTGGAGATGAG 572

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NAME/KEY: CDS  
LOCATION: 11..1594  
US-09-005-051-36

Query Match 10.5%; Score 179.6; DB 4; Length 2007;  
Best Local Similarity 56.2%; Pred. No. 2,8e-42;  
Matches 360; Conservative 0; Mismatches 274; Indels 6; Gaps 1;

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OY 116 ATGGCAAGTGAAGCGCTTAACGTTTAACTGTGTACATGATTCCTCTACAGTTTG 175
DB 39 AAGGTACTTTAAAGAAAGAAAGCAATTAAGTGAAGAAAGAAATGTTCCATATTT 98
OY 176 AAGGTATACCGTACCGCCAGCGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 235
DB 99 CTGGATTCATATGCAAGCAACCTCGTGTAGGTATTAAGATTAAAGCCACCTCAAGCTG 158
OY 236 CAACACCCCTGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 295
DB 159 CAGAACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 218
OY 296 ATTTTAAAGCGGCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 355
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OY 476 TGTGTATACATACATATGTTGGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 535
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OY 536 ACCTTAATGCGCGGTAATGCGGCTTAAGATCAAGTCAATGCGCTGTGTGTGTGTGTGTGT 595
DB 459 AA-----GCGCCTGCAATGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 512
OY 596 AAATATATGCGCCACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 655
DB 513 AAACAATATGCAATCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 572
OY 656 CCGGTGCTGCTTACCCATACATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 715
DB 573 CAGGTGTGCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 632
OY 716 GTGTATATATATGTCGGGTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 755
DB 633 AAGCATCTCAAAAGTGAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 672

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Job time : 47.518 secs

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Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 11, 2003, 01:07:17 ; Search time 94.5276 Seconds  
(without alignments)  
15895.765 Million cell updates/sec

Title: US-09-776-910-9  
Perfect score: 1713  
Sequence: 1 atgaattcaacgttagttl.....aacatagagattatttttag 1713

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapept 1.0

Searched: 593429 seqs, 438583890 residues

Total number of hits satisfying chosen parameters: 1186858

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database:

Published Applications, NA:\*

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- 2: /cgn2\_6/ptodata/2/pubpna/ECT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*
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- 13: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*
- 14: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	88.8	5.2	1691	9 US-10-083-590-13	Sequence 13, Appl
2	77.2	4.5	1611	9 US-09-738-626-1254	Sequence 1254, Ap
3	62.2	3.6	1967	10 US-09-748-739A-1	Sequence 1, Appl
4	62.2	3.6	2381	10 US-09-880-107-2271	Sequence 2271, Ap
5	62.2	3.6	2416	10 US-09-748-739A-3	Sequence 3, Appl
6	62.2	3.6	2416	10 US-09-748-739A-5	Sequence 5, Appl
7	62.2	3.6	2416	10 US-09-748-739A-7	Sequence 7, Appl
8	62.2	3.6	2416	10 US-09-748-739A-16	Sequence 16, Appl
9	62.2	3.6	2444	9 US-09-893-519A-112	Sequence 112, App
10	57.8	3.4	657	10 US-09-974-300-1107	Sequence 1107, Ap
11	57.8	3.4	2508	10 US-09-934-323-1	Sequence 1, Appl
12	57.6	3.4	4667	10 US-09-934-323-1	Sequence 1038, Ap
13	56.8	3.3	2191	9 US-09-954-531-1038	Sequence 3854, Ap
14	56.8	3.3	2191	10 US-09-880-107-3854	Sequence 271, Appl
15	56.8	3.3	2484	9 US-10-102-806-271	Sequence 271, Appl
16	55.4	3.2	1641	10 US-09-895-860-3	Sequence 3, Appl
17	55.4	3.2	2087	10 US-09-895-860-1	Sequence 1, Appl
18	55.4	3.2	2428	9 US-09-418-176-1	Sequence 1, Appl
19	55.4	3.2	2428	10 US-09-969-347-220	Sequence 220, App

20	55.4	3.2	3824	9 US-10-036-041-22	Sequence 22, Appl
21	55.4	3.2	3824	9 US-10-028-072-541	Sequence 541, Appl
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33	55.4	3.2	3824	9 US-10-140-474-541	Sequence 541, Appl
34	55.4	3.2	3824	9 US-10-035-719-22	Sequence 22, Appl
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36	55.4	3.2	3824	9 US-10-143-114-541	Sequence 209, Appl
37	55.4	3.2	3824	9 US-10-230-163-209	Sequence 209, Appl
38	55.4	3.2	3824	9 US-10-140-002-541	Sequence 541, Appl
39	55.4	3.2	3824	9 US-10-036-160-22	Sequence 22, Appl
40	55.4	3.2	3824	9 US-10-142-419-541	Sequence 541, Appl
41	55.4	3.2	3824	9 US-10-218-631-209	Sequence 209, Appl
42	55.4	3.2	3824	9 US-10-230-338-209	Sequence 209, Appl
43	55.4	3.2	3824	9 US-10-036-958-22	Sequence 22, Appl
44	55.4	3.2	3824	9 US-10-036-150-22	Sequence 22, Appl
45	55.4	3.2	3824	9 US-10-123-262-541	Sequence 541, Appl

#### ALIGNMENTS

RESULT 1  
US-10-083-590-13  
Sequence 13, Application US/10083590  
Publication No. US20030027257A1  
GENERAL INFORMATION:  
APPLICANT: IATROU, Kostas  
APPLICANT: FARRELL, Patrick J.  
TITLE OF INVENTION: SEQUENCES FOR IMPROVING THE EFFICIENCY OF SECRETION OF  
TITLE OF INVENTION: NON-SECRETED PROTEINS FROM MAMMALIAN AND INSECT CELLS  
FILE REFERENCE: 028722-207  
CURRENT APPLICATION NUMBER: US/10/083,590  
CURRENT FILING DATE: 2002-02-27  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/256,694  
PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-24  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/136,421  
PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-20  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/056,871  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 13  
LENGTH: 1691  
TYPE: DNA  
ORGANISM: Heliothis virescens  
US-10-083-590-13

Query Match 5.2%, Score 88.8, DB 9, Length 1691;  
Best local similarity 53.6%, Pred. No. 6.4e-13;  
Matches 211: Conservative 0; Mismatches 177; Indels 6; Gaps 1;  
QY 368 CCGAAGCTAAAGCTCCCGTTAGTATACATACAGTGGTGTATATATCGGTAA 427  
DB 380 CCACACCTTACGGCTTACCTCGGTTCATACATGATGGAGATTTGCTTGGCTCG 439  
QY 428 ATCATCTGATATGATGCTGCTGATTTATTCATTAAAGATGTGCTGTTACAA 487  
DB 440 GCACAGGACGACACGACGACGACGACGACGACGACGACGACGACGACGACG 499  
QY 488 TACATATGTTGGAGCTCTAGCTTCTAAGTTTAAATTCGAAGACCTTATGTC 547  
DB 500 TTATTTACAGATTGACGCTTCTGCTTCTGCTCCATGACACACACA-----AAATTC 553

QY 548 CCGTAATGCCGCGCTTAAGATCAAGTCAATGGCTTGGCTGATTAATAATATTCG 607  
Db 554 CCGGGAATGCCGCTCCGATAGTAAACCTGCTGGCTGATCAAGAGAGAGCCCA 613  
QY 608 CCAATTTGGGCAATCCCGATTAATATTAACATCTTTGGTGAAGTCCGCTGCTG 667  
Db 614 AGAATTTCCGAG 673  
QY 668 CTACCCATCAATGATGTTAAACGAAACAGAGAGAGAGAGAGAGAGAGAGAG 727  
Db 674 CTGCGCATCTACTAGCTCTTTCTAAAGCTACTGAGAGAGAGAGAGAGAGAG 733  
QY 728 TGTGGGTAATGCTATTTGCTCAATGGCTATATAC 761  
Db 734 TGAGCGGAACAGAGATGAGCTACTCTTACTATAC 767

## RESULT 2

US-09-738-626-1254  
Sequence 1254, Application US/09738626  
Publication No. US20020197605A1  
GENERAL INFORMATION:  
APPLICANT: NAKAGAWA, SATOSHI  
APPLICANT: MIZOGUCHI, HIROSHI  
APPLICANT: ANDO, SEIKO  
APPLICANT: HAYASHI, MIKIO  
APPLICANT: OCHIAI, KEIKO  
APPLICANT: YOKOI, HARUHIKO  
APPLICANT: TATEISHI, NAOKO  
APPLICANT: SENOH, AKIHIRO  
APPLICANT: IKEDA, MASATO  
APPLICANT: OZAKI, AKIO  
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
FILE REFERENCE: 249-125  
CURRENT APPLICATION NUMBER: US/09/738,626  
CURRENT FILING DATE: 2000-12-18  
PRIOR APPLICATION NUMBER: JP 99/377484  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: JP 00/159162  
PRIOR FILING DATE: 2000-04-07  
PRIOR APPLICATION NUMBER: JP 00/280988  
PRIOR FILING DATE: 2000-08-03  
NUMBER OF SEQ ID NOS: 7059  
SOFTWARE: PatentIn ver. 3.0  
SEQ ID NO 1254  
LENGTH: 1611  
TYPE: DNA  
ORGANISM: Corynebacterium glutamicum  
US-09-738-626-1254

Query Match 4.5%; Score 77.2; DB 9; Length 1611;  
Best Local Similarity 50.2%; Pred. No. 6.4e-10;  
Matches 277; Conservative 0; Mismatches 263; Indels 12; Gaps 3;

QY 177 GGGTATACCGTACGCCCAACGCCAGTGGTACCTGAGATTAAACCCAGCCAGC 236  
Db 78 GGGATTCCTACGAGCGCAACACTGGGGAATATCGCTCCGGGACACCCGCCGCC 137  
QY 237 AACACCCGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 293  
Db 138 CAGAAATGGAGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 197  
QY 294 TGATTTTAAACGGGCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 353  
Db 198 GTACTCTGAGCAGATAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 257  
QY 354 GAATATCTAATCCGAAACCTAAGCTCCGTTTATGATATACATACATGCTGCTG 413  
Db 258 G-----CTGATTCCTCCAGAAAGCTTCTGTTGCTGCTGCTGCTGCTGCTG 311  
QY 414 TATATGCTGA---AATCATGCTGATGATGCTGCTGCTGCTGCTGCTGCTGCTG 470

Db 312 CATCATGGGCTCATCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 371  
QY 471 TGTGCTGTTGATTAACATACATATGCTTGGAGCTCTAGCTTTTAACTTAATTC 530  
Db 372 TGTGCTGTTGATTAACATACATATGCTTGGAGCTCTAGCTTTTAACTTAATTC 431  
QY 531 AGAAGACCTTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 590  
Db 432 CGTGGGAGAGAGATTCGATACCAACCCGCTCCAGATGAGCTCTGCTGCTGCTG 491  
QY 591 GATTAATAATAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 650  
Db 492 GGTGACCGCTAATATGCAAGCATTCGTTGGGAGATTCGTTGCAACGCTCAAG 551  
QY 651 AAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 710  
Db 552 ATCCGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 611  
QY 711 CCATGCTGCTAT 722  
Db 612 CCACCGCGCCAT 623

## RESULT 3

US-09-748-739A-1  
Sequence 1, Application US/09748739A  
Patent No. US20020119489A1  
GENERAL INFORMATION:  
APPLICANT: Lockridge, Oksana  
APPLICANT: Watkins, Jeffrey D.  
TITLE OF INVENTION: Butyrylcholinesterase Variants and  
METHODS OF USE  
FILE REFERENCE: P-IX 4143  
CURRENT APPLICATION NUMBER: US/09/748,739A  
CURRENT FILING DATE: 2000-12-06  
NUMBER OF SEQ ID NOS: 31  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 1967  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Human Butyrylcholinesterase variant  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (86)...(1891)  
US-09-748-739A-1

Query Match 3.6%; Score 62.2; DB 10; Length 1967;  
Best Local Similarity 54.8%; Pred. No. 5.6e-06;  
Matches 190; Conservative 0; Mismatches 148; Indels 9; Gaps 3;

QY 325 GAGGATGCTATACCTAGTGTGCTATACGATTAATCTAATCCGAACTAAAGTCC 384  
Db 437 GAGACTGTTTATATCTAATATGATGATTCAGACCTAAAC---AAAAATCCACT 493  
QY 385 GTTTAGTATACATACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 444  
Db 494 GATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 553  
QY 445 GGTCCGATTAATTCATTAAGAA---TGTGCTGCTGATTAACATCAATATGCTG 501  
Db 554 GATGGCAATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 613  
QY 502 GGAGCTGATGCTTCTAAGTTTAATTCAGAGAGCTTAATGCTGCTGCTGCTGCTG 561  
Db 614 GGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 670  
QY 671 TTAATGATCAAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 730  
Db 622 AATCCGATTAATTAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 668



Db 731 AATCCATAAAGTGTACTCTCTTTGGAGAAAGTCAGAGCAGCTTC 777

RESULT 4  
US-09-880-107-2271

; Sequence 2271, Application US/09880107  
; Patent No. US20020142981A1

; GENERAL INFORMATION:

; APPLICANT: Horne, Darci T.

; APPLICANT: Vockley, Joseph G.

; APPLICANT: Scherf, Uwe

; APPLICANT: Gene Logic, Inc.

; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer

; FILE REFERENCE: 44921-5028-WO

; CURRENT APPLICATION NUMBER: US/09/880,107

; CURRENT FILING DATE: 2001-06-14

; PRIOR FILING DATE: 2000-06-14

; PRIOR APPLICATION NUMBER: US 60/211,379

; PRIOR FILING DATE: 2000-10-02

; NUMBER OF SEQ ID NOS: 3950

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2271

; LENGTH: 2381

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:  
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 M16474

US-09-880-107-2271

Query Match 3.6%; Score 62.2; DB 10; Length 2381;

Best Local Similarity 54.8%; Pred. No. 6.2e-06;

Matches 190; Conservative 0; Mismatches 148; Indels 9; Gaps 3;

Db 325 GAGGATTTCTATACCTAGTGTCTATACGAATATCTAAATCCGAAACCTAAACGCTCC 384

Db 427 GAAGACTGTTATATCTAAATGATGATTCAGACCTAACCC---AAAAATGCCACT 483

Qy 385 GTTTAGTATACATACATGCTGCTGTTTATATATCGGTCAAAATCATCTGATATGTA 444

Db 484 GTATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 543

Qy 445 GGTCCCTATATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 501

Db 544 GATGGCAAGTTTCTGCTGGGTGGAAGATATCTATGTCATGAACTATAGGCTG 603

Qy 502 GAGCTCTAGCTTTCTAAGTTTAAATTCAGAACCTTAATGTCGGGTAAATGCCGCG 561

Db 604 GGTCCCTAGGATTTCTAGCTTT---GCCAGGAATCCTGAGCTCCAGGAGACATGGGT 660

Qy 562 CTTAAGATCAAGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 621

Db 661 TTTATTTATGATCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720

Qy 622 AATCCCATATATTTATACAGTCTTTGTTGGAAGTCCGCGTCTGCTGCTGCTGCTG 668

Db 721 AATCTTAAAGTGTACTCTCTTTGGAGAAAGTCAGAGCAGCTTC 767

RESULT 5  
US-09-748-739A-3

; Sequence 3, Application US/09748739A

; Patent No. US20020119489A1

; GENERAL INFORMATION:

; APPLICANT: Lockridge, Oksana

; APPLICANT: Watkins, Jeffrey D.

; TITLE OF INVENTION: Butyrylcholinesterase Variants and

; FILE REFERENCE: P-IX 4143

; CURRENT APPLICATION NUMBER: US/09/748,739A

; CURRENT FILING DATE: 2000-12-06

; NUMBER OF SEQ ID NOS: 31

Query Match 3.6%; Score 62.2; DB 10; Length 2416;

Best Local Similarity 54.8%; Pred. No. 6.3e-06;

Matches 190; Conservative 0; Mismatches 148; Indels 9; Gaps 3;

Db 325 GAGGATTTCTATACCTAGTGTCTATACGAATATCTAAATCCGAAACCTAAACGCTCC 384

Db 481 GAAGACTGTTATATCTAAATGATGATTCAGACCTAACCC---AAAAATGCCACT 537

Qy 445 GGTCCCTATATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 501

Db 598 GATGGCAAGTTTCTGCTGGGTGGAAGATATCTATGTCATGAACTATAGGCTG 657

Qy 502 GAGCTCTAGCTTTCTAAGTTTAAATTCAGAACCTTAATGTCGGGTAAATGCCGCG 561

Db 658 GGTCCCTAGGATTTCTAGCTTT---GCCAGGAATCCTGAGCTCCAGGAGACATGGGT 714

Qy 562 CTTAAGATCAAGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 621

Db 715 TTTATTTATGATCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 774

Qy 622 AATCCCATATATTTATACAGTCTTTGTTGGAAGTCCGCGTCTGCTGCTGCTGCTG 668

Db 775 AATCTTAAAGTGTACTCTCTTTGGAGAAAGTCAGAGCAGCTTC 821

RESULT 6  
US-09-748-739A-5

; Sequence 5, Application US/09748739A

; Patent No. US20020119489A1

; GENERAL INFORMATION:

; APPLICANT: Lockridge, Oksana

; APPLICANT: Watkins, Jeffrey D.

; TITLE OF INVENTION: Butyrylcholinesterase Variants and

; FILE REFERENCE: P-IX 4143

; CURRENT APPLICATION NUMBER: US/09/748,739A

; CURRENT FILING DATE: 2000-12-06

; NUMBER OF SEQ ID NOS: 31

Query Match 3.6%; Score 62.2; DB 10; Length 2416;

Best Local Similarity 54.8%; Pred. No. 6.3e-06;

Matches 190; Conservative 0; Mismatches 148; Indels 9; Gaps 3;

Db 325 GAGGATTTCTATACCTAGTGTCTATACGAATATCTAAATCCGAAACCTAAACGCTCC 384

Db 481 GAAGACTGTTATATCTAAATGATGATTCAGACCTAACCC---AAAAATGCCACT 537

Qy 445 GGTCCCTATATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 501

Db 598 GATGGCAAGTTTCTGCTGGGTGGAAGATATCTATGTCATGAACTATAGGCTG 657

Qy 502 GAGCTCTAGCTTTCTAAGTTTAAATTCAGAACCTTAATGTCGGGTAAATGCCGCG 561

Db 658 GGTCCCTAGGATTTCTAGCTTT---GCCAGGAATCCTGAGCTCCAGGAGACATGGGT 714

Qy 562 CTTAAGATCAAGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 621

Db 715 TTTATTTATGATCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 774

Qy 622 AATCCCATATATTTATACAGTCTTTGTTGGAAGTCCGCGTCTGCTGCTGCTGCTG 668

Db 775 AATCTTAAAGTGTACTCTCTTTGGAGAAAGTCAGAGCAGCTTC 821

QY 385 GTTTTACTATACATACATGCTGCTGTTTATATATCGTGAAATCATCGTATATGAT 444  
DB 538 GTATTGATATGATTTATGCTGCTGTTTCAACTGGAACATCATCTTACATGTTTAT 597  
QY 445 GGTCTGATTTTTCATTAAAAAGA---TGTGCTGTTGATTAACATACATATCGTTG 501  
DB 598 GATGCAAGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 657  
QY 502 GGACCTGATGTTTCTTAAGTTTAAATTCAGAACCTTAATGCTGCTGCTGCTGCTG 561  
DB 658 GTTGCCCTAGATTTCTTAAGTTT---GCCAGGAATCTCTAGGCTCCAGGACATGGGT 714  
QY 562 CTAAAGATCAAGTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 621  
DB 715 TTATTTGATCAACAGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 774  
QY 622 AATCCGATATATTAACGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 668  
DB 775 AATCCTAAAGTGAATCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 821

## RESULT 7

US-09-748-739A-7  
; Sequence 7, Application US/09748739A  
; Patent No. US20020119489A1  
; GENERAL INFORMATION:  
; APPLICANT: Lockridge, Oksana  
; APPLICANT: Watkins, Jeffrey D.  
; TITLE OF INVENTION: Butyrylcholinesterase Variants and  
; TITLE OF INVENTION: Methods of Use  
; FILE REFERENCE: P-IX 4143  
; CURRENT APPLICATION NUMBER: US/09/748,739A  
; CURRENT FILING DATE: 2000-12-06  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 2416  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Human Butyrylcholinesterase variant  
; NAME/KEY: CDS  
; LOCATION: (214)...(1935)  
US-09-748-739A-7

Query Match 3.6%; Score 62.2; DB 10; Length 2416;  
Best Local Similarity 54.8%; Pred. No. 6.3e-06;  
Matches 190; Conservative 0; Mismatches 148; Indels 9; Gaps 3;

QY 325 GAGGATGCTATACATACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 384  
DB 481 GAGGATGCTATACATACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 537  
QY 385 GTTTTACTATACATACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 444  
DB 538 GTATTGATATGATTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 597  
QY 445 GGTCTGATTTTTCATTAAAAAGA---TGTGCTGTTGATTAACATACATATCGTTG 501  
DB 598 GATGCAAGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 657  
QY 502 GGACCTGATGTTTCTTAAGTTTAAATTCAGAACCTTAATGCTGCTGCTGCTGCTG 561  
DB 658 GTTGCCCTAGATTTCTTAAGTTT---GCCAGGAATCTCTAGGCTCCAGGACATGGGT 714  
QY 562 CTAAAGATCAAGTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 621  
DB 715 TTATTTGATCAACAGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 774  
QY 622 AATCCGATATATTAACGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 668  
DB 775 AATCCTAAAGTGAATCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 821

DB 775 AATCCTAAAGTGAATCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 821

## RESULT 8

US-09-748-739A-16  
; Sequence 16, Application US/09748739A  
; Patent No. US20020119489A1  
; GENERAL INFORMATION:  
; APPLICANT: Lockridge, Oksana  
; APPLICANT: Watkins, Jeffrey D.  
; TITLE OF INVENTION: Butyrylcholinesterase Variants and  
; TITLE OF INVENTION: Methods of Use  
; FILE REFERENCE: P-IX 4143  
; CURRENT APPLICATION NUMBER: US/09/748,739A  
; CURRENT FILING DATE: 2000-12-06  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 16  
; LENGTH: 2416  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-748-739A-16

Query Match 3.6%; Score 62.2; DB 10; Length 2416;  
Best Local Similarity 54.8%; Pred. No. 6.3e-06;  
Matches 190; Conservative 0; Mismatches 148; Indels 9; Gaps 3;

QY 325 GAGGATGCTATACATACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 384  
DB 481 GAGGATGCTTTTATCTTAATATGATTCAGACCTTAACCC---AAAAATGCCACT 537  
QY 385 GTTTTACTATACATACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 444  
DB 538 GTATTGATATGATTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 597  
QY 445 GGTCTGATTTTTCATTAAAAAGA---TGTGCTGTTGATTAACATACATATCGTTG 501  
DB 598 GATGCAAGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 657  
QY 502 GGACCTGATGTTTCTTAAGTTTAAATTCAGAACCTTAATGCTGCTGCTGCTGCTG 561  
DB 658 GTTGCCCTAGATTTCTTAAGTTT---GCCAGGAATCTCTAGGCTCCAGGACATGGGT 714  
QY 562 CTAAAGATCAAGTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 621  
DB 715 TTATTTGATCAACAGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 774  
QY 622 AATCCGATATATTAACGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 668  
DB 775 AATCCTAAAGTGAATCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 821

## RESULT 9

US-09-893-519A-112  
; Sequence 112, Application US/09893519A  
; Publication No. US20030027243A1  
; GENERAL INFORMATION:  
; APPLICANT: ANADYS PHARMACEUTICALS, INC.  
; APPLICANT: THOMPSON, Craig  
; APPLICANT: MOORE, Jeffrey  
; APPLICANT: BURMAN, Ed T.  
; APPLICANT: BRADLEY, John  
; APPLICANT: DESTIVA, Thameira  
; APPLICANT: HARRIS, Sandra  
; APPLICANT: KOMARNITSKY, Svetlana  
; APPLICANT: MENDILLO, Marc  
; APPLICANT: MOORE, Daniel  
; APPLICANT: MCCOY, Melissa  
; APPLICANT: SANDERSON, Karen  
; APPLICANT: HAO, Tariq  
; APPLICANT: ZHU, Shuhao  
; APPLICANT: LONG, Fan  
; APPLICANT: DAVIDOV, Eugene

;; TITLE OF INVENTION: ANTIFUNGAL COMPOUNDS AND METHODS OF USE  
;; FILE REFERENCE: 0342/1G548-US2  
;; CURRENT APPLICATION NUMBER: US/09/893,519A  
;; CURRENT FILING DATE: 2001-06-28  
;; PRIOR APPLICATION NUMBER: US 60/215,164  
;; PRIOR FILING DATE: 2000-06-29  
;; PRIOR APPLICATION NUMBER: US 60/224,457  
;; PRIOR FILING DATE: 2000-08-10  
;; NUMBER OF SEQ ID NOS: 146  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 112  
;; LENGTH: 2444  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
;; PUBLICATION INFORMATION:  
;; DATABASE ACCESSION NUMBER: Human Genbank/NM\_000055  
;; DATABASE ENTRY DATE: 2001-02-03  
;; RELEVANT RESIDUES: (1)..(2444)  
US-09-893-519A-112

Query Match 3.6%; Score 62.2; DB 9; Length 2444;  
Best Local Similarity 54.8%; Pred. No. 6.3e-06;  
Matches 190; Conservative 0; Mismatches 148; Indels 9; Gaps 3;

QY 325 GAGGATTGCTATACCTAAGTGTCTATACGAATATCTAAATCCCGAACTAAACGTCC 384  
DB 509 GAAAGACTGTTATATCTAATGATGATTCACACCTTAACG---AAAAATGCCACT 565  
QY 385 GTTTATATACATACATACATGCGTGTGTTTATATCGGTGAATCATCTGATATAT 444  
DB 566 GTATTGATATGATTTATGAGTGCGTTTCACAACTGGAACATCATCTTACATGTTAT 625  
QY 445 GGTCCGATATATTTTATTAATAAAGA--TGTCGTGTTGATTAACATACATATCGTTG 501  
DB 626 GATGGCAAGTTTCGGTGGTGGTGAAGAGTATTTAGTGTCAATGACATATAGGTCG 685  
QY 502 GGACCTAGTGTGTTTCAAGTTTAAATTCAGAGACCTTAATGCCCCGTAATGCCGC 561  
DB 686 GTGCCCTGATGATTTCTAGCTTT---GCCAGGAATCTGAGCGCTCAGGGAACATGGGT 742  
QY 562 CTTAAGATGATGATGATGCGCTGTTGATTAATAATATGCGCACTTGGTGGC 621  
DB 743 TTATTTATACACAGTTGGCTCTTCAGTGGGTCAAAAAATATATAGAGCTTTGGTGA 802  
QY 622 AATCCCATATATATACAGTCTTTGTAAGAGCCGCGTCTGCTG 668  
DB 803 AATCCTAAGATGATCTCTTTGGAGAAAGTGCAGGACGACCTTC 849

RESULT 10  
US-09-974-300-1107  
;; Sequence 1107, Application US/09974300  
;; Patent No. US20020146721A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Berka, Randy M.  
;; APPLICANT: Clausen, Ib Groth  
;; TITLE OF INVENTION: Methods For Monitoring Multiple Gene  
;; FILE REFERENCE: 10085-500-US  
;; CURRENT APPLICATION NUMBER: US/09/974,300  
;; CURRENT FILING DATE: 2001-10-05  
;; PRIOR APPLICATION NUMBER: 09/680,598  
;; PRIOR FILING DATE: 2000-10-06  
;; PRIOR APPLICATION NUMBER: 60/279,526  
;; PRIOR FILING DATE: 2001-03-27  
;; NUMBER OF SEQ ID NOS: 8481  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 1107  
;; LENGTH: 657  
;; TYPE: DNA  
;; ORGANISM: Bacillus licheniformis  
US-09-974-300-1107

Query Match 3.4%; Score 57.8; DB 10; Length 657;  
Best Local Similarity 49.9%; Pred. No. 4.2e-05;  
Matches 174; Conservative 0; Mismatches 172; Indels 3; Gaps 1;

QY 377 AACGTCCTGTTTATGATACATACATGTTGTTTATTCGG---TGAATATCATC 433  
DB 30 ATCGCTGTTTATGATGATTCATGAGGGCGCTTTTATGCGCGCGGAGATGAC 89  
QY 434 GTGATATGATGTCCTGATTTATTCATTAAGAAAGATGCTGTTGATATACATACAT 493  
DB 90 CGCTATATAGCGGACTCATCTGCAAGACAGGAAGATGATCTGTGATCATCATATT 149  
QY 494 ATCGTTTGGAGCTCTAGGTTTCTAATTAATTACAGAACCTTAATGTCGCCGGA 553  
DB 150 ATGCGCTGATGCTGTTGCTGTTTTCATCTATCTCATATGATATTCCTACAGAGA 209  
QY 554 ATCCGCGCTTAAAGATCAAGTCATGCGCTTGGCTTGAATTAATAATTCGCCCACT 613  
DB 210 ATCTTGCCCTGCTGATCAAAATCGCGCTCTGAGTGGTGAAGACATATATCGCTTCT 269  
QY 614 TTGTCGCAATCCCATATATATACATCTTTGGTGAAGTGCCTGCTGCTTACCC 673  
DB 270 TTGGCGAGACCTCATCTACATTTAGCGTTTGGAGAGTCGCGGATGATGACATCG 329  
QY 674 ACTACATGATGTTAACCGAACAACCTCGCGCTTTTCCATCGTGAT 722  
DB 330 CTTCGCTTTTGGGATGCCGAAAGGAGGCTTTTCAACAGGCAAT 378

RESULT 11  
US-09-934-323-3  
;; Sequence 3, Application US/09934323  
;; Patent No. US20020150910A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Curtiss, Roy A. J.  
;; TITLE OF INVENTION: 33410, A NOVEL HUMAN CARBOXYESTERASE  
;; FILE REFERENCE: 10448-081001  
;; CURRENT APPLICATION NUMBER: US/09/934,323  
;; CURRENT FILING DATE: 2001-08-21  
;; PRIOR APPLICATION NUMBER: US 60/726,774  
;; PRIOR FILING DATE: 2000-08-21  
;; NUMBER OF SEQ ID NOS: 8  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 3  
;; LENGTH: 2508  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-09-934-323-3

Query Match 3.4%; Score 57.6; DB 10; Length 2508;  
Best Local Similarity 54.2%; Pred. No. 0.0001;  
Matches 117; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

QY 530 CAGAAACCTTAATGTCGCCGTAATGCGGCTTAAGATGAAGTCAATGCTTGCCT 589  
DB 671 CCGGGAGCCAGGCTGCAAAAGCAATATGAGCTCTGTGACCAAGTCCAGGCTCGCCT 730  
QY 590 GGATTAATAAATAATGCGCAACTTTGTTGTCGAATCCGATATATTAACGCTTTGGTG 649  
DB 731 GGTCAGTGAATAACATCGCCACTTTGGGGGCGACCCGAGGATTCACATCTTTGGTT 790  
QY 650 AAGTCCGCTGCTGCTTACCCACTACATGATGTTAACGCAAAACCTGCGCTTT 709  
DB 791 CCGGGGAGGCGCTCTGCTGATCACTTCTGATCTCTCCACCATTCAGAGGCGCTGT 850  
QY 710 TCCATGCTGATATGATGCGGTAATGATATTT 745  
DB 851 TCCAGAAAGCCATCGCCGAGAGTGGCACCGCATTT 886

RESULT 12  
US-09-934-323-1

Sequence 1, Application US/09934323  
Patent No. US20020150910A1  
GENERAL INFORMATION:  
APPLICANT: Curtis, Roy A. J.  
TITLE OF INVENTION: 33410, A NOVEL HUMAN CARBOXYLESTERASE  
TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF  
FILE REFERENCE: 10448-081001  
CURRENT APPLICATION NUMBER: US/09/934,323  
CURRENT FILING DATE: 2001-08-21  
PRIOR APPLICATION NUMBER: US 60/226,774  
PRIOR FILING DATE: 2000-08-21  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 4667  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (420)...(2924)  
US-09-934-323-1

Query Match 3.4%; Score 57.6; DB 10; Length 4667;  
Best Local Similarity 54.2%; Pred. No. 0.00014;  
Matches 117; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

QY 530 CAGAGACCTTAATGTCGGCGGTATGCGGCTTAAGATCAAGTCAATGCGCTTGGCT 589  
DB 1090 CCGGGACACGAGCTCAAAAGGCTATGAGGCTCTGACCAATCCAGGCGCTGCT 1149  
QY 590 GGATTAATAATGTCGCGCACTTGTGCAATCCGCAATATTAATTAAGTCTTGGTG 649  
DB 1150 GGCTCAGTAAGAAACATGCGCCACTTTGGGGGAGACCCGAGGATATCAATCTTGGTT 1209  
QY 650 AAGTCCGCGTCTCCCTTCAACCTCAATGATGTTAACGACAACTCGGCTCTT 709  
DB 1210 CCGGGGACGAGGCGCTCTGCGTCAACCTTCGATCTCTCCACCATTCAGAAAGGCTGT 1269  
QY 710 TCCATGCTGATTAATGTCGGGTATGCTATTT 745  
DB 1270 TCCAGAGGCGCATGCGCCAGAGAGTGGCAGCCGCAATTT 1305

RESULT 13  
US-09-954-531-1038  
Sequence 1038, Application US/09954531  
Patent No. US2002015180A1  
GENERAL INFORMATION:  
APPLICANT: Weaver, Zoe  
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cand  
FILE REFERENCE: 689290-77  
CURRENT APPLICATION NUMBER: US/09/954,531  
CURRENT FILING DATE: 2002-05-02  
PRIOR APPLICATION NUMBER: US/60/233,133  
PRIOR FILING DATE: 2000-09-18  
PRIOR APPLICATION NUMBER: US/60/234,009  
PRIOR FILING DATE: 2000-09-20  
PRIOR APPLICATION NUMBER: US/60/234,034  
PRIOR FILING DATE: 2000-09-20  
PRIOR APPLICATION NUMBER: US/60/234,509  
PRIOR FILING DATE: 2000-09-22  
PRIOR APPLICATION NUMBER: US/60/234,567  
PRIOR FILING DATE: 2000-09-22  
NUMBER OF SEQ ID NOS: 1392  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 1038  
LENGTH: 2191  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-954-531-1038

Query Match 3.3%; Score 56.8; DB 9; Length 2191;

Best Local Similarity 53.2%; Pred. No. 0.00015;  
Matches 215; Conservative 0; Mismatches 177; Indels 12; Gaps 4;

QY 322 TCAGAGAGTGTCTATACCTAAGTCTCTATACGAATATCTAATCCGAA--ACTAA 378  
DB 436 TCTGAGAGACTGCTTACCTACGATCTACACGCGCCCAAGCCATGAGGCTCTAAC 495  
QY 379 CGTCCGTTTATATACATACATGAGTGGTGTATTATATGCGTAATCATGCTGAT 438  
DB 496 CTGCGGATGATGCTGTGATCCAGGTGGTGGCTGTTTGG--GCATGGCTTCTTGT 553  
QY 439 ATGATGCTGCTATATTTCAATTAAGATGATGCTGTGATTAATACATACATTCGT 498  
DB 554 ATGATGCTGCTATGCTGCTGCT--TGAGAAAGCTGTGATGATCATACAGTACCC 612  
QY 499 TTGGAGCTCTAGCTTTTCTAATTTAATTCAGAAAGACCTTAATGTCGCGGTATGCG 558  
DB 613 CTGGGTCTCTGGGCTT-----CTTCAGCATGAGAGACAGCAACGCGCAACTGG 666  
QY 559 GGCCTTAAGATCAAGCATGAGCTTGGCTTGGATTAATAATTAATGCGCAACTTGGT 618  
DB 667 GGCTACCTGACCAAGTGGCTGCTACAGCTGCTGCTCAGCAAGATATCGCCACTTGA 726  
QY 619 GCGAATCCGATATATATTAACAGTCTTTGGTGAAGTCCGCGTCTCTACCACTAC 678  
DB 727 GCGAACCCTGACGCTGACCATTTTGGGAGTCTGCGGCTGCGACGAGTGTCTTGG 786  
QY 679 ATGATGTTACCGAACAACCTCGGCTTTTCCATCGTGTAT 722  
DB 787 CTGTGTGTGTCCTCATATCCCAAGGACTCTTCCAGGAGCCAT 830

RESULT 14  
US-09-880-107-3854  
Sequence 3854, Application US/09880107  
Patent No. US20020142981A1  
GENERAL INFORMATION:  
APPLICANT: Horne, Darci T.  
APPLICANT: Vockley, Joseph G.  
APPLICANT: Scherf, Uwe  
TITLE OF INVENTION: Gene Logic, Inc.  
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer  
FILE REFERENCE: 44921-5028-WO  
CURRENT APPLICATION NUMBER: US/09/880,107  
CURRENT FILING DATE: 2001-06-14  
PRIOR APPLICATION NUMBER: US 60/211,379  
PRIOR FILING DATE: 2000-06-14  
PRIOR APPLICATION NUMBER: US 60/237,054  
PRIOR FILING DATE: 2000-10-02  
NUMBER OF SEQ ID NOS: 3950  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 3854  
LENGTH: 2191  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: Genbank Accession No. US20020142981A1 Y09616  
US-09-880-107-3854

Query Match 3.3%; Score 56.8; DB 10; Length 2191;  
Best Local Similarity 53.2%; Pred. No. 0.00015;  
Matches 215; Conservative 0; Mismatches 177; Indels 12; Gaps 4;

QY 322 TCAGAGAGTGTCTATACCTAAGTCTCTATACGAATATCTAATCCGAA--ACTAA 378  
DB 436 TCTGAGAGACTGCTTACCTACGATCTACACGCGCCCAAGCCATGAGGCTCTAAC 495  
QY 379 CGTCCGTTTATATACATACATGAGTGGTGTATTATATGCGTAATCATGCTGAT 438  
DB 496 CTGCGGATGATGCTGTGATCCAGGTGGTGGCTGTTTGG--GCATGGCTTCTTGT 553  
QY 439 ATGATGCTGCTATATTTCAATTAAGATGATGCTGTGATTAATACATACATTCGT 498

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Db 554 ATGATGCTTCATGCTGGCTGCT-76GAGAACGTGGTGTGTCATCATTCACATACCGC 612
QY 499 TTGGAGCTCTAGCTTTTCTTAAGTTAAATTCAGACACCTTAATGTGCCGGTAATGCC 558
Db 613 CTGGGTGCTCGGGCTT-----CTTCAGCACTGTGACACAGCAGCAACCGGGAACCTGG 666
QY 559 GGCCTTAAAGATCAATGATGAGCCCTTGGATTAATAAATAATTCGCCCACTTTGGT 618
Db 667 GGCTACCTGTGACCAAGTGGCTGACACCTGCTGGGTCCAGACAGATATGCGCACTTTGA 726
QY 619 GGCATCCCGATATATATACAGTCTTTGGTGAAGTCCGGTGTGCTCTACCCACTAC 678
Db 727 GGCACACCTGTGACCTGTGACCATTTTGGGAGTGTGCGGAGTGGCAGAGTGTCTTGC 786
QY 679 ATGATGTTAACCGAACAACTCGCGGTCTTTCCATGCTGTAT 722
Db 787 CTGTGTGTGTCCCATATCCCAAGGACTCTTCCACGAGCCAT 830

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## RESULT 15

```

US-10-102-806-271
; Sequence 271, Application US/10102806
; Publication No. US20030054421A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA103P1C1
; CURRENT APPLICATION NUMBER: US/10/102,806
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 09/925,298
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05881
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 846
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 271
; LENGTH: 2484
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (194)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (623)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (2396)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (2484)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-102-806-271

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Query Match 3.3%; Score 56.8; DB 9; Length 2484;
Best Local Similarity 53.2%; Pred. No. 0.00016;
Matches 215; Conservative 0; Mismatches 177; Indels 12; Gaps 4;

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QY 322 TCAGAGGATGTTCTAATCTAGTGTCTATAGCAATATCTAATCCGAA--ACTAAA 378
Db 950 TCTGAGAGACTGCTCTGACTCTACATCTACACGCGCCCATAGCCATGAGGCTCTAAC 1009
QY 379 GCTCCGCTTTATATACATACATGATGATGATGATGATGATGATGATGATGATGATGAT 438
Db 1010 CTGCGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1067
QY 439 ATGATGCTCTGATATTTCTAATAAAGATGATGATGATGATGATGATGATGATGATGAT 498
Db 1068 ATGATGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1126
QY 499 TTGGAGCTCTAGTGTCTAATGTTAATTCAGAACCTTAATGTGCCCGGTATGCC 558

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Db 1127 CTGGGTGCTCGGGCTT-----CTTCAGCACTGTGACACAGCAGCAACCGGCACTGG 1180
QY 559 GGCCTTAAAGATCAATGATGAGCCCTTGGATTAATAAATAATTCGCCCACTTTGGT 618
Db 1181 GGCTACCTGTGACCAAGTGGCTGACACCTGCTGGGTCCAGACAGATATGCGCACTTTGA 1240
QY 619 GGCATCCCGATATATATACAGTCTTTGGTGAAGTCCGGTGTGCTCTACCCACTAC 678
Db 1241 GGCACACCTGTGACCTGTGACCATTTTGGGAGTGTGCGGAGTGGCAGAGTGTCTTGC 1300
QY 679 ATGATGTTAACCGAACAACTCGCGGTCTTTCCATGCTGTAT 722
Db 1301 CTGTGTGTGTCCCATATCCCAAGGACTCTTCCACGAGCCAT 1344

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Search completed: April 11, 2003, 13:24:04
Job time : 105.528 secs

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GenCore version 5.1.4.p5.4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 4, 2003, 09:08:22 ; Search time 44.0154 Seconds

(without alignments)  
1725.596 Million cell updates/sec

Title: US-09-776-910-13

Perfect score: 3045

Sequence: 1 MFPLKQFIRLKLCKVCNVN.....PEMDKIKGASIFDKKLEF 570

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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- 2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*
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- 22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*
- 23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3017	99.1	570	18	AAW17767
2	2348	77.1	570	16	AAW17767
3	2348	77.1	570	18	AAW17767
4	2335	76.7	570	18	AAW17767
5	2335	76.7	570	18	AAW17767
6	1844.5	60.6	572	22	ABBS7850
7	1330	43.7	554	22	ABBS7866
8	1311	43.1	572	22	ABBS7867
9	1298.5	42.6	567	22	ABBS7857
10	1277.5	42.0	554	22	ABBS9161

11	1267.5	41.6	566	22	ABBS1983
12	1236.5	40.6	565	22	ABBS7746
13	1217	40.0	530	22	ABBS7868
14	1204	39.5	542	22	ABBS7790
15	1194.5	39.2	602	23	AAW47598
16	994	32.6	551	22	ABBS7788
17	948.5	31.1	541	22	ABBS7789
18	899	29.5	568	22	ABBS7831
19	795	26.1	528	22	AAW57862
20	795	26.1	528	22	AAE12916
21	793	26.0	513	19	AAW57863
22	741.5	24.4	562	22	ABBS7708
23	735.5	24.2	550	19	AAW57864
24	735.5	24.2	550	19	AAW57865
25	735.5	24.2	550	19	AAW57853
26	735.5	24.2	550	19	AAW57854
27	735.5	24.2	550	22	AAE12910
28	735.5	24.2	550	22	AAE12923
29	733.5	24.1	530	19	AAW57855
30	733.5	24.1	530	19	AAW57877
31	733.5	24.1	530	22	AAE12911
32	723.5	23.8	505	19	AAW57851
33	722.5	23.7	505	19	AAW57852
34	722.5	23.7	505	22	AAE12909
35	721.5	23.7	495	19	AAW57869
36	693	22.8	530	19	AAW57866
37	693	22.8	530	19	AAW57867
38	690.5	22.7	527	22	ABBS64915
39	662	21.7	527	22	ABBS6353
40	641.5	21.1	584	23	ABBS6766
41	635	20.9	575	23	ABBS79538
42	624	20.5	570	19	AAW57860
43	624	20.5	570	19	AAW57879
44	624	20.5	570	22	AAE12915
45	624	20.5	595	19	AAW57859

## ALIGNMENTS

RESULT 1  
AAW17767  
ID AAW17767 standard; Protein: 570 AA.

AC AAW17767 ;

DT 08-AUG-1997 (first entry)

DE Md-alpha-E7 malathion resistant mutant.

XX Malathion carboxylesterase; organophosphate; insecticide;  
pesticide; remediation; bioremediation; decontamination.

OS Musca domestica Rutgers strain.

XX Key Location/Qualifiers

FT Misc-difference 251 /note= "Ser-251 is tryptophan in the susceptible  
allele expression product"

FT

PN W0919176-A1.

PD 29-MAY-1997.

XX 22-NOV-1996; 96MO-AU00746.

PF 23-NOV-1995; 95AU-0006751.

PR (CSIR ) COMMONWEALTH SCI & IND RES ORG.

PA Boyce T, Brownlie JC, Campbell PM, Claudianos C;  
Newcomb RD, Oakeshott JG, Robin GC, Russell RJ, Smyth K;

DR WPI; 1997-298113/27.  
 DR N-PSDB; AAT68597.  
 XX DNA encoding enzyme that degrades organophosphate pesticides -  
 PT useful for decontamination of soil, water, food etc  
 XX  
 XX Disclosure: Fig 3; 52pp; English.  
 XX  
 CC A polypeptide (AAW17767) is the expression product of a malathion  
 CC resistant allele of the *Musca domestica* Md-alpha-E7 gene, and  
 CC contains a Ser for Trp substn. at amino acid position 251. The  
 CC enzyme is capable of hydrolysing carboxylester and/or  
 CC diethylloxon organophosphates and can be formulated for use  
 CC in bioremediation strategies for treatment of soil or water.  
 CC  
 XX  
 XX Sequence 570 AA;  
 SQ

Query Match 99.1%; Score 3017; DB 18; Length 570;  
 Best Local Similarity 99.3%; Pred. No. 6.8e-276;  
 Matches 566; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MFLKOFIFRLKCYKCMVNTYNTRLSTNETQIIDTEYGOIKGYKMTVYDSDYSFES 60  
 DB 1 MFLKOFIFRLKCYKCMVNTYNTRLSTNETQIIDTEYGOIKGYKMTVYDSDYSFES 60  
 QY 61 IPYAKPVGELRFKAPQRPVPEWEGVRDCCGPANRSVQTDFTSGKPTGSEDCLYLVNTND 120  
 DB 61 IPYAKPVGELRFKAPQRPVPEWEGVRDCCGPANRSVQTDFTSGKPTGSEDCLYLVNTND 120  
 QY 121 LNPDKRRPVYVFIHGDFIFGEANRWNGPDPYEMKRPVLYVYQRLGVLGFLSLKSEN 180  
 DB 121 LNPDKRRPVYVFIHGDFIFGEANRWNGPDPYEMKRPVLYVYQRLGVLGFLSLKSEN 180  
 QY 181 NVPGNAGLKDOVMALRWYKSNIAIFGSDVNTVFGESAGASTHYMMITEQTRGLFHRG 240  
 DB 181 NVPGNAGLKDOVMALRWYKSNIAIFGSDVNTVFGESAGASTHYMMITEQTRGLFHRG 240  
 QY 241 IMMSGNSMCWASTECQSRALTMARVGYKGEDNEKDILEFLMKANPYDLIKEBPQVLT 300  
 DB 241 IMMSGNSMCWASTECQSRALTMARVGYKGEDNEKDILEFLMKANPYDLIKEBPQVLT 300  
 QY 301 ERMQKVMPEPGPTVEPYOTADCVKPIREWKSAMGNSIPTLLGNSTYGLLSKSTAK 360  
 DB 301 ERMQKVMPEPGPTVEPYOTADCVKPIREWKSAMGNSIPTLLGNSTYGLLSKSTAK 360  
 QY 361 QYPEVVKELSCVNYVPELADSESAPELTERAAIVKKAHVDEGPTPLDNFMELCSFY 420  
 DB 361 QYPEVVKELSCVNYVPELADSESAPELTERAAIVKKAHVDEGPTPLDNFMELCSFY 420  
 QY 421 FLFPMHRLQLRFNHTAGTPILYLRFDSEELINPYRIMRFGKGVKGVSHADELTLYLFW 480  
 DB 421 FLFPMHRLQLRFNHTAGTPILYLRFDSEELINPYRIMRFGKGVKGVSHADELTLYLFW 480  
 QY 481 NILSKRLKESREYKTIERRMGIWTEFAATGKPYSNIDLAGMENLTPDIKSDVYKCLN 540  
 DB 481 NILSKRLKESREYKTIERRMGIWTEFAATGKPYSNIDLAGMENLTPDIKSDVYKCLN 540  
 QY 541 IGDELKVMDEPMOKIKOGASIFDKKELF 570  
 DB 541 IGDELKVMDEPMOKIKOGASIFDKKELF 570

RESULT 2  
 AAR78142  
 ID AAR78142 standard; Protein: 570 AA.  
 XX  
 AC AAR78142;  
 XX  
 DT 22-DEC-1995 (first entry)  
 XX  
 DE OP-sensitive esterase E3.  
 XX  
 KW Esterase; E3; bioremediation; organophosphate; carbamate;

KW Insecticide; pesticide; water decontamination; meat decontamination.  
 XX  
 XX *Lucilia cuprina*.  
 OS  
 XX W09519440-A1.  
 PN  
 XX 20-JUL-1995.  
 PD  
 XX  
 XX 13-JAN-1995; 95NO-AU00016.  
 PF  
 XX 13-JAN-1994; 94AU-0003347.  
 PK  
 XX (CSIR ) COMMONWEALTH SCI & IND RES ORG.  
 PA  
 XX Boyce TM, Campbell PM, Newcomb RD, Oakeshott JG;  
 PI Parker AG, Robin GC, Russell RJ, Smyth K;  
 DR N-PSDB; AAQ91561.  
 DR WPI; 1995-263870/34.  
 XX  
 XX Pure E3 esterase from *Lucilia cuprina* and related DNA - used to  
 PT eliminate residues of organo:phosphate and carbamate pesticides from  
 PT water, meat etc.  
 XX  
 PS Example 3; Page 12-17; 38pp; English.  
 XX  
 CC cDNA from organophosphate (OP)-sensitive *L. cuprina* pupa cDNA  
 CC library was amplified using cluster-specific esterase primers.  
 CC Isolated clone lc743, a probable full-length cDNA, was expressed  
 CC using a baculovirus vector in insect cells and shown to encode  
 CC an OP-susceptible E3 esterase useful in bioremediation.  
 CC  
 XX  
 XX Sequence 570 AA;  
 SQ

Query Match 77.1%; Score 2348; DB 16; Length 570;  
 Best Local Similarity 74.2%; Pred. No. 1.1e-212;  
 Matches 423; Conservative 73; Mismatches 74; Indels 0; Gaps 0;

QY 1 MFLKOFIFRLKCYKCMVNTYNTRLSTNETQIIDTEYGOIKGYKMTVYDSDYSFES 60  
 DB 1 MFLKOFIFRLKCYKCMVNTYNTRLSTNETQIIDTEYGOIKGYKMTVYDSDYSFES 60  
 QY 61 IPYAKPVGELRFKAPQRPVPEWEGVRDCCGPANRSVQTDFTSGKPTGSEDCLYLVNTND 120  
 DB 61 IPYAKPVGELRFKAPQRPVPEWEGVRDCCGPANRSVQTDFTSGKPTGSEDCLYLVNTND 120  
 QY 121 LNPDKRRPVYVFIHGDFIFGEANRWNGPDPYEMKRPVLYVYQRLGVLGFLSLKSEN 180  
 DB 121 LNPDKRRPVYVFIHGDFIFGEANRWNGPDPYEMKRPVLYVYQRLGVLGFLSLKSEN 180  
 QY 181 NVPGNAGLKDOVMALRWYKSNIAIFGSDVNTVFGESAGASTHYMMITEQTRGLFHRG 240  
 DB 181 NVPGNAGLKDOVMALRWYKSNIAIFGSDVNTVFGESAGASTHYMMITEQTRGLFHRG 240  
 QY 241 IMMSGNSMCWASTECQSRALTMARVGYKGEDNEKDILEFLMKANPYDLIKEBPQVLT 300  
 DB 241 IMMSGNSMCWASTECQSRALTMARVGYKGEDNEKDILEFLMKANPYDLIKEBPQVLT 300  
 QY 301 ERMQKVMPEPGPTVEPYOTADCVKPIREWKSAMGNSIPTLLGNSTYGLLSKSTAK 360  
 DB 301 ERMQKVMPEPGPTVEPYOTADCVKPIREWKSAMGNSIPTLLGNSTYGLLSKSTAK 360  
 QY 361 QYPEVVKELSCVNYVPELADSESAPELTERAAIVKKAHVDEGPTPLDNFMELCSFY 420  
 DB 361 QYPEVVKELSCVNYVPELADSESAPELTERAAIVKKAHVDEGPTPLDNFMELCSFY 420  
 QY 421 FLFPMHRLQLRFNHTAGTPILYLRFDSEELINPYRIMRFGKGVKGVSHADELTLYLFW 480  
 DB 421 FLFPMHRLQLRFNHTAGTPILYLRFDSEELINPYRIMRFGKGVKGVSHADELTLYLFW 480  
 QY 481 NILSKRLKESREYKTIERRMGIWTEFAATGKPYSNIDLAGMENLTPDIKSDVYKCLN 540  
 DB 481 NILSKRLKESREYKTIERRMGIWTEFAATGKPYSNIDLAGMENLTPDIKSDVYKCLN 540





CC a substr. of the tryptophan residue at amino acid position 251.  
 CC The enzyme is capable of hydrolyzing carboxylester and/or  
 CC dimethylloxon organophosphates and can be formulated for use in  
 CC bioremediation strategies for treating soil or water.

SO Sequence 570 AA;

Query Match 76.7%; Score 2335; DB 18; Length 570;  
 Best Local Similarity 74.0%; Pred. No. 1.9e-211;  
 Matches 422; Conservative 73; Mismatches 75; Indels 0; Gaps 0;

QY 1 MTFLEQFIRLKLVCYKCNKNTNRLSTNETQIITDEYGOIKGKRYVYDSDYSFES 60  
 DB 1 MNFNLSLMERKAKKIKCKENKFLNRLTNEVVAETEGYKGVKRLVYDSDYSFEG 60  
 QY 61 IPIYAKPVGELRFAKAPORPVWEGVRDCCGPANRSVOTDFISGKPTSEDELTANYTND 120  
 DB 61 IPIYAPVPELRFKAPORPTPMDCVRDCCNHNKSKSVQVDFITTKVCGSECLTLYSTNN 120  
 QY 121 LNPDKRRPVWVETIHGSDPIFGSEANRNFPGDYTKKRPVLTVOYRLGVGLFSLKSENT 180  
 DB 121 LNPETKRPVLYIHGGFIIIGENHRDMYGPDIYIKKDVVLINIQYRLGALGFLSNEEDL 180  
 QY 181 NVPGNAGLKDQVVALRWKSNIAIFGSDVDNITVFESAGASTHYMMLTEQTRGLFHGG 240  
 DB 181 NVPGNAGLKDQVVALRWKSNIAIFGSDVDNITVFESAGASTHYMMLTEQTRGLFHGG 240  
 QY 241 IMNSGNSMCWASTECOSRALYMAKRVYKGEDNEKDLLEFLKANPYDLIKEEPOVLTLP 300  
 DB 241 IMNSGNAICPXANTQCOHRAFTLAKLAGYKGEDNDKDVLEFLKAKPODLIKEEVLTLP 300  
 QY 301 ERMOKNMFEPFGPTVEPYQADCVKPRPIREMYKSAWNSIPTLIGNTSYEGLSKSVAK 360  
 DB 301 EERTNKVMFPFGPTVEPYQADCVLPKHPREMYKTAWNSIPTLIGNTSYEGLEFSTILK 360  
 QY 361 QYEVYKELSCVNYVPELADSEASAPETLERAAIVKKAHVDGETPTLIDNEMELCSYFY 420  
 DB 361 QMPMLVYKELSCVNYVPELADSEASAPETLERAAIVKKAHVDGETPTLIDNEMELCSHYY 420  
 QY 421 FLFPMHRLDQLRNHTAGPTIYLRPDSEELINPYRIMRGKGVKGVSHADELTLYLFW 480  
 DB 421 FWFPMHRLDQLRNHTAGPTIYLRPDSEELINPYRIMRGKGVKGVSHADELTLYLFW 480  
 QY 481 NILSKRLPKESREYKTIETRMVGIWTEFATGKPYNSNDIAGENMLTMDPIKSSDDVYKCLN 540  
 DB 481 NOLAKRMPKESREYKTIETRMVGIWTEFATGKPYNSNEIEGMENTVMDPIKSSDEVYKCLN 540  
 QY 541 IGDELKYMDDPEMDKIKOGASIFDKKKELF 570  
 DB 541 ISDELKIMDIVPEMDKIKOWESMEFEXHRDLF 570

RESULT 5  
 AAM17768  
 ID AAM17768 standard; Protein: 570 AA.  
 AC AAM17768;  
 XX

DT 08-AUG-1997 (first entry)

DE Malathion carboxylesterase RM8Con.

KM Malathion carboxylesterase; organophosphate; insecticide;  
 KW pesticide; remediation; bioremediation; decontamination; esterase;  
 KX Lucilia cuprina.

OS Lucilia cuprina.

PN MO9719176-A1.

PD 29-MAY-1997.

PF 22-NOV-1996; 96MO-AU00746.

XX 23-NOV-1995; 95AU-0006751.  
 PR (CSIR) COMMONWEALTH SCI & IND RES ORG.  
 PA Boyce T, Brownlie JC, Campbell PM, Claudianos C,  
 PI Newcomb RD, Oakeshott JG, Robin GC, Russell RJ, Smyth K;  
 DR WPI: 1997-298113/27.

XX DNA encoding enzyme that degrades organophosphate pesticides -  
 PT useful for decontamination of soil, water, food etc  
 PS Claim 6; Fig 1; 52pp; English.

CC A malathion carboxylesterase (AAM17768), designated RM-8Con, differs  
 CC from the esterase (AAM17765) of a malathion susceptible clone of  
 CC Lucilia cuprina by a substr. of the tryptophan residue at amino  
 CC acid position 251 by a leucine residue. This mutation is situated  
 CC at the base of the active site gorge, 6.5 Angstroms from the active  
 CC site serine. The RM8Con amino acid sequence is a consensus deduced  
 CC from the DNA sequences of 3 resistant clones (RM8 A-C) and their  
 CC comparison to reference susceptible clone Lc743 (AAR68596) of  
 CC Lc-alpha-E7. The enzyme is capable of hydrolyzing carboxylester  
 CC and/or dimethylloxon organophosphates and can be formulated for use  
 CC in bioremediation strategies for treatment of soil or water.

SO Sequence 570 AA;

Query Match 76.7%; Score 2335; DB 18; Length 570;  
 Best Local Similarity 74.0%; Pred. No. 1.9e-211;  
 Matches 422; Conservative 73; Mismatches 75; Indels 0; Gaps 0;

QY 1 MTFLEQFIRLKLVCYKCNKNTNRLSTNETQIITDEYGOIKGKRYVYDSDYSFES 60  
 DB 1 MNFNLSLMERKAKKIKCKENKFLNRLTNEVVAETEGYKGVKRLVYDSDYSFEG 60  
 QY 61 IPIYAKPVGELRFAKAPORPVWEGVRDCCGPANRSVOTDFISGKPTSEDELTANYTND 120  
 DB 61 IPIYAPVPELRFKAPORPTPMDCVRDCCNHNKSKSVQVDFITTKVCGSECLTLYSTNN 120  
 QY 121 LNPDKRRPVWVETIHGSDPIFGSEANRNFPGDYTKKRPVLTVOYRLGVGLFSLKSENT 180  
 DB 121 LNPETKRPVLYIHGGFIIIGENHRDMYGPDIYIKKDVVLINIQYRLGALGFLSNEEDL 180  
 QY 181 NVPGNAGLKDQVVALRWKSNIAIFGSDVDNITVFESAGASTHYMMLTEQTRGLFHGG 240  
 DB 181 NVPGNAGLKDQVVALRWKSNIAIFGSDVDNITVFESAGASTHYMMLTEQTRGLFHGG 240  
 QY 241 IMNSGNSMCWASTECOSRALYMAKRVYKGEDNEKDLLEFLKANPYDLIKEEPOVLTLP 300  
 DB 241 IMNSGNAICPXANTQCOHRAFTLAKLAGYKGEDNDKDVLEFLKAKPODLIKEEVLTLP 300  
 QY 301 ERMOKNMFEPFGPTVEPYQADCVKPRPIREMYKSAWNSIPTLIGNTSYEGLSKSVAK 360  
 DB 301 EERTNKVMFPFGPTVEPYQADCVLPKHPREMYKTAWNSIPTLIGNTSYEGLEFSTILK 360  
 QY 361 QYEVYKELSCVNYVPELADSEASAPETLERAAIVKKAHVDGETPTLIDNEMELCSYFY 420  
 DB 361 QMPMLVYKELSCVNYVPELADSEASAPETLERAAIVKKAHVDGETPTLIDNEMELCSHYY 420  
 QY 421 FLFPMHRLDQLRNHTAGPTIYLRPDSEELINPYRIMRGKGVKGVSHADELTLYLFW 480  
 DB 421 FWFPMHRLDQLRNHTAGPTIYLRPDSEELINPYRIMRGKGVKGVSHADELTLYLFW 480  
 QY 481 NILSKRLPKESREYKTIETRMVGIWTEFATGKPYNSNDIAGENMLTMDPIKSSDDVYKCLN 540  
 DB 481 NOLAKRMPKESREYKTIETRMVGIWTEFATGKPYNSNEIEGMENTVMDPIKSSDEVYKCLN 540  
 QY 541 IGDELKYMDDPEMDKIKOGASIFDKKKELF 570  
 DB 541 ISDELKIMDIVPEMDKIKOWESMEFEXHRDLF 570

XX	RESULT 6
ABBS57850	
ID	ABB57850 standard; Protein; 572 AA.
AC	ABB57850;
DT	26-MAR-2002 (first entry)
DE	Drosophila melanogaster polypeptide SEQ ID NO 342.
KW	Drosophila developmental biology; cell signalling; insecticide; pharmaceutical.
OS	Drosophila melanogaster.
PN	WO200171042-A2.
PD	27-SEP-2001.
PF	23-MAR-2001; 2001WO-US09231.
PR	23-MAR-2000; 2000US-191637P. 11-JUL-2000; 2000US-0614150.
PA	(PEKE ) PE CORP NY.
PI	Venter JC, Adams M, Li PWD, Myers EW;
DR	WPI: 2001-656860/75.
XX	N-PSDB; ABL01953.
PT	New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
PS	Disclosure: SEQ ID NO 342; 21pp + Sequence Listing; English.
CC	The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL01840-ABL16175), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-ABBS72072).
CC	The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
SQ	Sequence 572 AA:
Query Match	60.6%; Score 1844.5; DB 22; Length 572;
Best Local Similarity	59.9%; Pred. No. 4.3e-165;
Matches 338; Conservative 93; Mismatches 132; Indels 1; Gaps 1.	
Y	7 FIFRLKLCVKCMVNTYTRLSTNEFQIIDTEYGQIKGYKRMIVYDYSFESEIPYAKP 66
Db	7 FEERLRMRWKRTIEHKVVQVRGOSTNETRYADVETGYGRIGKRSLSDVDVPFFSFGICPYAP 66
Y	67 PYVEGLRFAAPORPVWEVGGVRCDCGPANNSVOTDFISGKFTSGEDCLYLNVYTNDLPDKR 126
Db	67 PVGEGLRFAAPORPPIWERVRDCSQPKDAVQVFDFDKVGESDECLYLVNYNNVYPDKA 126
Y	127 RVPMVFIHGCDTICEEARNMNGPPYPMKKPVLYLTVOYRGVLGFLSIKSSENINWPANA 186
Db	127 RPYVMVFIHGGCFTICEEARNEMTGPDTFEKEDVAVLTIOIRLGALGMSSLSKSELNPANA 186
Y	187 GLKDQVALNRWKNIAITFGGDVNITYVGSASAGASTHYMMITEQTRLFRGIIMMSGN 246
Db	187 GLKDQVALNRWKNNCASPBGDPNCITYVGESASAGASTHYMLTDQTQSFLFRGLIIGSS 246
Y	247 SMCSPA-STECOSRALTKAKRVGYGEDNEKDILFLMKANDYDLIKEEPVLTPERRMON 305

[illegible]

RESULT 7  
 ABB57866  
 ID ABB57866 standard; Protein; 554 AA.  
 XX  
 AC ABB57866;  
 XX  
 DT 26-MAR-2002 (first entry)  
 XX  
 DE Drosophila melanogaster polypeptide SEQ ID NO 390.  
 XX  
 KW Drosophila; developmental biology; cell signalling; insecticide;  
 KW pharmaceutical.  
 XX  
 OS Drosophila melanogaster.  
 XX  
 WO200171042-A2.  
 XX  
 PN 27-SEP-2001.  
 PD  
 XX  
 PF 23-MAR-2001; 2001WO-US09231.  
 XX  
 PR 23-MAR-2000; 2000US-191637P.  
 PR 11-JUL-2000; 2000US-0614150.  
 XX  
 PA (PEKE ) PE CORP NY.  
 XX  
 PI Venter JC, Adams M, Li PWD, Myers EW;  
 DR WPI: 2001-656860/75.  
 DR N-PSDB; ABL01969.  
 XX  
 PT New isolated nucleic acid detection reagent for detecting 1000 or more  
 PT genes from Drosophila and for elucidating cell signalling and cell-cell  
 PT interactions -  
 XX  
 PS Disclosure; SEQ ID NO 390; 21pp + Sequence Listing; English.  
 XX  
 XX The invention relates to an isolated nucleic acid detection reagent  
 CC capable of detecting 1000 or more genes from Drosophila. The invention is  
 CC useful in developmental biology and in elucidating cell signalling and  
 CC cell-cell interactions in higher eukaryotes for the development of  
 CC insecticides, therapeutics and pharmaceutical drugs. The invention  
 CC discloses genomic DNA sequences (ABL01840-ABL16175), expressed DNA  
 CC sequences (ABL01840-ABL16175) and the encoded proteins  
 CC (ABB57737-ABB72072).  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pctl\_sequences.  
 XX

SQ Sequence 554 AA:  
 Query Match 43.7%; Score 1330; DB 22; Length 554;  
 Best Local Similarity 47.6%; Pred. No. 1.7e-116;  
 Matches 264; Conservative 95; Mismatches 184; Indels 12; Gaps 7;

21 KTYNRLSTNEQIIDTEGQIKGVKRMVYDSDYSFESIPAKPPVELRKAQRPV 80  
 5 KYQQRRTSEKTVSTTYGPIKGVKRSIYGSTYSFERIPAKPPVELRKAQRPV 64  
 81 PWEVGRDCCGPNRNVQDTPISGKPTGSDCLVNTYNDLNDKRRPVPWFHGGDTF 140  
 65 VWEVRSCTSGQPKLQKHFEVEMTDGSDCLVNTYNTKLPYTKMPVWVWYGGGFGF 124  
 141 GEANRRWFGDPDPMKPPVLTVOYRLGVLFSLKSEMLNVPNGNGLKDOVALRWVS 200  
 125 GEASRECYSPDYLRDQVVISINRYLGLFLCLDDPELDVPGNGLKDOVALRWVA 184  
 201 NTAIFGVDNITVFEESAGASTHYMTTEQTRGLFHRGIMSGNSMSTECQSPRA 260  
 185 NCSRFQDSANITIFGDSAGASVHYMTTEQTHGLFHKALCMGNTLSPMAVTPORNMP 244  
 261 LMAKRVGKGDENEDILEFLKANPYDLKEEPOVLPERMKNQVMPFEGTTPYOT 320  
 245 YRLAVQAGYAGENNTRDVEFLKNAKSEITKANGLCIDDEEKERRIGSEFGEVIEPYVT 304  
 321 ADCVAPKPREMYKSAWGSNIPITLIGNTSYEGLLSKSAKQYEPVVEKESCVNVPWEL 380  
 305 SHCVAPKRIEMKRTAMSNIPILIGVSNEGLLYSETKNKCLNELDDCFVVPFIEL 364  
 381 ADSESAPELTERAIVKKAHVDGETPLD--NEMELCSYEFELFPMHRELQLRNHTA 437  
 365 -NMDRESALCREYGDDLRQCYGDKTPSLDTHLEYLQWNSHEFWEPIRYKTVLSRLQYAR 423  
 438 GTPPIVYRDPDSEELINRYIRMRGKGVKGVSHADELYLEWNLISKLPRKSERYKPT 497  
 424 SAPTYVYRDPDPSKH-FNHLRILSCGKVKRGTCGGDLSYLEFNSLARKLKNNHTREKCI 482  
 498 EMWVGITFEATTKPKPYSDIAGMENLTV--DPIKSSDVYKCLNIGDELKYMDELPEMD 554  
 483 ERLVGLMTLHFAACGNP--NFDPQEDL-WQVPDPAVEKHQKCLNLSDELKVIDVPLDK 539  
 555 KIKQGASIFDKKEL 569  
 540 KLMWSEFF-RRDEL 553

RESULT 8  
 ABB57867  
 ID ABB57867 standard; Protein; 572 AA.  
 XX  
 AC ABB57867;  
 XX  
 DT 26-MAR-2002 (first entry)  
 XX  
 DE Drosophila melanogaster polypeptide SEQ ID NO 393.  
 XX  
 KW Drosophila; developmental biology; cell signalling; insecticide;  
 XX  
 KW pharmaceutical.  
 XX  
 OS Drosophila melanogaster.  
 XX  
 PN WO200171042-A2.  
 PD  
 XX 27-SEP-2001.  
 PF 23-MAR-2001; 2001WO-US09231.  
 XX  
 PR 23-MAR-2000; 2000US-191637P.  
 XX  
 PR 11-JUL-2000; 2000US-0614150.  
 XX  
 PA (PEKE ) PE CORP NY.  
 XX

PI Venter JC, Adams M, Li PMD, Myers EW;  
 XX  
 DR WPI: 2001-656860/75.  
 XX  
 DR N-PSDB; AB01970.  
 XX  
 PT New isolated nucleic acid detection reagent for detecting 1000 or more  
 PT genes from Drosophila and for elucidating cell signalling and cell-cell  
 XX interactions -  
 PS  
 SQ Disclosure; SEQ ID NO 393; 21pp + Sequence Listing; English.  
 CC  
 CC The invention relates to an isolated nucleic acid detection reagent  
 CC capable of detecting 1000 or more genes from Drosophila. The invention is  
 CC useful in developmental biology and in elucidating cell signalling and  
 CC cell-cell interactions in higher eukaryotes for the development of  
 CC insecticides, therapeutics and pharmaceutical drugs. The invention  
 CC discloses genomic DNA sequences (AB16176-AB163051), expressed DNA  
 CC sequences (AB101840-AB16175) and the encoded proteins  
 CC (AB57737-AB72072).  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.int/pub/published\_pct\_sequences.  
 CC  
 XX  
 SQ Sequence 572 AA:  
 Query Match 43.1%; Score 1311; DB 22; Length 572;  
 Best Local Similarity 46.1%; Pred. No. 1.1e-114;  
 Matches 264; Conservative 95; Mismatches 184; Indels 30; Gaps 8;

21 KTYNRLSTNEQIIDTEGQIKGVKRMVYDSDYSFESIPAKPPVELRKAQRPV 80  
 5 KYQQRRTSEKTVSTTYGPIKGVKRSIYGSTYSFERIPAKPPVELRKAQRPV 64  
 81 PWEVGRDCCGPNRNVQDTPISGKPTGSDCLVNTYNDLNDKRRPVPWFHGGDTF 140  
 65 VWEVRSCTSGQPKLQKHFEVEMTDGSDCLVNTYNTKLPYTKMPVWVWYGGGFGF 124  
 141 GEANRRWFGDPDPMKPPVLTVOYRLGVL-----GFLSKSENLV 182  
 125 GEASRECYSPDYLRDQVVISINRYLGLTNDTKKKHIFNISLPGLCIDDEELDY 184  
 183 PGNAGLKDOYMLRWKNSNATFGGDVNTVFEESAGASTHYMTTEQTRGLFHRGIM 242  
 185 PGNAGLKDOYMLRWKNSNATFGGDVNTVFEESAGASTHYMTTEQTRGLFHRGIM 244  
 243 MSGNSMCSWASTECQSRALTMARVGYKGDENEDILEFLKANPYDLKEEPOVLPER 302  
 245 MSGNTLSPMAVTPORNMPYRLAVQAGYAGENNTRDVEFLKNAKSEITKANGLCIDDE 304  
 303 MOKKVPFPGPIYEPYQADCVKPIREMYKSAWGSNIPITLIGNTSYEGLLSKSAKQY 362  
 305 KKERIGSEFGEPIEPTVTSCHVAPKPIEMKRTAMSNIPILIGVSNEGLLYSETKN 364  
 363 PEVVKELSCVNVVPELADSESAPELTERAIVKKAHVDGETPLD--NFMELCSYF 419  
 365 PKCLNELDDCFVVPFIEL-NMDRESALCREYGQDLQCYGDKTPSLDTHLEYLQWNSHE 423  
 420 YLEFPMHRELQLRFNHTAGTPVLYRFPDSEELINRYIRMRGKGVKGVSHADELYLEF 479  
 424 YWFEPYIRTVLSRLQYARSAPTYLYRFPDPSKH-FNHLRILSCGKVKRGTCGGDLSYLE 482  
 480 WNLISKLRFRESREKYTIEMWVGIWTEFATTKPKPYSDIAGMENLTV--DPIKSSDVY 536  
 483 YNSLARKLKNNHTREKYCIERLWGLMTHFAACGNP--NFDPQEDL-WQVPDPAVEKHOL 539  
 537 KCLNIGDELKVMDELPEMDKIKQASIFDKKEL 569  
 540 KCLNISDELKVIDVPLDKLMWSEFF-RDEL 571

RESULT 9  
 ABB57857  
 ID ABB57857 standard; Protein; 567 AA.  
 XX

XX ABB57857;  
 XX 26-MAR-2002 (first entry)  
 DT Drosophila melanogaster polypeptide SEQ ID NO 363.  
 XX Drosophila melanogaster polypeptide SEQ ID NO 363.  
 DE Drosophila melanogaster polypeptide SEQ ID NO 363.  
 XX Drosophila melanogaster polypeptide SEQ ID NO 363.  
 KM Drosophila melanogaster polypeptide SEQ ID NO 363.  
 OS Drosophila melanogaster.  
 XX WO200171042-A2.  
 XX 27-SEP-2001.  
 PD 23-MAR-2001: 2001WO-US09231.  
 PF 23-MAR-2000: 2000US-191637P.  
 XX 11-JUL-2000: 2000US-0614150.  
 PR (PEKE ) PE CORP NY.  
 XX Venter JC, Adams M, Li PWD, Myers EW;  
 PI WPI: 2001-656860/75.  
 DR N-PSDB: ABL01960.  
 XX New isolated nucleic acid detection reagent for detecting 1000 or more  
 PT genes from Drosophila and for elucidating cell signalling and cell-cell  
 PT interactions -  
 PS Disclosure: SEQ ID NO 363; 21pp + Sequence Listing; English.  
 XX The invention relates to an isolated nucleic acid detection reagent  
 CC capable of detecting 1000 or more genes from Drosophila. The invention is  
 CC useful in developmental biology and in elucidating cell signalling and  
 CC cell-cell interactions in higher eukaryotes for the development of  
 CC insecticides, therapeutics and pharmaceutical drugs. The invention  
 CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA  
 CC sequences (AB101840-AB16175) and the encoded proteins  
 CC (ABB57737-ABB72072).  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 CC Sequence 567 AA;  
 SQ

Query Match 42.6%; Score 1298.5; DB 22; Length 567;  
 Best Local Similarity 46.8%; Pred. No. 1.7e-113;  
 Matches 261; Conservative 91; Mismatches 187; Indels 19; Gaps 7;

21 KTTNRLSTNETOITDTEYGOIKGYKMTYVDSYSFESIPYAKPPVGEIRKAPRPV 80  
 14 KTNQRLRSNDKVIADTYGKVKYKQSIYNNYSEGIPIFAKPPVGEIRKAPRPV 73  
 81 PBEGRVDCGCPNRSVQIDFISGRKMTYVDSYSFESIPYAKPPVGEIRKAPRPV 140  
 74 HNSDKRCHVRAKPCQVNIYKQVGSSEDCILNVTYRELPHRPPLVLTWITGGQFM 133  
 141 GEANRMWFGPDYFMKKPVLVTVQYRLGVLGFLSLKSENLVNPGNAGIKDQVALRWVKS 200  
 134 GERSRLYSPDYIMMEHVLYISYRLGALSLADELDVPGNAGIKDQVALRWVKS 193  
 201 NIAIFGVDNITVFGESAGGASTHYMTTETRLRLHRCIMGNSMCSMASSTEQ-SR 259  
 194 NCOFFGDDNITVFGESAGGASTHYMTTDOAKGLFHTIIMSGLAPMAQIPTHINW 253  
 260 ALTMARVKGKEDNKOILFEFLMKANPYDLIKEPQVLT-PEMQNKVMEFPGPTPEPY 318  
 254 PYRLAQTGTGDANDRDIFAHLLKCKCKSMKVAEDITIMBERQRLTMSFQPTIEPY 313  
 319 QTADCVVPRKIREMKSAMGNSIPTLIGNTSEGLLSKSVAKQYEVVYKELESCVNIYPM 378

DB 314 LPHCYIPKSPLEMMRDCKGNSIPWVIGNSPESGLMPPEVNMKPELLCOJGDENLAPQ 373  
 QY 379 ELADSERAPETLERAAIVKKA---HVDGEFP---TLDNFEILCSYFELFPMRFLQLR 432  
 DB 374 DAHDEQ-----QRKAFKVKVRELYFGDRPGRKTLLEYSDLSYKFEWGHIRTLISR 427  
 QY 433 FNTTACTPIYLYRFPDSEELINPYRIMFGRGVGSHADELYLFWNILSKRLPRESR 492  
 DB 428 AHHAPLAPFLFRFDPDSKH-FNIMRLITCGKRVKGTCHADDSLTFYNAAKKLKRTA 486  
 QY 493 EYKTIEMVGIWTFEATTKP---YSNDIAGMENLWDPKISDVKYKCLNIGDELAKVM 548  
 DB 487 EFKTIKRLVSMVYHFAISDPPNIPMWCODEKOPRGAWLPIKDDKVRQCLNISHDHYI 546  
 QY 549 DLEPMKIKOGASIFDKK 566  
 DB 547 DLEPAEKRLIMDCTIDRE 564

## RESULT 10

ABB59161  
 ID ABB59161 standard; Protein; 554 AA.

ABB59161;  
 AC 26-MAR-2002 (first entry)

DT Drosophila melanogaster polypeptide SEQ ID NO 4275.  
 XX Drosophila melanogaster polypeptide SEQ ID NO 4275.  
 DE Drosophila melanogaster polypeptide SEQ ID NO 4275.  
 XX Drosophila melanogaster polypeptide SEQ ID NO 4275.  
 KM Drosophila melanogaster polypeptide SEQ ID NO 4275.  
 OS Drosophila melanogaster.  
 XX WO200171042-A2.  
 XX 27-SEP-2001.  
 PD 23-MAR-2001: 2001WO-US09231.  
 PF 23-MAR-2000: 2000US-191637P.  
 XX 11-JUL-2000: 2000US-0614150.  
 PR (PEKE ) PE CORP NY.  
 XX Venter JC, Adams M, Li PWD, Myers EW;  
 PI WPI: 2001-656860/75.  
 DR N-PSDB: ABL03264.  
 XX New isolated nucleic acid detection reagent for detecting 1000 or more  
 PT genes from Drosophila and for elucidating cell signalling and cell-cell  
 PT interactions -  
 PS Disclosure: SEQ ID NO 4275; 21pp + Sequence Listing; English.

The invention relates to an isolated nucleic acid detection reagent  
 CC capable of detecting 1000 or more genes from Drosophila. The invention is  
 CC useful in developmental biology and in elucidating cell signalling and  
 CC cell-cell interactions in higher eukaryotes for the development of  
 CC insecticides, therapeutics and pharmaceutical drugs. The invention  
 CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA  
 CC sequences (AB101840-AB16175) and the encoded proteins  
 CC (ABB57737-ABB72072).  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 CC Sequence 554 AA;  
 SQ

Query Match 42.0%; Score 1277.5; DB 22; Length 554;  
 Best Local Similarity 46.2%; Pred. No. 1.5e-111;

Matches 250; Conservative 106; Mismatches 170; Indels 15; Gaps 9;

```

QY 20 NKYNRYLSTNETOIIDTEYGOIKGKRMYYD-DSYSSFSIYAKPPGELFRAPOR 78
   ||||| | :|||:||||:| :||| :|||:|||||:|||||
Db 8 HKVOGYRLSTHTYILDITKYGVGLOKRYTDEKEPFARPEGITFARPGDLFRAPOR 67
QY 79 PVPEHGVADCCGPRNRSVQDTEFISGKPTGSEDCLYLVNTDLPDRRPMVFHIGGDF 138
   ||||| | :|||:||||:| :||| :|||:|||||:|||||
Db 68 PEMOGVILNCTNRSKPMORMMLGIVEGSEDCIHLNVYKALKSEKPLPIYWIYGGGF 127
QY 139 IFGEANRWMEGPDYFMKKPVLYVQYRLVGLFSLKSENLPNGAGLKQVMAALRWY 198
   ||||| | :|||:||||:| :||| :|||:|||||:|||||
Db 128 QKGASNDIYSPDYFMKKPVYFAVAINRLAALGFLSLKDPKLDVPGNAGLKQVMAALRWY 187
QY 199 KSNIAIFGGVDNITVFESAGASTHYMMITTEQTRGLFHRGIMSGNSMCMASTECOS 258
   ||||| | :|||:||||:| :||| :|||:|||||:|||||
Db 188 SONIAHFNQDPNNITLMGESASASVHYMMITTEQTRGLFHRGIMSGNSMCMASTECOS 247
QY 259 RALTMARVGYKGEDEKDLLEFLMKANPYDLKEEPQVLTPERMQKNVPPGPTVEPY 318
   ||||| | :|||:||||:| :||| :|||:|||||:|||||
Db 248 WAPRLAONLGTGDEKADVLSEFLSKVCARQIAIDQVITNDEVSFLLFAFGPIVEPY 307
QY 319 QTADCVPRKPIREMYKMSANGSIPTLIGNTSYEGILSKSVAKOYPEVYKLESCVYVPM 378
   ||||| | :|||:||||:| :||| :|||:|||||:|||||
Db 308 ETDHCVPYKHKHKLDSAMGNDLPVIVGNSFEGLESYQLVKRDPAALKNFH---NILPR 364
QY 379 ELAD-SERSAPETLERAAIYKKAHVDE--TPPLDNF--MELCSYFYFLFPMHFLQLRN 434
   ||||| | :|||:||||:| :||| :|||:|||||:|||||
Db 365 EVETSSLEGGDILLVRR--LKOLYFNNEQESMEKEFALNIFSHRQIMHDTFRFLIARQS 422
QY 435 HTAGTPIYLRFPDSEELINPPIRMFGYGVASHADELYLFPNITLSKRLPKESREY 494
   ||||| | :|||:||||:| :||| :|||:|||||:|||||
Db 423 YAKRTPTLYLRFPDSEPH--FNQPRRLVCGRDIRGVAHADELSTLEFNITIAKSLDKSSMEY 481
QY 495 KTERVAVGIVTEPATTTGKPYSDIAGMENLTWDPK--KSDDYKCLINIGDELKVMDLPEM 553
   ||||| | :|||:||||:| :||| :|||:|||||:|||||
Db 482 KTERVAVGIVTEPATTTGKPYSDIAGMENLTWDPK--KSDDYKCLINIGDELKVMDLPEM 553
QY 554 D 554
   ||||| | :|||:||||:| :||| :|||:|||||:|||||
Db 539 D 539

```

RESULT 11  
 ABB61983  
 ID ABB61983 standard; Protein: 566 AA.

AC ABB61983;

DT 26-MAR-2002 (first entry)

DE Drosophila melanogaster polypeptide seq ID NO 12741.

KW Drosophila: developmental biology; cell signalling; insecticide;

OS Drosophila melanogaster.

PN WO200171042-A2.

PD 27-SEP-2001.

PE 23-MAR-2001; 2001WO-US09231.

PR 23-MAR-2000; 2000US-191637P.

PR 11-JUL-2000; 2000US-0614150.

PA (PEKE ) PE CORP NY.

PI Venter JC, Adams M, Li PWD, Myeats EW,

DR WPI; 2001-656860/75.

DR N-PSDB; ABL06086.

XX New isolated nucleic acid detection reagent for detecting 1000 or more  
 PT genes from Drosophila and for elucidating cell signalling and cell-cell  
 PT interactions -  
 PS  
 PS Disclosure: SEQ ID NO 12741; 21pp + Sequence Listing; English.  
 XX  
 CC The invention relates to an isolated nucleic acid detection reagent  
 CC capable of detecting 1000 or more genes from Drosophila. The invention is  
 CC useful in developmental biology and in elucidating cell signalling and  
 CC cell-cell interactions in higher eukaryotes for the development of  
 CC insecticides, therapeutics and pharmaceutical drugs. The invention  
 CC discloses genomic DNA sequences (AB101840-AB16175) and the encoded proteins  
 CC (AB57737-AB572072).  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WPI  
 CC at ftp.wipo.int/pub/published\_pcl\_sequences.  
 XX  
 SQ Sequence 566 AA;

Query Match 41.6%, Score 1267.5; DB 22; Length 566;  
 Best Local Similarity 47.0%; Pred. No. 1,4e-110;  
 Matches 259; Conservative 92; Mismatches 187; Indels 13; Gaps 8;

```

QY 7 FTFRLKLCVCKVKNKYTNRYLSTNETOIIDTEYGOIKGKRMYYD-DSYSSFSIYAK 65
   ||||| | :|||:||||:| :||| :|||:|||||:|||||
Db 7 FSDKRLKAKITIGKRVVQYKLGOTKELAVKYOQLGQQRRTLYDEPYSSFEGIPFAQ 66
QY 66 PVGELFRKADQRPVMEGVADCCGPRNRSVQDTEFISGKPTGSEDCLYLVNTDLPDR 125
   ||||| | :|||:||||:| :||| :|||:|||||:|||||
Db 67 PPGVGLFRFRAQPPSSWGQVDCYARREKPMQNRSTNAAGSEDCIHLNVYKALKSEK 126
QY 126 RRPVAVFHGGDFEFGENRWMEGPDYFMKKPVLYVQYRLVGLFSLKSENLPNGN 185
   ||||| | :|||:||||:| :||| :|||:|||||:|||||
Db 127 PLPVAVWVLFGGGFOYGASRELYGPDYFMKHDILVTINRVGVLGLSLKDELKIPGN 186
QY 186 AGLKDQVMAALRWKSNIAIFGGVDNITVFESAGASTHYMMITTEQTRGLFHRGIMSG 245
   ||||| | :|||:||||:| :||| :|||:|||||:|||||
Db 187 AGLKDQVMAALRWKSNIAIFGGVDNITVFESAGASTHYMMITTEQTRGLFHRGIMSG 246
QY 246 NSMCSMASTECOSRALTMARVGYKGE--DNEKDLLEFLMKANPYDLKEEPQVLTPERMQ 304
   ||||| | :|||:||||:| :||| :|||:|||||:|||||
Db 247 SALCAMATQDPKWPORLKGELGAGNLESEKELLEFPQOIPASKLAQYCNSTVTOEOR 306
QY 305 NKVMEPPGPTVEPYQTADCVPRKPIREMYKMSANGSIPTLIGNTSYEGILSKSVAKOYDE 364
   ||||| | :|||:||||:| :||| :|||:|||||:|||||
Db 307 DYEILAFAPVIEPYVGDQVPIKSOQDQLSSANGNSIPMITIGTSFEGLFSTYTTLDDP- 365
QY 365 VVKELESCVNVVWELADERSAPETLERAAIYKKAHVDE--ETPTLDFMELCSYFY 421
   ||||| | :|||:||||:| :||| :|||:|||||:|||||
Db 366 -LYVLSAFAIIPROYDA--IDKEELAEVRLRKSYFDDPDRASMELEYECLHILSIKNE 423
QY 422 LFPNHRFLQLRFNHTAGTPIYLRFPDSEELINPPIRMFGYGVASHADELYLFPN 481
   ||||| | :|||:||||:| :||| :|||:|||||:|||||
Db 424 WHDIHRTLLARLAVATNLPYTLRFDMDSPH--FNHRYILKCGKRVAGVCHADDISIFMG 482
QY 482 ILSKRLPKESREYKTERVAVGIVTEPATTTGKPYSDIAGMENLTWDPKSDYVYKCLNI 541
   ||||| | :|||:||||:| :||| :|||:|||||:|||||
Db 483 ILSKRLPKESREYKTERVAVGIVTEPATTTGKPYSDIAGMENLTWDPKSDYVYKCLNI 541
QY 542 GDELKVMDLPE 552
   ||||| | :|||:||||:| :||| :|||:|||||:|||||
Db 539 ADGLERFLPE 549

```

RESULT 12  
 ABB57746  
 ID ABB57746 standard; Protein: 565 AA.

AC ABB57746;

DT 26-MAR-2002 (first entry)



Db 5 GPARGVKRNITMGSYFSEKIFPAKPPVLDLRFKAPEAVEPWDEIDTSPADKPLQTH 64  
 QY 100 FISGPTGSEDCLYLNYTNDLPDKRRPVVFIHGDDIFEGANRNMWCPDYFMKKPVY 159  
 Db 65 MFRKRYAGSEDCLYLNYVVDLPDKRRPVVVIYGGYGVGASGSDMSDPDFMSKDVY 124  
 QY 160 LTVVQRLVGLVGLSLKSENLVPGNAGLKDQYVALRWKSNIAIFGCDNTVFGESA 219  
 Db 125 IVTVVYRLGALGFLSLDDPOLNVPNGNAGLKDQYVALRWKSNIAIFGCDNTVFGESA 184  
 QY 220 GGASTHMTTEQTRGIFHFGIMSGNSKMSASTECQSALTMARVGTGKEDNCKDL 279  
 Db 185 GGASTHMTTEQTRGIFHFGIMSGNSKMSASTECQSALTMARVGTGKEDNCKDL 244  
 QY 280 EFLTKANPYDLKEEPOVLTPERMOKNMFPPGTPVEPYQTADCVKPKFIREVKSAMGN 339  
 Db 245 EFLRSMGSGEIKATATVLSNDEKHHRIELFAGFPVVEPTTEHTVYAKQPHLMQMSWH 304  
 QY 340 STEPLGNTSYEGLLSKSAKQKPEVYVLESCVNTVPEMLADSEKSAPELLEKAT-VK 398  
 Db 305 RITPMFGGYSFEGELLYPEVSRPAPLDEVGCKNLPSDL--GLNLDKRLRENYGLQK 362  
 QY 399 KAHVDETP---TLDFMELCSYFFFLFPMHRLQLRFNHAGTPYLYRFDDESELI 454  
 Db 363 KAYF-GDEPCONANMKFLELCYREFMHPYIAALNRQSS-APTLYKRDHDS-KLC 419  
 QY 455 NPYRIRFGRGVKGVSHADELYLFENILSKRLPKESREYKTERVWGIWTEFATGKPY 514  
 Db 420 NAIKRYLCHOMRGVCHGDLCTIFHSMLSHOSAPSPHKYITGVWVDTGFAHGDPN 479  
 QY 515 SNDIAGENLWDPITKSDDYKCLINIGDELVMGLPEMDKIK 557  
 Db 480 CEST---KSLKRAPIENVTN-FKCLNTIGDQFEVMALEPLOTKE 518  
 RESULT 14  
 ABB57790  
 ID ABB57790 standard; Protein; 542 AA.  
 AC ABB57790;  
 DT 26-MAR-2002 (first entry)  
 DE Drosophila melanogaster polypeptide SEQ ID NO 162.  
 DX  
 KM Drosophila: developmental biology; cell signalling; insecticide;  
 KM pharmaceutical.  
 OS Drosophila melanogaster.  
 XX  
 PN WO2001/1042-A2.  
 PD 27-SEP-2001.  
 PF 23-MAR-2001; 2001WO-US09231.  
 PR 23-MAR-2000; 2000US-191637P.  
 PR 11-JUL-2000; 2000US-0614150.  
 PA (PEKE ) PE CORP NY.  
 PI Venter JC, Adams M, Li PWD, Myers EW;  
 DR WPI: 2001-656860/75.  
 DR N-PSDB: ABL01893.  
 XX  
 PT New isolated nucleic acid detection reagent for detecting 1000 or more  
 PT genes from Drosophila and for elucidating cell signalling and cell-cell  
 PT interactions -  
 PS Disclosure: SEQ ID NO 162; 21pp + Sequence Listing; English.  
 XX The invention relates to an isolated nucleic acid detection reagent  
 CC

CC capable of detecting 1000 or more genes from Drosophila. The invention is  
 CC useful in developmental biology and in elucidating cell signalling and  
 CC cell-cell interactions in higher eukaryotes for the development of  
 CC insecticides, therapeutics and pharmaceutical drugs. The invention  
 CC discloses genomic DNA sequences (AB116176-AB130511), expressed DNA  
 CC sequences (AB101840-AB116175) and the encoded proteins  
 CC (AB57737-AB72072).  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 CC  
 CC Sequence 542 AA;  
 SO  
 Query: Match 39.5%; Score 1204; DB 22; Length 542;  
 Best Local Similarity 47.5%; Pred. No. 1,3e-104;  
 Matches 257; Conservative 79; Mismatches 179; Indels 26; Gaps 11;  
 QY 28 STNETQIIDTEYGOIKGVKRMVYDSDYSFESIPYAKPPVGLRFAKPPVPMWEGVGD 87  
 Db 5 SSIETCELLPVGQIKGVKRLSLVDDPYFSEKIPFAKPLGELRFAKPPVPMWEGVGD 64  
 QY 88 CCGPANKRVOQDFISGKPTGSEDCLYLNYTNDLPDKRRPVVFIHGDDIFEGANRNMW 147  
 Db 65 CTHAEKPTQGLLTRELEGGECLYLVYSKOLSKSEKPLPVVVIYGAFTVGEATREL 124  
 QY 148 FGPDYFMKKPVVLYTVQVRLGLVGLSLKSENLVPGNAGLKDQYVALRWKSNIAIFG 207  
 Db 125 YGPYFMRKDVVLYTLNVRVDCGLFSLKPSLKVPGNAGLKDQYVALRWKSNIAIFG 184  
 QY 208 DVNITVFGESAGASTHYMMITEQTRGIFHFGIMSGNSKMSASTECQSALTMARV 267  
 Db 185 DDSNITVFGESAGGCSHFMMCTEOTRGLFHKAIPMGVHANNPAPDFAFLAQN 244  
 QY 268 GYKGEDEKDLFELMKANPYDLKEEPOVLTPERMOKNMFPPGTPVEPYQTADCVK 327  
 Db 245 GFTGENDAKVLEYLQGVPAADLVNH--NLTPHRRNGLLFAGFPVVEPYQTADCVK 302  
 QY 328 PIREVKSAMGNSIPTLIGNTSYEGLLSKSAKQKPEV--VVELBSC---VNYVPWEL 380  
 Db 303 PVEVMDAWMSNNPVMVLTGTSFEGLE-----MYPAVSANLKAADLSODPRLVADV 356  
 QY 381 ADSEKSAPELLEKATVKKAHVDETP---LNFMELCYFFFLFPMHRLQLRFNHAG 437  
 Db 357 R-TVSSSEKENLEYSQRLMAKAYFGYSPSSPELLNMDLFYSKTFMWHGFNTFNARLT 414  
 QY 438 GTPYLYRFDDESEELINPRIMRFGGVK-GVSHADELYLFENILSKRLPKESREYK 496  
 Db 415 KAPTYRRFPDSDPN-FNFRAKFCGDKIKTGAHADDSLFLRNAGSMKLDKTSAYRT 473  
 QY 497 IERWGIWTEFATGKPYSDIAGMENLWDPITKSDDYKCLINIGDELVMGLPEMDK 556  
 Db 474 IERMIGIWTAFATSNCPBEIGHLE--WKPSKNDP-KRVINISSDVTIIDLPYEXL 529  
 QY 557 K 557  
 Db 530 Q 530  
 RESULT 15  
 AAM47598  
 ID AAM47598 standard; Protein; 602 AA.  
 AC AAM47598;  
 DT 12-FEB-2002 (first entry)  
 DE Drosophila cell cycle progression protein #27.  
 DX  
 KM Antiproliferative; cytoskeletal; cardiact; immunosuppressive; meiosis;  
 KM antiinflammatory; antiparasitic; antineoplastic; antifungal; mitosis;  
 KM cell cycle progression protein; tumour; proliferative disorder;  
 KM cardiovascular; autoimmune; dermatological disorder.  
 CC



XX Drosophila sp.  
 OS  
 OS W020017274-A2.  
 PN  
 XX  
 PD 04-OCT-2001.  
 XX  
 PE 23-MAR-2001; 2001WO-GB01297.  
 XX  
 PR 24-MAR-2000; 2000GB-0007268.  
 XX  
 PA (CYCL-) CYCLACEL LTD.  
 XX  
 PI Deak P, Glover DM, Midgley C;  
 XX  
 DR WPI: 2002-055132/07.  
 XX  
 PT Polynucleotides encoding cell cycle progression proteins, useful for  
 XX treating a tumor or a proliferative disorder -  
 PS  
 XX  
 XX Claim 8; Page 164; 213pp; English.  
 CC The present invention relates to Drosophila cell cycle progression  
 CC proteins (AAM47572-AAM47608) and their coding sequences  
 CC (ABA90366-ABA90520). The coding sequences and proteins are useful for  
 CC identifying a substance capable of affecting the function of the  
 CC corresponding gene, a substance capable of inhibiting the cell division  
 CC cycle, or capable of inhibiting mitosis and/or meiosis. They can also be  
 CC used in a method for treating a tumor or proliferative disorder,  
 CC cardiovascular disorders (such as restenosis and cardiomyopathy),  
 CC autoimmune disorders such as (glomerulonephritis and rheumatoid  
 CC arthritis), dermatological disorders (such as psoriasis),  
 CC antiinflammatory, antifungal and antiparasitic disorders (such as  
 CC malaria).  
 CC  
 SQ Sequence 602 AA:

Query Match 39 2%; Score 1194.5; DB 23; Length 602;  
 Best Local Similarity 45.4%; Pred. No. 1.2e-103;  
 Matches 246; Conservative 98; Mismatches 175; Indels 23; Gaps 10;

QY 21 KYNVRLSTNEFIIDTEYGOIKGVKRMVYDSDYSPESIPYAKPPVGLRFAQRPV 80  
 DB 67 KYEQRRLSTAIYVITKSGPVGVKRMVIMGSGYSPFEKIPFAKPPVGLRFAQRPV 126  
 QY 81 PWEGVRDCCCPANRSVOTDFISGKPTGSEDCILYNTDNLNPKRRPVMVFIHGDFLF 140  
 DB 127 PMDOELDCTSPADKPLQTHMFFRKVAGSEDCILYNTDNLNPKRRPVMVFIHGDFLF 186  
 QY 141 GEANRMWFGPDYFMKPPVLTVOYRGLVGFELSKSENLNPGNAGLKDQVVALRMVKS 200  
 DB 187 GEASR---GLD-----VAVTVAIRLGAAGFLSLDDPOLNVPNGNLKQDIMALRMVQO 237  
 QY 201 NIAIFGGDVNITVFGESAGCSTHYMTTEOTRGLEFHGIMSGNSMCMSTECOSRA 260  
 DB 238 NIEAFGGDSNNITLFGESAGCSTHYMTTEOTRGLEFHGIMSGNSMCMSTECOSRA 297  
 QY 261 LTMARRGYKGENEKEKILFEIKKANPYDLKEPEVLTPERMQNKVMFPFGPTVEPYOT 320  
 DB 298 YRLAQKLGTYGDNKKAIFELNSMGSCEIVKATAYLSNDEKHHRIIFAFGPEVEPYT 357  
 QY 321 ADVVPRPIREMYKSGNSIPFLIGNTSYGLLSKSVAKOYPEVKELESCVNVYFWEL 380  
 DB 358 EHTVVAQPHLMQNSHRIIPMFGTSEGLLFYEVSRRAPTLDEVGNCKNLIPSDL 417  
 QY 381 ADSERSAPETLERAI-VKKAHVDETP---TIDNFMELCSYFLEPMHFLQLEFNH 435  
 DB 418 --GLNLPKLENYGLQKAYF-GDEPCNANMKFLELCSTREHNPITRAALNVRQ 474  
 QY 436 TAGTPYLYRDPDESEITINPYRIMRFGRGVYSHADELYTLFWNTLSKRLPKESREYK 495  
 DB 475 SS-APTYLYRDPDHS-KLCNARIYVLCGHQMRGVCHGDDLCYIFHSMLSHOSAPDSPEHK 532

QY 496 TIERMGIINTERATGCKPYSDNDIAGMENTWDPKIKSDPDVYKCLNICDELKYMDELPEMDK 555  
 DB 533 VITGMDVMTSFAAHQDPNCEST---KSLKFAPIENVTN-FKCLNIGDQFEVMALELOK 588  
 QY 556 IK 557  
 DB 589 IE 590

Search completed: April 4, 2003, 09:13:01  
 Job time: 45.0154 secs

1. The first part of the report is a general introduction to the subject of the study. It discusses the importance of the study and the objectives of the research. It also provides a brief overview of the methodology used in the study.

2. The second part of the report is a detailed description of the methodology used in the study. It discusses the data collection methods, the sample size, and the statistical analysis techniques used.

Mon Apr 14 10:18:09 2003

us-09-776-910-13.rpr

Page 1

GenCore version 5.1.4-p5-4578  
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OM protein - protein search, using sw model

Run on: April 4, 2003, 09:10:33 ; Search time 19.0734 Seconds  
(without alignments)  
2872.940 Million cell updates/sec

Title: US-09-776-910-13

Perfect score: 3045  
Sequence: 1 MTFIKQPIFKLQVCKMVN.....PEMDIKQKASIEDKKELF 570

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues  
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08  
Maximum Match 1008  
Listing first 45 summaries

Database :  
1: PIR.73:\*  
2: PIR.1:\*  
3: PIR.2:\*  
4: PIR.3:\*

pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	959.5	31.5	540	2 S53370	carboxylesterase (
2	954.5	31.3	540	2 A35986	esterase B1 - sout
3	945.5	31.1	540	2 S53371	carboxylesterase (
4	861.5	28.3	503	2 S53372	carboxylesterase (
5	607	19.9	578	2 P89068	protein T28C12.4b
6	607	19.9	578	2 T32053	hypothetical prote
7	602.5	19.8	564	2 A33325	juvenile-hormone e
8	575	18.9	489	2 B68680	para-nitrobenzyl e
9	553.5	18.2	547	2 S36787	carboxylesterase (
10	545	17.9	547	2 T25690	juvenile hormone e-
11	544	17.9	552	2 S55233	hypothetical prote
12	544	17.9	552	2 S36786	carboxylesterase (
13	542	17.8	561	2 T47655	carboxylesterase (
14	529	17.4	548	2 T32907	hypothetical prote
15	523	17.2	597	2 A33668	sterol esterase (E
16	518	16.9	602	1 ACH014	cholinesterase (EC
17	515.5	16.9	614	2 JH0314	acetylcholinestera
18	512.5	16.8	581	2 C39768	cholinesterase (EC
19	512	16.8	562	2 S27782	esterase precursor
20	511	16.8	596	1 ACRYE	acetylcholinestera
21	508.5	16.7	603	2 S70849	cholinesterase (EC
22	507.5	16.7	545	2 S58980	carboxylesterase (
23	505.5	16.6	545	2 S58979	carboxylesterase (
24	505.5	16.6	545	2 S58972	carboxylesterase (
25	505.5	16.6	545	2 S58962	carboxylesterase (
26	505.5	16.6	545	2 S58963	carboxylesterase (
27	504.5	16.6	545	2 S58977	carboxylesterase (
28	504.5	16.6	545	2 S58973	carboxylesterase (
29	504.5	16.6	614	2 JH0811	acetylcholinestera

30	503.5	16.5	545	2 S58975	carboxylesterase (
31	501.5	16.5	545	2 S58970	carboxylesterase (
32	500.5	16.4	511	2 D70944	probable lipf prot
33	500.5	16.4	545	2 S58976	carboxylesterase (
34	500	16.4	559	1 JC5408	carboxylesterase (
35	500	16.4	561	2 S71597	carboxylesterase (
36	499.5	16.4	545	2 S58980	carboxylesterase (
37	499.5	16.4	557	2 A47162	thioesterase B (E
38	499	16.4	562	2 S27800	elastase precursor
39	498.5	16.4	539	2 T32052	hypothetical prote
40	498.5	16.4	545	2 S58978	carboxylesterase (
41	498.5	16.4	545	2 S10367	carboxylesterase (
42	497.5	16.3	545	2 S58974	carboxylesterase (
43	497.5	16.3	545	2 S58971	carboxylesterase (
44	496.5	16.3	545	2 S58969	carboxylesterase (
45	495.5	16.3	545	2 S58968	carboxylesterase (

## ALIGNMENTS

### RESULT 1

S53370  
C:Species: Culex pipiens quinquefasciatus (southern house mosquito)  
C:Date: 15-Jul-1995 #sequence #revision 08-Sep-1995 #text\_change 21-Jul-2000  
C:Accession: S53370; S44211  
R:Vaughan, A.; Rodriguez, M.; Hemingway, J.  
Biochem. J. 305, 651-658, 1995  
A:Title: The independent gene amplification of electrophoretically indistinguishable  
A:Reference number: S53370; MUID:95134253; PMID:7530448  
A:Accession: S53370  
A:Molecule type: mRNA  
A:Residues: 1-540 <VAD>  
A:Cross-references: EMBL:Z32694; NID:9475067; PIDD:CAA83643.1; PID:9475068  
A:Experimental source: strain PeIR  
C:Superfamily: cholinesterase; cholinesterase homology  
C:Keywords: carboxylic ester hydrolase

Query Match 31.5% Score 959.5; DB 2; Length 540;  
Best Local Similarity 37.3%; Pred. No. 1.3e-65;  
Matches 205; Conservative 111; Mismatches 211; Indels 23; Gaps 10;

QY	31	ETQIIDREYQIKVGRMTVYDDSYSESTIYAPAPPGELRFKAPQRPVMEGRDC--	88
DB	4	ESLTVQTKYGVGRKRSVSLGQEVYFQGIYAPAPPEGLRFKAPVPPQWTFELDCSQ	63
QY	89	-CGPA---NSVQTFISCKPTGSEDCILYNTDNDKRRPVVFHGGDFIFGEAN	144
DB	64	QCEPCYHFRRLQ-----KIYGCEDSLKINVPFAKINSKPLPVMLYIYGGFTGTS	117
QY	145	RNMFGPDYFMKPVVLTVOYRIGVIGFSLKSENLNVGNGMGLDOVALRWKSNIAI	204
DB	118	TELYGPDPLVQKDIIVSFNIRIGALIGLCCSEQGVGNGMGLDONAIWLVENIAA	177
QY	205	FGGDVNTITVGEASGASTHYMTTEOTRGLFRHGMNSGNSWASTECOSRALIMA	264
DB	178	FGGDKRKYTLVGHSGAASVQYHILSDASKDLFRALVMSGTYNSWSTLRRNVEKIA	237
QY	265	KRVGYKGEDNEKDLLEFLKAPNPDYDIKEPOVLTPEBRMKNKVPFPGFTVEPYQADCV	324
DB	238	KALGMGQGESGALRFLKAPKPBEDIVANOKELTHDDMDIDFTFPGFVEVEYLTQCM	297
QY	325	VKRPTEEMKSAWNSIPTLIGNTSYEGLLSKSAKQPEVYKELSCVYVWELADSE	384
DB	298	IKPEPEMKATMGKIDIMIGTSEEGILLQIKILOPELISHPHLEFNVPNNL---	354
QY	385	RSAPETLERAIVKKAHVDGETPTLDN---FMELCSYVYFFPMHRLQIRFNHTACTPI	441
DB	355	ISMEKRIEFAKIKORYPDSSPMENNIQYHMSDVFVHGHRTLIARAASRAR-T	413
QY	442	YLRFDDSEELLNPRIMRFGYGVSHADELYLEFWNLISKRLPESREYVYTIEMV	501

Db 414 FVYRICLOS-EFYNHYRIMIDPKLRGTAHADELSTYLFNSFQVPEKTEFYEIGIQLTV 472  
 QY 502 GIWTEFATGKPYSDIAGMENLTWDPKRSDDVYKCLNI-GDELKVMDELPEMDKIKOGA 560  
 Db 473 DVFTAFVINGDP-NCGMIATAGSVFEEPNQOTKPTFKCLNTIANDGVAFVDYDPADRLDMMD 531  
 QY 561 SIFDKKLELF 570  
 Db 532 AMY-VNDEL 540

## RESULT 2

A35986  
 esterase B1 - southern house mosquito  
 C:Species: Culex pipiens quinquefasciatus (southern house mosquito)  
 C:Date: 16-Nov-1990 #sequence\_revision 13-Jan-1993 #text\_change 21-Jul-2000  
 R:Accession: A35986  
 R:Mouches, C.; Pauplin, Y.; Agarwal, M.; Lemieux, L.; Herzog, M.; Abadon, M.; Beysat-Ar  
 Proc. Natl. Acad. Sci. U.S.A. 87, 2574-2578, 1990  
 A:Title: Characterization of amplification core and esterase B1 gene responsible for ins  
 A:Reference number: A35986; MUID:90207238; PMID:2320576  
 A:Accession: A35986  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-540 <MOU>  
 A:Cross-references: GB:M32328; NID:9156687; PIDN:AAA28289.1; PID:9156688  
 A:Note: the authors translated the codon CGT for residue 213 as Ala, and CGT for residue  
 C:Superfamily: cholinesterase; cholinesterase homology

Query Match 31.38; Score 954.5; DB 2; Length 540;  
 Best Local Similarity 36.98; Pred. No. 3, 1e-65;  
 Matches 203; Conservative 113; Mismatches 211; Indels 23; Gaps 10;

QY 31 ETQIDITEYQIKGKRVMTYDSDYSFSESIIPYAKPVEELRKAQRPVMEGVRDC-- 88  
 Db 4 ESLVOTKYGVRKRVNLSLGOEYVFOGIPYARABGELRKAQVPOKMTETLDCQ 63  
 QY 89 -CGPA---NRSYQDPFISGKPTGSEDCILYNTYNDLNDPKRRPVWFHGGDFJEGAN 144  
 Db 64 QCEPCYHFRRLQ-----KIVCEDSLKINFAKEINPSPLPMLYIGGFGTEGSG 117  
 QY 145 RNMFGPDYFMKRVVLTVOYRGLVGLFLSKENLWPNAGLKQOVALRMVKSNIAT 204  
 Db 118 TELYGDPLVQKDIYLVSEFYRIGALGFLCCQSDQGVPGNAGLKQOVALRMVLENTIA 177  
 QY 205 FCGDVNDITVFESAGSAGSTHYMTTEOTRGLFHRGIMSGNSCWSASTECOSRALTMA 264  
 Db 178 FGDDPKRYTLVGHSGAASVOYHLISDASKDLFORRIYMSGSTVSMSTRORNWVEKLA 237  
 QY 265 KRVGYGEDNEKDLLEFLKAPYDLKEEPOVLTPERMQKVFPRGPTVEPYQTADCV 324  
 Db 238 KALGMDGGGSGALRFLRAKPEDIVAHQKLLTDQMODDITFPFGPTVEPYLTQCI 297  
 QY 325 VKPRIREMVSAMGNSIPTLLIGNTSYEGLSKSVAKOYPEVVELESVYVWELADSE 384  
 Db 298 IKRPFEMARTAMGDKIDIMIGTSEGLLQKIKLPELLSHPHLFGNVPNL--K 354  
 QY 385 RSAPETLERAAIVKKAHVDEPTLDN--FMELCSYFYLFPMHFLOLRNHTAGTPI 441  
 Db 355 ISMEKRIFFAKLRKORYYPPDISPMENNLGYVHMSDRVFWHGLHTILARAARSAR-T 413  
 QY 442 YLYRFDSEELINPYRIRFGKGVSHADELTLYLFNNILSKRLPKRESREYKTIEMV 501  
 Db 414 FVYRICLOS-EFYNHYRIMIDPKLRGTAHADELSTYLFNSFQVPEKTEFYEIGIQLTV 472  
 QY 502 GIWTEFATGKPYSDIAGMENLTWDPKRSDDVYKCLNI-GDELKVMDELPEMDKIKOGA 560  
 Db 473 DVFTAFVINGDP-NCGMIATAGSVFEEPNQOTKPTFKCLNTIANDGVAFVDYDPADRLDMMD 531  
 QY 561 SIFDKKLELF 570  
 Db 532 AMY-VNDEL 540

## RESULT 3

S53371  
 carboxylesterase (EC 3.1.1.1) B1 - southern house mosquito  
 C:Species: Culex pipiens quinquefasciatus (southern house mosquito)  
 C:Date: 01-Aug-1995 #sequence\_revision 01-Sep-1995 #text\_change 21-Jul-2000  
 R:Accession: S53371  
 R:Vaughan, A.; Rodriguez, M.; Hemingway, J.  
 Biochem. J. 305, 651-658, 1995  
 A:Title: The independent gene amplification of electrophoretically indistinguishable  
 A:Reference number: S53370; MUID:95134253; PMID:7530448  
 A:Accession: S53371  
 A:Molecule type: mRNA  
 A:Residues: 1-540 <YAU>  
 A:Cross-references: EMBL:222695; NID:9475069; PIDN:CAA83644.1; PID:9780238  
 A:Experimental source: Strain MRES  
 C:Superfamily: cholinesterase; cholinesterase homology  
 C:Keywords: carboxylic ester hydrolase

Query Match 31.18; Score 945.5; DB 2; Length 540;  
 Best Local Similarity 36.78; Pred. No. 1, 5e-64;  
 Matches 202; Conservative 112; Mismatches 213; Indels 23; Gaps 10;

QY 31 ETQIDITEYQIKGKRVMTYDSDYSFSESIIPYAKPVEELRKAQRPVMEGVRDC-- 88  
 Db 4 ESLVOTKYGVRKRVNLSLGOEYVFOGIPYARABGELRKAQVPOKMTETLDCQ 63  
 QY 89 -CGPA---NRSYQDPFISGKPTGSEDCILYNTYNDLNDPKRRPVWFHGGDFJEGAN 144  
 Db 64 QCEPCYHFRRLQ-----KIVCEDSLKINFAKEINPSPLPMLYIGGFGTEGSG 117  
 QY 145 RNMFGPDYFMKRVVLTVOYRGLVGLFLSKENLWPNAGLKQOVALRMVKSNIAT 204  
 Db 118 TELYGDPLVQKDIYLVSEFYRIGALGFLCCQSDQGVPGNAGLKQOVALRMVLENTIA 177  
 QY 205 FCGDVNDITVFESAGSAGSTHYMTTEOTRGLFHRGIMSGNSCWSASTECOSRALTMA 264  
 Db 178 FGDDPKRYTLVGHSGAASVOYHLISDASKDLFORRIYMSGSTVSMSTRORNWVEKLA 237  
 QY 265 KRVGYGEDNEKDLLEFLKAPYDLKEEPOVLTPERMQKVFPRGPTVEPYQTADCV 324  
 Db 238 KALGMDGGGSGALRFLRAKPEDIVAHQKLLTDQMODDITFPFGPTVEPYLTQCI 297  
 QY 325 VKPRIREMVSAMGNSIPTLLIGNTSYEGLSKSVAKOYPEVVELESVYVWELADSE 384  
 Db 298 IKRPFEMARTAMGDKIDIMIGTSEGLLQKIKLPELLSHPHLFGNVPNL--K 354  
 QY 385 RSAPETLERAAIVKKAHVDEPTLDN--FMELCSYFYLFPMHFLOLRNHTAGTPI 441  
 Db 355 ISMEKRIFFAKLRKORYYPPDISPMENNLGYVHMSDRVFWHGLHTILARAARSAR-T 413  
 QY 442 YLYRFDSEELINPYRIRFGKGVSHADELTLYLFNNILSKRLPKRESREYKTIEMV 501  
 Db 414 FVYRICLOS-EFYNHYRIMIDPKLRGTAHADELSTYLFNSFQVPEKTEFYEIGIQLTV 472  
 QY 502 GIWTEFATGKPYSDIAGMENLTWDPKRSDDVYKCLNI-GDELKVMDELPEMDKIKOGA 560  
 Db 473 DVFTAFVINGDP-NCGMIATAGSVFEEPNQOTKPTFKCLNTIANDGVAFVDYDPADRLDMMD 531  
 QY 561 SIFDKKLELF 570  
 Db 532 AMY-VNDEL 540

## RESULT 4

S53372  
 carboxylesterase (EC 3.1.1.1) B - southern house mosquito (fragment)  
 C:Species: Culex pipiens quinquefasciatus (southern house mosquito)  
 C:Date: 15-Jul-1995 #sequence\_revision 01-Sep-1995 #text\_change 20-Sep-1999  
 R:Accession: S53372; S44212  
 R:Vaughan, A.; Rodriguez, M.; Hemingway, J.  
 Biochem. J. 305, 651-658, 1995  
 A:Title: The independent gene amplification of electrophoretically indistinguishable

A:Title: The independent gene amplification of electrophoretically indistinguishable



Best Local Similarity 32.08; Pred. No. 3.5e-38;

Accession: 140510  
Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 158, 'P', 60-94, 'Q', 96-149, 'D', 151-229, 'A', 231-241, 'S', 243-245, 'R', 247-250, 'R'

A:Cross-references: EMBL:U06089; NID:g468045; PIDN:AAA81915.1; PID:g468046

A:Experimental source: strain NRRL B8079

C:Genetics:

A:Gene: pnbA

C:Superfamily: cholinesterase; cholinesterase homology

C:Keywords: carboxylic ester hydrolase

F:24-478/Domain: cholinesterase homology &lt;CH&gt;

Query Match 18.9%; Score 575; DB 2; Length 489;  
 Best Local Similarity 30.7%; Pred. No. 3, 7e-36;  
 Matches 170; Conservative 90; Mismatches 209; Indels 84; Gaps 23;

QY 33 QIDTEYQIKVKRMVYDSDYSSESTIYAPRPGVGLAFKAPQRPVEGYRDCGPA 92  
 D 4 QIVTYQYKVGKGT-----ENGVMKMGIPYAKPPVGOMRKAPEPEVEDVLDATAYG 58  
 QY 93 NRSVQ-TDETS-----GKPTGSEDCILNYTNDLNPDKRRPVYVFIHGDFEGEARNRW 147  
 D 59 SICQPSDLSLSTTELPQSEDCILYVNVAPD-TPSKNLPYVYVHIGAFYLGAGSEPL 117  
 QY 148 F-GPDYFKKRPVLYVYQYRLGVLGLSLKSENLVPGNAGLKDQVALLRWKSNIAIFG 206  
 D 118 YDGSKLAQGEVIVYVTLNRYLGLPGLHLSSENEAYSDNLGLDQAAALMKVRENISAFG 177  
 QY 207 GDVNTIYFGSAGASTHYMTETQTRGLFHRGIMSGNSMCMASSTECOSRALTMAR 266  
 D 178 GDDPNVYVFGSAGMSIALAMPAAKGLFQKAIMESGSR-TMKEQAAISTAAFLQY 236  
 QY 267 VGYGGEDEKRIEFLMKANPYDLKEPEQYLPERRMKNKMPFGPTVEPYOTADCV 326  
 D 237 LGI-----NEGQ-LDKLHVSAEDLLKADQRIAEK-ENIFQLFQPALDPK-----TLR 285  
 QY 327 KPIREMYKSAWNSIPILIGTSTYGLISVANKQYREYVKELESCVNYVPMELADSE 386  
 D 286 EEPEKALIEGAASGIPILITGTTRDEGYLF-----FPP-----DSDVH 322  
 QY 387 APEPLERA-----AIYKKAHVDEGPTPLDPMELCSYEFELPMPHRLQRENTAGT 439  
 D 323 SQETDIALEYLQKPLAEKV-ADLYPRSLSEQIHMMTDLLFMRPAVAYASQSHY---A 378  
 QY 440 PIYLYRFPDSEELINPYRIRFRGKGVGSHADELYLFNFI--LSKRLPKE-SREKT 496  
 D 379 PYWYRFRPMHKK--PRY-----NKAFHLELPFVFNGLDGLSMAMAELTIDEVKQ 427  
 QY 497 IERNV-GIWEFATTKPYSDNDIAGMENLWDPPIKSDVYKCLNIGDELKVMDLPEMDK 555  
 D 428 LSHTIOSAMITFAKTGNP-----STEAVNMPAY--HEETRETLIDSEITENDPESEK 479  
 QY 556 IKQGSIFDKKE 568  
 D 480 ROK--LFPSKGE 489

## RESULT 9

carboxylesterase (EC 3.1.1.1) FE4 precursor - green peach aphid

C:Species: Myzus persicae (green peach aphid)

C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999

C:Accession: S36787

R:Field, L.M.; Williamson, M.S.; Moores, G.D.; Devonshire, A.L.

A:Title: Cloning and analysis of the esterase genes conferring insecticide resistance in

A:Reference number: S36786; MUID:93384534; PMID:8373371

A:Accession: S36787

A&gt;Status: preliminary

A:Molecule type: mRNA

A:Cross-references: EMBL:X74555; NID:g397512; PIDN:CAA52649.1; PID:g397513

C:Superfamily: Cholinesterase; cholinesterase homology

C:Keywords: carboxylic ester hydrolase

F:52-552/Domain: cholinesterase homology &lt;CH&gt;

Query Match 18.2%; Score 553.5; DB 1; Length 564;  
 Best Local Similarity 31.5%; Pred. No. 2e-34;  
 Matches 178; Conservative 81; Mismatches 231; Indels 75; Gaps 26;

QY 8 IFRLKLVCKMVKYTNRLSTNETQIIDTEYQIKVKRMVYDSDYSSESTIYAPR 67  
 D 8 LNLFLFFICFLP-----CSASNTPKVQVHSGELIAGGEFYVNGRKIKYFGLIYAS 61  
 QY 68 VGELEKAPQRPVMEGVNDCCGPANRSVQTFISG-KPTGSEDCILNYTNDLNPDKR 126  
 D 62 VONNRKEPEQVQPMGVNNAVTPGSACLGIEFGSKLIGEDDLFLNYTPKLPQENS 121  
 QY 127 ----RPVYFIHGDFIEGEARNRMEGPDYFM-KRPVLYVYQYRLGVLGLSLKSE 181  
 D 122 AGDLNAVYHIHGGGYFEEG--ILGPHYLLDNNDYFVSYNTYRLVGLFASGTDGVL- 178  
 QY 182 VPQNAKLDQVALLRWKSNIAIFGSDVNTIYFGSAGASTHYMTETQTRGLFHGI 241  
 D 179 -PGNGLKQVALLKWIQONIVAFGSDPNSVITIGMSAGASSVNHLLISPMKGLFNRAI 237  
 QY 242 MMSGNSMCMASSTECOSRALTMARVGYKGE-----DNEKILFLMKANPYDLKEEP 295  
 D 238 IQSGSAFCHWSTAE-----NWAQKTKYLANLIGCTTNSVEIIECL-RSRPAKAIASY 290  
 QY 296 QVLTPERMKNKVPFPGPTVE--PYQTADCVYKPIREMYKSAWNSIPTLIGNTSYEGL 353  
 D 291 LNMFWRR--NFPPTPGPIYEVAGYE-----KFLPDPEKLVPHDIPVLSIAQDEGL 341  
 QY 354 LSKSVAKQYREYVKELESCVN-VYPMELADSESAEPL--ERAAIVKKAHVDEGPT--- 407  
 D 342 IF-STFLGLENGENEELNNMNEHLPHILDYNTTISNENLRFPTADIKFEYV-GDKPLSK 399  
 QY 408 -TLDNFMELCSYFLEFPMHRLQLEFNHTAG---PIYLYRFPDSEELINPYRIRP- 462  
 D 400 ETKSNLSKMSIDSGFYGTSKAAQ-----HAAKNTAPVYFIEGYSGN-----YSVA 450  
 QY 463 ----GRGVKGVSHADELYLFNWLISKRLPKRSRYKTIERNVGIWEFATTKPYSD 517  
 D 451 DPKSYSG--SSPHGDETNVYL-KVDGFYVDNEEDRKMKITVYNIMATFIKSGVP---D 505  
 QY 518 IAGMENLWDPPIKSD-DVYKCLNI 541  
 D 506 TENSE--IWLDPVSKNPADLEFRFKI 528

## RESULT 10

juvenile hormone esterase-related protein - cabbage looper

C:Species: Trichoplusia ni (cabbage looper)

C:Date: 23-Aug-1995 #sequence\_revision 19-Oct-1995 #text\_change 07-May-1999

C:Accession: S55233

R:Jones, G.; Venkataraman, V.; Ridley, B.; O'Mahony, P.; Turner, H.

A:Title: Structure, expression, and gene sequence of a juvenile hormone esterase-relat

A:Reference number: S55233; MUID:95031924; PMID:7945209

A:Accession: S55233

A&gt;Status: preliminary

A:Molecule type: mRNA

A:Residues: 1547 &lt;ON&gt;

C:Superfamily: juvenile-hormone esterase

Query Match 17.9%; Score 545; DB 2; Length 547;  
 Best Local Similarity 28.5%; Pred. No. 8, 7e-34;  
 Matches 153; Conservative 99; Mismatches 222; Indels 62; Gaps 19;

QY 14 CVKCMVKNKYNRLSTNETQIIDT-----EYQIKVKRMVYDSDYSSESTIYAPR 69  
 D 17 CVNCMELMNPIDORHANQRPQCDVRAQLDSGWCSTRSAGEVQYASFGIDYADQPLG 76  
 QY 70 ELRFKAPQRPVMEGVNDCCGPANRSVQTFEI--SGKPTG-SEDCILYLVN-----YTN 119  
 D 77 QLRKEQLPLKPMNGVLETIEEGPICQYDEITGRMGQPLAMSEACIYANVHPFNMYTS 136

[illegible]

Query Match	17.9%	Score 544	DB 2:	Length 552:
Best Local Similarity	31.4%	Pred No. 1.1e-33:		
Matches 176; Conservative	79;	Mismatches 221;	Indels 84;	Gaps 26

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0Y      8 IFRLLCYKCMWKNKYTNRLSTNEFOI IDTEGOKYKRYMTVDDSYSESIPYAKMP 67
Db      8 L1NLFLFGICFLT-----CASNPNKYQVHSGELAGFEITYNGRKIYISLGIPIYASPP 61
QY      68 VGLERFKAPORPVMEVGRDCCGPANRSVOTDETISG -KPTGSEDCLYLVNTYDNLNPKR 126
Db      62 YONNFKPEPOAPOLGVMWNAIVTSGSACLGIEFGSGSKIIIOEDCELIANVTYTPKLPQENS 121
QY      127 ----RPWVFIFHGCGEFGIEGANRMMFGGDYDM -KKPVLYLYQYRLVLGTLKSXENLN 181
Db      122 AGDLNMYVTHIHGGGYIFEG--ILYGFHYLDNNDFYVYSINRLVYLGAAGSDGYLT 179
QY      182 VPGNAGLDOYMAIRWYKSNIAIFEGGDVNTFEVSAGASASTHYMMITECTRLTFRGI 241
Db      180 --GNNGKLDQYAAALKWIGIONIVARGGDPNSVTIIIGMSAGASVANHILISPMKGLFRAI 237
QY      242 MMSGSMKCSASTECQSHALTMARVGYKGE-----DNEKDIIEFLMKANPDLIKEEP 295
Db      238 IQSGSAFCHWSTAE-----NVAACTRYIANLMGCPITNSSEIIEVC- RSRPAKAIKSY 290
QY      296 QYLTPFERMQUKVPMEFGTVE--LYOTADCVPRPIREMWKSAMGNSIPLTIGTSTYEG 353
Db      291 LNMFMWR--NPPFPFGGTVAQYE-----KFLPDIEKLVPHIIPALISIAODEGL 341
QY      354 LSKSVANQYFVUKLELSCVN-VYPMELADSEARSAPETL--ERAATYKKAHVDETP-- 407

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Db 342 IF-STFLENGENFNNNNNEHLPHILDVNTYISNENLFKAQDICEYF-GDKRISK 399  
Qy 408 -TLDNPELCSYFFLEPMRPFQLRPNHAG--TPIYLRPDSEELINRYLRMR- 462  
Db 400 ETKSNLSKMSIDRSFGYTSKAAO---HIAAKNTAPVYFEGYSGN---YSYVAF 450  
Qy 463 -----GRVGVSHADLFYTL-----FNNILSKRLPKESREYTIEMVGTWTEFATGK 512  
Db 451 DKPSYSNG-SSPHRGEDETSLVKMDGY-----VYDNEEDRKMTKTMVIMATFIKSCV 503  
Qy 513 PYSNDIAGMENTLWDPKRS 532  
Db 504 P---DTENSE--IWLPSKN 518

## RESULT 13

S47655  
carboxylesterase (EC 3.1.1.1) precursor - golden hamster  
C:Species: Mesocricetus auratus (golden hamster)  
C>Date: 26-Dec-1994 #sequence\_revision 03-Aug-1995 #text\_change 20-Jun-2000  
C:Accession: S47655  
R:Gene, T.: Isobe, M.; Takabatake, E.; Wang, C.Y.  
Biochim. Biophys. Acta 1207, 138-142, 1994  
A:Title: Cloning and sequence analysis of a hamster liver cDNA encoding a novel putative  
A:Reference number: S47655; MID:94318665; PMID:8043605  
A:Accession: S47655  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-561 <SON>  
A:Cross-references: EMBL:D28566; NID:9531238; PIDN:BA05913.1; PID:9531239  
C:Superfamily: cholinesterase; cholinesterase homology  
C:Keywords: carbonyl ester hydrolase  
F:58-546/Domain: cholinesterase homology <CHE>  
F:227,459/Active site: Ser, His status predicted

Query Match 17.8%; Score 542; DB 2; Length 561;

Best Local Similarity 30.4%; Pred. No. 1.5e-33;  
Matches 173; Conservative 87; Mismatches 204; Indels 106; Gaps 25;

Qy 34 IIDTEYQIQIKVMKYTD--DSTYSESIPIYAKPYGELFRKAPQRPVMEGVRDCCGP 91  
Db 33 IRTNHTQGVNRG-KLVYVEGVTVGYAFGLIPFAKRPVGPILFAPPEPEPMSGVRDGTSE 91  
Qy 92 ANRSVQTDFTSGK-----PT--GSECLYLVNVT--NDLNDKRRPVVFIHGDFI 139  
Db 92 PAMCLQIDDFMKPQISKERKILPTISSECLYINITTPRAHAGSMLPVMWTHGSAV 151  
Qy 140 FGEANRMWFGPDYMKRPVVLVTVQYRLGVGLSLKSENINLVPGNAGLKDQVVALRMVK 199  
Db 152 MGNMAMN-DGSLAATIEDIVISYQYRLGILGFSTGDEHAR--GNMGYLDQVVALHMVQ 208  
Qy 200 SNIAIFGSDVNTVFGESAGASTHYMTTEQIRGLFHRIIMSGMSMSMASTECOSR 259  
Db 209 QNIAISFGNPGQVITIFGVSAGTSVSSLVSPMSKGLFHGAIMOSGVALLPDLISDTPEA 268  
Qy 260 ALT--MAKRVGYKEDNEKDLIFLMAKANPYDLKEEPQVLTPEPMONKVMFPGPVP 317  
Db 269 VYTPVAVANOSCEAKDSRA-LVHCLRE-----KTEAEILIA-----INQVFI-----MTP 311  
Qy 318 YQADACVVPKPIRMVKSAMGNSIPTLIGNTSYE-----GL--LSNSVAKQ-PREV 365  
Db 312 GVNQGIPLRHPQELASVDHFPVPSIIGVSDCGMCPFLMGLDHWIKITRETLPAF 371  
Qy 366 VKELESCVNYVPELAD-----SESAPELTERALVKKAHNDGEPILDNEMELCSY 418  
Db 372 LKSRAEHM-MLRPPCSDLIMQYMGDVEDPQTQA-----QERLEMKD 413  
Qy 419 FYFLPMPMRFTQLRPNHAGTPIYLRPDSEELIN---PYRIMRFGKGVKSHADE 474  
Db 414 PMEVLPDA---LKAVAFQSHAPVYFEPQHOSSFTKKNDARPSVR-----ADHGCH 462  
Qy 475 LTYL---FNNILSKRLPKESREYKTIEMVGTWTEFATGKPYSDIAGMENTLWDPK 530

Db 463 VAFVGSDFWGL--KIDLTEEEKLLNRMKMYANFARHGNPNS-----EGLPWDEL 513  
Qy 531 KSDDYKCLNT-----GDELKVMIDLPEMDKI 556  
Db 514 VHDQTLKIDLPAYGRALKSKRLHFWTKI 543

## RESULT 14

T32907  
hypothetical protein F56C11.6 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans  
C>Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 31-Jan-2000  
C:Accession: T32907

R:Fin-Wollam, A.; Wohlmann, P.; Morris, M.  
submitted to the EMBL Data Library, January 1998

A:Description: The sequence of C. elegans cosmid F56C11.

A:Reference number: 221244

A:Accession: T32907

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-548 <TIN>

A:Cross-references: EMBL:AF043697; PIDN:AA097558.1; GSPDB:GN00019; CESP:F56C11.6

A:Experimental source: strain Bristol N2; clone F56C11

C:Gene(s):

A:Gene: CESP:F56C11.6

A:Map position: 1

A:Introns: 29/3; 84/3; 264/1; 340/1; 398/3; 447/1; 490/2

A:Superfamily: cholinesterase; cholinesterase homology

Query Match 17.4%; Score 529; DB 2; Length 548;  
Best Local Similarity 29.8%; Pred. No. 1.5e-32;  
Matches 177; Conservative 91; Mismatches 207; Indels 118; Gaps 28;

Qy 32 TQIDTEYQIQIKVMKYTDSDSYSESIPIYAKPYGELFRKAPQRPVMEGVRDCCGP 91  
Db 12 TAVHDTGCPRLKGVGYEGDGSVBSGLPIPAEPGLARKKAYAHKKWTEPLDCYAF 71  
Qy 92 ANRSVQTD-----FTSGKPTGSEDCILYLVNVT-----NDLNDKRRPVVFIHGDFI--- 139  
Db 72 GPRSPONDELQGFVTVTKVSEHCLSLNVFIPKMSNMPD--GFPVWFIHGGEFAVHS 130  
Qy 140 ---FGEAN--RMWFGPDYMKRPVVLVTVQYRLGVGLSLKSENINLVPGNAGLKDQVMA 194  
Db 131 SSNYGASIAARN-----LCITKDVVVVITNRYLGVGFPTTGDEVCOR--GNGLMDQPA 182  
Qy 195 LRWVKNIAIFGSDVNTVFGESAGASTHYMTTEQIRGLFHRIIMSGMSMSMAST 254  
Db 183 LEWVQENIOSFRQDPDNTVIFGOSAGASVDLCLSPHSRGLFPNRAIPMAGNCEDFAMR 242  
Qy 255 ECOSRA---LTMARVGYKEDNE-KDLEFLMAKANPYDLKEEPQVLTPEPMONK 306  
Db 243 TSGQQAQSLSEFRARYLQWGSDDNDSDDLQFDQQLYKI-----EMGINPKRGFHSQAG 298  
Qy 307 VMEFPGPYVEPQTDACVVPKPIRMVKSAMGNSIPTLIGNTSYBEL--LSNSVAKQYPE 364  
Db 299 SLX-FVPNFD-----GDFFPKPLNQNRKAPKQWIT--GTYKYBELFIAGALSKNPE 350  
Qy 365 VVKE-----LESCVNVVPELADSESAPELTERALVKKAHNDGEPILDNEMELCSY 419  
Db 351 GIKKEMGRIFKEC-----DYGERA-----DDVLQWVYF 379  
Qy 420 YF--LFP-----MARELQV--RPNHTAGT-----PIYLRPDSEELINXY 457  
Db 380 YFKGVAPRKHDEKMMHDIYFQIGYSINTGYRLANIMTDLQHDVYVYQGDYHNSA---GF 436  
Qy 458 RIMRFGRGKGVSHADELYLFM-NILSKRLPKESREYKTIEMVGTWTEFATGKPYRN 516  
Db 437 GVFRLMLPEFGSGTHCTEMRYVLCKGIISKFRPND--DKKMLHMTYTFNFAKKGPNGE 495  
Qy 517 DIAGMENTLWDPKISGSDVYKCLNIGDELKVMIDLPEMDKIKOGASTFDDKKEL 569  
Db 496 N---OETGEW---QKHDSAHPRFHKITLDDSEME--DYQERRAEMLDKRLAL 541

## RESULT 15

A33668

sterol esterase (EC 3.1.1.13) precursor - bovine (fragment)

C:Species: Bos primigenius taurus (cattle)

C:Date: 09-Mar-1990 #sequence\_revision 09-Mar-1990 #text\_change 18-Jun-1999

C:Accession: A33668

R:Kyger, E.M.; Wiegand, R.C.; Lange, L.G.

Biochem. Biophys. Res. Commun. 164, 1302-1309, 1989

A:Title: Cloning of the bovine pancreatic cholesterol esterase/lysophospholipase.

A:Reference number: A33668; PMID:90073663; PMID:2590203

A:Accession: A33668

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-597 &lt;KYG&gt;

A:Cross-references: GB:M28402; NID:9598081; PIDN:AAA56788.1; PID:9598082

C:Superfamily: cholinesterase; cholinesterase homology

C:Keywords: carboxylic ester hydrolase

F:48-583/Domain: cholinesterase homology &lt;CHE&gt;

Query Match 17.2%; Score 523; DB 2; Length 597;

Best Local Similarity 30.1%; Pred. No. 4.9e-32;

Matches 167; Conservative 67; Mismatches 211; Indels 109; Gaps 22;

```
OY 37 TEYGOIKGV-KRMTYDSDYSFESIPYAKPVGELRFKAPQRPVPEWEGVRCOCGPANRS 95
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 26 TEGFVEGVNKKLSLFGSDVDFKGIQFPAAPKA---LEKPERHPGMOGLKAKSFKKRC 82
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 96 VQTFDISGKPTGSEDCILNYTNDLNDPKRR-----PVMVFTHGDFIRGE----- 142
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 83 IQATLTOSTYGNEDCLTLNTV---PQGRKEVSHDLPVMIWYIGAFIMGASOGANFL 138
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 143 ANRNFEGPDYEMKKPVVLVTVQYRLGLGLSLKSENLNPNAGLKDQVALRWKNSNI 202
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 139 SNYLDGGEIATRGVNIYVTFNYRGVPLGFLSTGDSNL--PGNYGLMDQHMAIWAVKNI 196
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 203 AIFGGDVNITVEGSGAGASTHYMTIEQTRGLFHRGIMSGNSMGMASTECQSRALT 262
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 197 EAFGGDPNITLFGESAGASVSLQTLSPYNNKGLIKRAISOSGVGLCPWA---IQODPLF 253
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 263 MAKR---VGKKGEDNEKDILEFLMKANPYDLKEEPQVLTPEKONKVMFPFGPT--- 314
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 254 WAKRIAELVGGCPVDTSK--MAGCLKIT-----DPRALT---LAYKL--PLGSTIEPK 299
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 315 -----VEPYQTADCVVPKPIRENVKSA-----WNSIPLILIGNTSYEGL 353
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 300 LHYLSFVPIIDGDFIPDDPVNLYANADVDYIAGTNDMDGHLFVGMDVPAL--NSNKQDV 357
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 354 LSKSVAKQYP--EYKKELESC-----VNYVPWELADSRSAPEFLERAATYKKAHVDGET 406
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 358 TEEDPYKLVSGLTYKGLRGANATYEYTEPW---AODSSQETR-----KKTVDLET 407
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 407 PTLNFMELCSYFELFPMHREQLRFNHTAGTPILYLFREFDSEELINPYRIRFGRGV 466
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 408 DIL-----FLIPKTAIVAOHSHAKSANTYTYLFSQPSRMPITYPKM----- 449
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 467 KGVSHADELYLENNILSKRLPKESREXYKTIERNVGIWTEPATGKPYSDNDIAGMENLTV 526
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 450 -GADHADLQYVFGKPFATPLGVRADRTVSKAMIAWTNFAFGDPTGHSIVPAN--W 506
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 527 DPIKSSDDVYKCLN 540
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 507 DPTYLEDNDNYLEIN 520
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

Search completed: April 4, 2003, 09:17:18  
Job time : 21.0734 secs

GenCore version 5.1.4\_p5\_4578  
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OM protein - protein search, using sw model

Run on: April 4, 2003, 09:09:07 ; Search time 10.6371 Seconds  
(without alignments)  
2222.559 Million cell updates/sec

Title: US-09-776-910-13

Perfect score: 3045

Sequence: 1 MFLKQFIFRLKLCVKMNV.....PEMDKIKGASIFDKKELF 570

Scoring table: BIOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	954.5	31.3	540	EST1_CULPI	P16854 culex pipie
2	600.5	19.7	564	EST1_HELYI	P12992 heliothis v
3	572	18.8	489	P1967A_BACSU	P37967 bacillus su
4	553.5	18.2	564	EST1_MYZPE	P35502 myzus persi
5	544	17.9	552	EST1_MYZPE	P35501 myzus persi
6	542	17.8	561	EST1_MESUN	P04419 mesocricetu
7	523	17.2	597	BAL_BOVIN	P30122 bos taurus
8	520.5	17.1	574	CHLE_HORSE	P81908 equus caball
9	518	17.0	602	CHLE_HUMAN	P06276 homo sapien
10	515.5	16.9	614	ACES_MOUSE	P21836 mus musculu
11	512.5	16.8	581	CHLE_MOUSE	P21927 oryctolagus
12	512.5	16.8	633	ACES_ELEBL	P04456 caenorhabdi
13	512	16.8	562	EST1_CAEBR	P04058 torpeda cal
14	511	16.8	586	ACES_TORCA	P00311 mus musculu
15	508.5	16.7	603	CHLE_MOUSE	P02035 bungarus fa
16	507.5	16.7	581	ACES_BUNFA	P37136 rattus norv
17	504.5	16.6	614	ACES_RAT	P37136 rattus norv
18	502.5	16.5	545	EST1_DROPS	P25726 drosophila
19	501	16.5	629	ACES_LEPDE	P02677 lepidoptera
20	500	16.4	634	EST1_RAT	P063010 rattus norv
21	500	16.4	634	ACES_BRARE	P09463 brachydanio
22	499.5	16.4	557	SASB_ANAPL	P044791 anas platyr
23	499.5	16.4	562	EST1_CAEBL	P04457 caenorhabdi
24	498.5	16.4	611	EST1_RAT	P16303 rattus norv
25	498.5	16.4	611	ACES_FELCA	P062763 felis silve
26	496.5	16.3	613	ACES_BOVIN	P23795 bos taurus
27	492	16.2	590	ACES_TORCA	P07692 torpeda mar
28	491.5	16.1	566	EST1_PIG	P02950 sus scrofa
29	490.5	16.1	544	EST1_DROME	P08171 drosophila
30	488	16.0	554	EST1_MOUSE	P063880 mus musculu
31	488	16.0	561	EST1_RAT	P04573 rattus norv
32	485.5	15.9	561	EST1_RAT	P063108 rattus norv
33	484.5	15.9	584	ACES_RABIT	P029499 oryctolagus

## ALIGNMENTS

RESULT 1	EST1_CULPI	STANDARD;	PRT;	540 AA.
AC	P16854			
DT	01-AUG-1990 (Rel. 15, Created)			
DT	01-AUG-1990 (Rel. 15, Last sequence update)			
DT	01-FEB-1994 (Rel. 28, Last annotation update)			
DE	Esterase B1 precursor (EC 3.1.1.1).			
GN	B1.			
OS	Culex pipiens (House mosquito).			
OC	Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;			
OC	Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematoceera;			
OC	Culicoidae; Culex.			
OX	NCBI_TaxID=7175;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=NEW-R;			
RX	MEDLINE=90207238; PubMed=2320576;			
RA	Mouches C., Pauplin Y., Agarral M., Lemieux L., Herzog M.,			
RA	Abadon M., Baysat-Arnaouty V., Hyrien O., de Saint Vincent B.R.,			
RA	Georgiou G.P., Pasteur N.;			
RT	*Characterization of amplification core and esterase B1 gene			
RT	responsible for insecticide resistance in Culex.*;			
RT	Proc. Natl. Acad. Sci. U.S.A. 87:2574-2578(1990).			
RT	-1- FUNCTION: OVERPRODUCTION OF NONSPECIFIC ESTERASES IS A COMMON			
CC	-1- FUNCTION: OVERPRODUCTION OF ORGANOPHOSPHATE INSECTICIDES.			
CC	-1- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a			
CC	carboxylic anion.			
CC	-1- MISCELLANEOUS: THERE ARE TWO SUCH ESTERASES: A AND B. ALLELES OF			
CC	BOTH A AND B ARE KNOWN.			
CC	-1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.			
CC	-1- This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
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CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>			
CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).			
CC	EMBL; M32328; AAA28289.1; -			
CC	PIR; A35986; A35986.			
DR	HSSP; P21836; IMAA.			
DR	InterPro: IPR002018; CarbesteraseB.			
DR	InterPro: IPR000379; Ser-estrs_site.			
DR	Pfam: PF00135; Coesterase_1.			
DR	PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.			
DR	PROSITE: PS00941; CARBOXYLESTERASE_B_2; FALSE-NEG.			
KW	Hydrolase; serine esterase; Glycoprotein; Multigene family; Signal.			
KW	SIGNAL			
FT	CHAIN	1	540	ESTERASE B1.
FT	ACT_SITE	191	191	BY SIMILARITY.
FT	ACT_SITE	442	442	BY SIMILARITY.
FT	DISULFID	68	81	BY SIMILARITY.
FT	CARBOYD	452	452	N-LINKED (GLCNAC... ) (POTENTIAL).
FT	SEQUENCE	540 AA;	60806 MM;	F73B25B3AV157C95 CRC64;

34	480.5	15.8	542	1	EST6_DROSI	Q08662 drosophila
35	480.5	15.8	599	1	BAL_MOUSE	O64285 mus musculu
36	480.5	15.8	612	1	BAL_RAT	P07880 rattus norv
37	480	15.8	549	1	EST1_RAT	P10959 rattus norv
38	479.5	15.7	562	1	EST2_MOUSE	O64176 mus musculu
39	479.5	15.7	567	1	EST1_HUMAN	P23141 homo sapien
40	479	15.7	545	1	ESTC_DROPS	P25725 drosophila
41	477.5	15.7	649	1	ACES_DROME	P07140 drosophila
42	475.5	15.6	542	1	EST6_DROMA	P47982 drosophila
43	475.5	15.6	742	1	BAL_HUMAN	P19835 homo sapien
44	473.5	15.6	614	1	ACES_HUMAN	P22303 homo sapien
45	471.5	15.5	547	1	EST4_DROPS	P25727 drosophila

Query Match 31.3%; Score 954.5; DB 1; Length 540;  
 Best Local Similarity 36.9%; Pred. No. 4.4e-66;  
 Matches 203; Conservative 113; Mismatches 211; Indels 23; Gaps 10;

31 EQGIDTEGQIKGKRMVYDDSYSESPYAKPVGELRFAKQRPVMEGVRD-- 88  
 Db ESTVQTKIPVGRKRNVLGQEVYSEFGIPYARAPGELRFAKQRPVMEGVRD 63

89 -CGPA---NRSVQDTFISGKPTGSEDCYLVNTDLPDRRPMVYHGGDFFGAN 144  
 Db OCEPCYHDDRQ-----KIVGCEDSIKINFAKIPSPPLPMLTYGGGTEGTS 117

145 RMEFEDYFMKKPVVTVQYRLVGLFSLKSENLANVGNAGIKDQYMAWRVKSNAI 204  
 Db TELVGPDLVQKDIYLVSNFRIGALGFLCCQSEDDGVPGNAGIKDQYMAWRV 177

205 FGGVDNITVFEGESAGSTHYMTEDTRGLFRGIMSGNSMCNASTCCSRALMTA 264  
 Db FGGDKRTVTLGHSAGASVQYHLISDASKDLFQRRIYMSGSTYSWSLFRQRMV 237

265 KRVGKGEDEKDLLEFLMKANPYDLKEBPQVLPERRQKVMFPPGPTVEPYQTADCV 324  
 Db KAIMDGGGSGALRFLRRKAPEDIVAHQEKLLTDQMODDITFPPTVEPYLTQCI 297

325 VPKPIREWKSAMGNSITPLIGNTSYGLSKSVAKQYPEVKELESCVNVPELADSE 384  
 Db IPKAPFEKARTAWGDKIDIMIGTSEGLLLQKIKLHPHLLSHPLFNGVNPNL--K 354

385 RSAPETLERAIVKAVHDETPLDN--FMELCSYFYLFPFHRLQIRFNTAGTPT 441  
 Db ISMERKLEPAKTKQRYRPSIPSEMNNLGVHMSDRVWGHGHTILAAARSRR--T 413

442 YLYFDDSEETINPYIRMGKGVSHADELTFLFNNILSKLPKESREKTYTERV 501  
 Db FYVRIQDS--EFYHYRIMIDPKLRGTAHADELSTYLFSEFTQVPEKFEFRGIDTV 472

502 GIMTEFATGKPYSDNLAGMENLWPIKRSDDVYKCLN--GELKAVMDLPENDKIKGA 560  
 Db DVSAFPIYNDP--NCGTKAGVGFEPNQTKEPFCCLNTIANDGVAFVDPDADRLMD 531

561 SIFDKKKELF 570  
 Db 532 AMY-VNDEL 540

RESULT 2  
 ESTD\_HELVI  
 ID ESTD\_HELVI STANDARD; PRT; 564 AA.  
 AC P12992;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE Juvenile hormone esterase precursor (EC 3.1.1.59) (JH esterase).  
 OS Heliothis virescens (Noctuid moth) (Owllet moth).  
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
 OC Insecta; Pelegrina; Neoptera; Endopterygota; Lepidoptera; Glossata;  
 OC Diptera; Noctuoidea; Noctuidae; Heliothinae; Heliothis.  
 OC NCBI\_TaxID=7102;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 20-54.  
 RX MEDLINE=89308671; PubMed=2745451;  
 RA Hanzik T.N., Yehia A.I.A.-A., Harshman L.G., Hammock B.D.;  
 RT "Isolation and sequencing of cDNA clones coding for juvenile hormone  
 RT esterase from *Heliothis virescens*. Evidence for a catalytic mechanism  
 RT for the serine carboxylesterases different from that of the serine  
 RT proteases.";  
 RT J. Biol. Chem. 264:12419-12425(1989).  
 RN [2]  
 RP REVISIONS.  
 RA Hanzik T.N.;  
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.  
 CC -I- FUNCTION: JH ESTERASE PLAYS A CRUCIAL ROLE IN THE DECREASE OF

CC JH ACTIVITY IN LEPIDOPTERAN INSECTS, BY HYDROLYZING THE METHYL  
 CC ESTER OF JH. IT IS ALSO INVOLVED IN THE TRANSPORT OF JH.  
 CC -I- CATALYTIC ACTIVITY: Methyl (2E,6E)-(10R,11S)-10,11-epoxy-3,7,11-  
 CC trimethyltrideca-2,6-dienoate + H<sub>2</sub>O = (2E,6E)-(10R,11S)-10,11-  
 CC epoxy-3,7,11-trimethyltrideca-2,6-dienoate + methanol  
 CC -I- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL: J04955; AAB8629.1; -  
 CC PIR: A34325; A34325.  
 CC HSP: P37967; 10E3.  
 CC InterPro: IPR002018; Carboxylesterase.  
 CC InterPro: IPR000379; Ser-estrs-site.  
 CC Pfam: PF00135; Coesterase; 1.  
 CC PROSITE: PS00122; CARBOXYLESTERASE\_B\_1; 1.  
 CC PROSITE: PS00941; CARBOXYLESTERASE\_B\_2; FALSE NEG.  
 CC K1: Hydrolase; Serine esterase; Glycoprotein; Signal.  
 CC SIGNAL 1 19  
 CC CHAIN 20 564 JUVENILE HORMONE ESTERASE.  
 CC FT ACT\_SITE 220 220 BY SIMILARITY.  
 CC FT ACT\_SITE 351 351 BY SIMILARITY.  
 CC FT ACT\_SITE 465 465 BY SIMILARITY.  
 CC FT DISULFID 89 109 BY SIMILARITY.  
 CC FT CARBOHYD 81 81 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 180 180 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 402 402 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 515 515 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT VARIANT 29 29 V->L.  
 CC FT VARIANT 52 52 F->P.  
 CC SQ SEQUENCE 564 AA; 62614 MW; D1405DD91914E8D CRC64;

Query Match 19.7%; Score 600.5; DB 1; Length 564;  
 Best Local Similarity 32.0%; Pred. No. 1e-38;  
 Matches 166; Conservative 97; Mismatches 210; Indels 45; Gaps 19;

29 TNEQGIT-DTEGQIKGKRMVYDDSYSESPYAKPVGELRFAKQRPVMEGVRD 87  
 Db TNSRSVVAHLDSGLIRGVR--SADGIRKASPLGVYAKQRPVMEGVRD 81

88 CGGPNRSVQDTFISGKPTGSEDCYLVNTDLPDRRPMVYHGGDFFGAN 144  
 Db ATNESPICFQTDVLYGRMAASENSEACTIVANIHVPMOSLPVRGTPPL-----RPLIVE 136

133 IHGGDFIRGEANRMWFGDPYFMKKPVVTVQYRLVGLFSLKSENLANVGNAGIKDOV 192  
 Db IHGGFARSGSHEDLHGEVLYTVNTYVITFNLYNFGSLSNMT--TKIPGNAGLRDOV 194

193 MALRWKSNLAIFGGVDNITVFEGESAGSTHYMTEDTRGLFRGIMSGNSMCNAST 252  
 Db TLLKRWYRNMAKNFGGDESDITIAQOSAGASAHLITLSTKATEGIFKRAILMSGMSYFF 254

253 STEGSRALTFMARRVYKGG--EDNEKDLLEFLMKANPYDLKEBPQVLPERRQKVMF 324  
 Db TTSPLFAAYISKOLLQTLGNETDPEITHQDL--PAELTANANAL-----TEQIGLFT 309

311 FGPVPE--PYQTADCVVPKPIREWKSAMGNSITPLIGNTSYGLSKSVAKQYPEVKELE 384  
 Db FLPTVESPLPGVTTIIDDPEITIAEGRKNVPLLLIGTSECEFTFRNRLNLDVKKIQ 369

370 ESCVNVYVPELADSEKAPETL--ERAAIVKAVHDETPLDNFMELCSYFYFLPMHFR 428  
 Db DNPITIIIPKLL--FMPPELLEMLAKTTERKYNG--TISIDNFVKSQSGDFEYPAKRL 426

429 LQLEFNHTAGTPIYLYRFDDSEETINPYIRMGKGVSHADELTFLFNNILSKLPKES 487  
 Db AKRR-AETGAPLILYRAFEAGONSITK-KVM--GLNHEGVGHIEDLYTVFVYNSKSEAL 482

QY 488 ---PRESREYKTIEMVGIWTEPATGKPYNSDIAGME 522  
 DB 483 HASPSEN-DYKMKNLMTGYFLNFKICSPCEODNNSLE 519

## RESULT 3

PNBA\_BACSU STANDARD; PRT; 489 AA.

AC P37967; 1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Para-nitrobenzyl esterase (EC 3.1.1.-) (PNB carboxy-esterase) (PNBE).  
 CN PNBA.  
 OS Bacillus subtilis.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OC NCBI\_TaxID=1423;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-22 AND 211-223.  
 RC STRAIN-NRRL B8079;  
 RA MEDLINE=95129891; PubMed=7828905;  
 RA Zock J., Cantwell C., Swartling J., Hodges R., Pohl T., Sutton K.,  
 RA Rostock P., Jr., McGilvray D., Queener S.;  
 RT "The Bacillus subtilis pnbA gene encoding p-nitrobenzyl esterase;  
 RT cloning, sequence and high-level expression in *Escherichia coli*.";  
 RL Gene 151:37-43(1994).  
 RN [2]  
 RP SEQUENCE OF 1-22 AND 211-223, AND CHARACTERIZATION.  
 RA Chen Y.-R., Usui S., Yu C.-A.;  
 RT "Purification and properties of p-nitrobenzyl esterase from *Bacillus*  
 RT subtilis.";  
 RL FASEB J. 6:A332-A332(1991).  
 RN [3]  
 RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).  
 RA MEDLINE=20006229; PubMed=10535917;  
 RA Spiller B., Gershenson A., Arnold F.H., Stevens R.C.;  
 RT "A structural view of evolutionary divergence.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 96:12305-12310(1999).  
 CC -1- FUNCTION: CATALYZES HYDROLYSIS OF SEVERAL BETA-LACTAM ANTIBIOTIC  
 CC PNB ESTERS TO THE CORRESPONDING FREE ACID AND PNB ALCOHOL.  
 CC -1- SUBUNIT: MONOMER.  
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.

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CC EMBL; 006089; AAA61915.1; -;  
 DR PDB; 1C7J; 29-MAR-00.  
 DR PDB; 1C7J; 29-MAR-00.  
 DR PDB; 1OE3; 21-JUL-99.  
 DR InterPro: IPR002018; Carboxylesterase.  
 DR InterPro: IPR000379; Ser-esterase-site.  
 DR Pfam: PF00135; Coesterase\_1.  
 DR PROSITE: PS00122; CARBOXYLESTERASE\_B\_1; 1.  
 DR PROSITE: PS00941; CARBOXYLESTERASE\_B\_2; 1.  
 KM Hydrolyase; Serine esterase; 3D-structure.  
 FT ACT\_SITE 189  
 FT ACT\_SITE 17  
 FT CONFLICT 17  
 SEQUENCE 489 AA; 53998 MW; 696B6EFEDA47269 CRC64;

Query Match 18.88; Score 572; DB 1; Length 489;  
 Best Local Similarity 30.68; Pred. No. 1.3e-36;  
 Matches 171; Conservative 89; Mismatches 203; Indels 96; Gaps 24;

QY 33 QIITEYQIQKGVKRMVYDSDYSFESIPAKPVGELRKPAPORPVPMEGVND----- 87  
 DB 4 QIVTVYQKVGKT-----ENGVIHKWGIPIYAKPPVGOMRKAPPEPEVMEVDVDAIATYG 58

QY 88 ---CCGPAKNSVQTDFTS-----GKPTGSEDCIYLNVTNDLNDPKRRPVWFIHGDFI 141  
 DB 59 PICPOP-----SDLLSTLSTELPRQSEDCIYVNVAPD-TTSQNLPMVWVHIGAFYLG 111  
 QY 142 EAMRNMF-GPDYPMKRVYLVQVIRGLVYGLFLSKSENLNPGNGLADQVVALWVKS 200  
 DB 112 AGSEPLDYDGSKLAAGSVIYVTLNTRIGRPGFHLTSSPDEAYSDNLQDQAALAKVRE 171  
 QY 201 NIAIFGGVDNITVFGESAGGASTHYMTTEQTRGLFHKGIMSGSKSMASTECSQA 260  
 DB 172 NISAFGSDPNVTVFGESAGGASTIAMLAMPARAKGLFQKAIMESGASR-TMKQQAAS 230  
 QY 261 LTMARKVYGEENKELIFELKANKYDILKEKPOLFPERQNKVMPFGPTVEPYQT 320  
 DB 231 AAFLOVIGI-----NESO-LDRLTVAEDLKAADQLRIK-ENIFQLEFGALDPK- 282  
 QY 321 ADCVVPKPIREMYKSANGNSIPTLIGNTSYGLSKSVAKQYDEYVKELESCVNYPMEL 380  
 DB 283 ---TLPEPEKSIAGASGIPLLIGTRDEGYLF-----FTP- 317  
 QY 381 ADSRSAPETLERA-----ATYKKAHVDGEPTLDMFELCSYFLPMPHRTQLRF 433  
 DB 318 -DSVHSGQETLDALELYLLGKPLAEKA-ADLYPRSLQSJHMTDLLFMRPAVYASAS 375  
 QY 434 NHTAGTPYLYRPFDESEELINPYRMRFGVGVSHADELYLVWNI--LSKRLPK- 490  
 DB 376 HY-----APVWMYRFPDHPK-PPY-----NKAFHALELPVFGNDGLERMAKEI 421  
 QY 491 SREYKTIEMV-GIWTPEATGKPYNSDIAGMENLTDPIKSDYVKCINIGDELKVM 549  
 DB 422 TDEVKQLSHTIQSAMITFAKGNP-----STEAVNMPAY--HEETREYVILSDIYEN 473  
 QY 550 LPEMKIKOGASIFDKKE 568  
 DB 474 DPESKRK-----LPSKGE 489

## RESULT 4

ESTF\_MYZPE STANDARD; PRT; 564 AA.

AC P35502;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 01-OCT-1994 (Rel. 30, Last annotation update)  
 DE Esterase FE4 precursor (EC 3.1.1.1) (Carboxylic-ester hydrolase).  
 OS Myzus persicae (Peach-potato aphid).  
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
 OC Insecta; Pterygota; Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha;  
 OC Aphidiformes; Aphidoidea; Aphididae; Macrosiphini; Myzus.  
 OC NCBI\_TaxID=13164;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 24-63.  
 RC STRAIN=Isolate 800F;  
 RA MEDLINE=93384534; PubMed=8373371;  
 RA Field L.M., Williamson M.S., Moores G.D., Devonshire A.L.;  
 RT "Cloning and analysis of the esterase genes conferring insecticide  
 RT resistance in the peach-potato aphid, *Myzus persicae* (Sulzer).";  
 RL Biochem. J. 294:569-574(1993).  
 CC -1- FUNCTION: OVERPRODUCTION OF NONSPECIFIC ESTERASES IS A COMMON  
 CC MECHANISM OF RESISTANCE TO ORGANOPHOSPHATE INSECTICIDES.  
 CC -1- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a  
 CC carboxylic anion.

CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.  
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CC EMBL: X74555; CAA52649.1; -  
 DR PIR: S36787; S36787.  
 DR HSSP: P21836; 1MAA.  
 DR InterPro: IPR002018; Carboxylesterase.  
 DR InterPro: IPR000379; Ser\_estr\_1-site.  
 DR Pfam: PF00135; Coesterase; 1.  
 DR PROSITE: PS00122; CARBOXYLESTERASE\_B\_1; 1.  
 DR PROSITE: PS00941; CARBOXYLESTERASE\_B\_2; FALSE NEG.  
 KW Hydrolyase; Serine esterase; Glycoprotein; Signal.  
 FT CHAIN 1 23  
 FT ACT\_SITE 24 564  
 FT ACT\_SITE 214 564  
 FT ACT\_SITE 339 564  
 FT ACT\_SITE 339 564  
 FT ACT\_SITE 463 564  
 FT ACT\_SITE 463 564  
 FT DISULFID 89 106  
 FT DISULFID 266 277  
 FT CARBOHYD 81 81  
 FT CARBOHYD 269 269  
 FT CARBOHYD 371 371  
 FT CARBOHYD 404 404  
 FT CARBOHYD 443 443  
 SO SEQUENCE 564 AA; 62757 MW; 128CC0EC3F2D9F1A CRC64;

Query Match Best Local Similarity 18.2%; Score 553.5; DB 1; Length 564;  
 Matches 178; Conservative 81; Mismatches 231; Indels 75; Gaps 26;

QY 8 IFRLLKVCWKYNTYRLSTNETQIIDTEYGOIKGKRMVYDDSYSPESIPYAKPP 67  
 DB 8 LINTLFLTGICFLT-----CSASNTPKYOVHSGELAGFEYTYNGRKIYSFLGIPYASPP 61  
 QY 68 VGLRFPKAPQRPVWEGVRCDCGGRANRSVQDTFISG-KPTGSEDCILVNTDNLNPKR 126  
 DB 62 VQNNRFEKPEQVQVPLGVMNATVGSACLGIEFGSGSKIIQOECLFLNVTYTPKLPQENS 121  
 QY 127 ----RPVVFTHGDFITGEANRMWFGPDYFM-KKPVLYTVQYRLGVLGFLSKSENLN 181  
 DB 122 AGDLNMTVTHHGGGYTGEG--ILYGPHTLLDNDNDEYVYSINRVLGAFSTGDEVL- 178  
 QY 182 VPGNAGLKDOYVALRWKNSNATIGSDVNTITVFGESAGASTHYMMITDQTRGLFHRGI 241  
 DB 179 -PGNGLKDOYVALRWKNSNATIGSDVNTITVFGESAGASTHYMMITDQTRGLFHRGI 241  
 QY 242 MASGNSMCMASTECQSRALTMARVKGKE-----DNEEDILEELMKANPVDLKEEP 295  
 DB 238 IQSGSAPCHNSTAB-----NVAOKTYIANLACPTNNSVEIYECVLRSPAKALAKSY 290  
 QY 296 QVLTPEKQKVPFPGPTVE--PYQTADCVPRPIREKVSAMGNSIPTLIGNTSYEGL 353  
 DB 291 LNFMPWR--NFPFPGPTVEVAGYE-----KFLPDIDPEKLVPHDIPILISADDEGL 341  
 QY 354 LSKVAQOYEVVKELESCVN-YVPMELADSESAPEVL--ERRAIVKKAHVDGEP-- 407  
 DB 342 IF-STPIGLENGENELNNMNEHPLHLLDNYTISNENLRFKTAODIKERYF-GDKPIK 399  
 QY 408 -TLDNEMELCSYEFLEPMHRLQLRNHTAG--PPIVYRRDPESEELINRYRIMRF- 462  
 DB 400 ETKSNLEKMSIDRSFGYGTSKAAO-----HTAANTAPVYIYEEGYSGN-----YTVAF 450  
 QY 463 -----GCGVGVSHADELYLNNILSKRLPKESREKTIERNVGIWTEFATGKPYSD 517  
 DB 451 DPKSYSG-SSPTHGDETNYVL-KVDGFTVYDNEEDRKMKTVMNIMATIKSGV--D 505  
 QY 518 IAGMENLTMDPIKSD-DVYKCLNI 541  
 DB 506 TENSE--TWLPVSKNPADLFRFTKI 528

RESULT 5  
 ESTE\_MYZPE  
 ID ESTE\_MYZPE  
 AC P35501; STANDARD; PRT; 552 AA.

DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 01-OCT-1994 (Rel. 30, Last annotation update)  
 DE Esterase E4 precursor (EC 3.1.1.1) (Carboxylic-ester hydrolase).  
 OS Myzus persicae (Peach-potato aphid).  
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
 OC Insecta; Pterygota; Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha;  
 OC Aphidiformes; Aphidoidea; Aphididae; Macrosiphini; Myzus.  
 OX NCBI\_TaxId-13164;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 24-63.  
 RC STRAIN-R3 / Isolate 794J;  
 RX MEDLINE-93384534; PubMed-8373371;  
 RA Field L.M., Williamson M.S., Moores G.D., Devonshire A.L.;  
 RT Cloning and analysis of the esterase genes conferring insecticide  
 RT resistance in the peach-potato aphid, Myzus persicae (Sulzer).  
 RL Biochem. J. 294:569-574(1993).  
 CC -1- FUNCTION: OVERPRODUCTION OF NONSPECIFIC ESTERASES IS A COMMON  
 CC MECHANISM OF RESISTANCE TO ORGANOPHOSPHATE INSECTICIDES.  
 CC -1- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a  
 CC carboxylic anion.  
 CC -1- MISCELLANEOUS: THIS ESTERASE CONFERS INSECTICIDE RESISTANCE.  
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.  
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DR EMBL: X74554; CAA52648.1; -  
 DR PIR: S36786; S36786.  
 DR HSSP: P21836; 1MAA.  
 DR InterPro: IPR002018; Carboxylesterase.  
 DR InterPro: IPR000379; Ser\_estr\_1-site.  
 DR Pfam: PF00135; Coesterase; 1.  
 DR PROSITE: PS00122; CARBOXYLESTERASE\_B\_1; 1.  
 DR PROSITE: PS00941; CARBOXYLESTERASE\_B\_2; FALSE NEG.  
 KW Hydrolyase; Serine esterase; Glycoprotein; Signal.  
 FT CHAIN 1 23  
 FT ACT\_SITE 24 552  
 FT ACT\_SITE 214 552  
 FT ACT\_SITE 339 552  
 FT ACT\_SITE 339 552  
 FT ACT\_SITE 463 552  
 FT ACT\_SITE 463 552  
 FT DISULFID 89 106  
 FT DISULFID 266 277  
 FT CARBOHYD 81 81  
 FT CARBOHYD 269 269  
 FT CARBOHYD 371 371  
 FT CARBOHYD 404 404  
 FT CARBOHYD 443 443  
 SO SEQUENCE 552 AA; 61348 MW; B97B67272DF7209 CRC64;

Query Match Best Local Similarity 17.9%; Score 544; DB 1; Length 552;  
 Matches 176; Conservative 79; Mismatches 221; Indels 84; Gaps 26;

QY 8 IFRLLKVCWKYNTYRLSTNETQIIDTEYGOIKGKRMVYDDSYSPESIPYAKPP 67  
 DB 8 LINTLFLTGICFLT-----CSASNTPKYOVHSGELAGFEYTYNGRKIYSFLGIPYASPP 61  
 QY 68 VGLRFPKAPQRPVWEGVRCDCGGRANRSVQDTFISG-KPTGSEDCILVNTDNLNPKR 126  
 DB 62 VQNNRFEKPEQVQVPLGVMNATVGSACLGIEFGSGSKIIQOECLFLNVTYTPKLPQENS 121  
 QY 127 ----RPVVFTHGDFITGEANRMWFGPDYFM-KKPVLYTVQYRLGVLGFLSKSENLN 181  
 DB 122 AGDLNMTVTHHGGGYTGEG--ILYGPHTLLDNDNDEYVYSINRVLGAFSTGDEVL 179  
 QY 182 VPGNAGLKDOYVALRWKNSNATIGSDVNTITVFGESAGASTHYMMITDQTRGLFHRGI 241

Db 180 --GNNGKQVAAKWKIQQNIVAFGDPNSVTITGMSAGASSVHNLISPMKGLFNRAI 237  
 QY 242 MMSGSMSCWASTECOSRATLMARVGYKGE-----DNEKDIIEFLMKANPYDLIKEEP 295  
 Db 238 IQSSGACCHWSTAE-----VNAOKTKYIANLMGCPINNSEIYECL-RSPAPAKIKSY 290  
 QY 296 QVLTPEKQKVMPEFGTYE--PYQTADCVVPRPIREMYKSAMGSIPTLIGNTSEGL 353  
 Db 291 LNFMPWR--NEPPTPFQGTVEAGYE-----KFLPDIPKELVPHDIPVLISIAQDEGL 341  
 QY 354 LSKSVANQYPRVVKLESCVN--VYPWELADSEBSAPETL--ERAATYKKAHVDETP--- 407  
 Db 342 IF-STFGLGENFENLNNMNEHLPHILDYNTTISNENLRKTKQDIEKFFY-GDKPISK 399  
 QY 408 -TLDNFELCSYFFFLPMPHRLQLRNHTAG--TPYLYRFPDSEETIINPYRIMRF- 462  
 Db 400 ETKNSLSMISDRSFGYGTSKAAQ-----HIAAKTAPVYEFEGYSGN-----YSYAF 450  
 QY 463 -----GRGVKGVSHADELYL-----FWNLISKRLPKESREYKTIEMVGIWTEFATGK 512  
 Db 451 DKPSYSRG-SSPTHGDETSYVLKMDGFY-----VYDNEEDRKMKIKTMVIMATFIKSGV 503  
 QY 513 PYSNDIAGMELTWDPPIKS 532  
 Db 504 P---DTENSE--TWLPVSKN 518

## RESULT 6

ESTL\_MESAU STANDARD; PRT; 561 AA.  
 ID ESTL\_MESAU STANDARD; PRT; 561 AA.  
 AC 06419;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Liver carboxylesterase precursor (EC 3.1.1.1).  
 OS Mesocricetus auratus (Golden hamster).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
 OC Mesocricetus.  
 NC NCB1\_TaxID=10036;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-Syrian golden; TISSUE-Liver;  
 RX MEDLINE=94318665; PubMed=8043605;  
 RA Some T., Isobe M., Takabatake E., Wang C.Y.;  
 RT "Cloning and sequence analysis of a hamster liver cDNA encoding a  
 RT novel putative carboxylesterase.";  
 RL Biochim. Biophys. Acta 1207:138-142(1994).  
 CC -1- FUNCTION: INVOLVED IN THE DETOXIFICATION OF XENOBIOTICS AND IN  
 CC THE ACTIVATION OF ESTER AND AMIDE PRODRUGS.  
 CC -1- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a  
 CC carboxylic anion.  
 CC -1- SUBCELLULAR LOCATION: Microsomal membrane, lumen of endoplasmic  
 CC reticulum.  
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: D28566; BAA05913.1; -  
 DR HSSP: P37967; 10E3.  
 DR InterPro: IPR002018; Carboxylesterase.  
 DR InterPro: IPR000379; Ser\_estr\_site.  
 DR Pfam: PF00135; Coesterase\_1.  
 DR PROSITE: PS00122; CARBOXYLESTERASE\_B\_1; 1.  
 DR PROSITE: PS00941; CARBOXYLESTERASE\_B\_2; 1.  
 DR Glycoprotein; Hydrolase; Serine esterase; Endoplasmic reticulum;  
 KW Signal; Multigene family.

FT SIGNAL 1 27  
 FT CHAIN 28 561  
 FT ACT\_SITE 227 227  
 FT ACT\_SITE 459 459  
 FT DISULFID 95 122  
 FT DISULFID 280 291  
 FT SITE 558 561  
 FT CARBOHYD 276 276  
 FT CARBOHYD 362 362  
 SO SEQUENCE 561 AA; 62330 MW; 48BA11E422475321 CRC64;

Query Match 17.8%; Score 542; DB 1; Length 561;  
 Best Local Similarity 30.4%; Pred. No. 3, 2e-34;  
 Matches 173; Conservative 87; Mismatches 204; Indels 106; Gaps 25;

QY 34 IIDTEYGOIKGVKRMVYD--DSYSEFISIPAKPVGGLRKAQRQRPVPMGVDCCGP 91  
 Db 33 IRNTHRGQVKG-KLVYKGVGVGVVAFGLIPAKPVGLRPAPEPPPMGSGVBDGTSE 91  
 QY 92 ANRSVOTDFISCK-----PT--GSEDCYLANYT-NDINPDKRRPVVFIHGDPFI 139  
 Db 92 PAMCLOTDFMRPQISKERKILPTISMSBDCLXNTYTAHAHESGNLPVWMIHGALY 151  
 QY 140 FGEANRMFGPDYEMKKPVVLYTVQYRLGVGLSLKSNLNVPGNAGLKDQVMAIRWK 199  
 Db 152 MGNASMN-DGSLLAATEDIIVISIQYRLGILGFFSTGDEHAR--GNWGGLDQVAAHLHWQ 208  
 QY 200 SNAIFGSDVDNTVFGESAGASTHYMMITDQRLGFRGIMGSMSCWASTECOSR 259  
 Db 209 QNTASFQGNQVTTIFGVSAAGTSVSLVSPSKGLFGALMGSGVALLPDLISDTPEA 268  
 QY 260 ALT--MAKRGYKGEEDNEKDIIEFLMKANPYDLIKEEPVLTPEKQKVMPEFGTYE 317  
 Db 269 VYIPVAVNAGSGCAKSKSEA-LVHCURE-----KTEAFILA-----INQVFI-----MTP 311  
 QY 318 YQTADCVVPRPIREMYKSAMGSIPTLIGNTSE-----GL--LSKSYAKO-YREV 365  
 Db 312 GVVDGIFELPRHPELQSLASVDPHVPISIIIGVDSQCGVGLPMGIDHVIKNTIRETLPAF 371  
 QY 366 VKLESCVNVVPELAD-----SRSAPETLERALYKKAHVGEPTLDFNEELCSY 418  
 Db 372 LKSRABHM-MLRPECSDLLMOEYMGVEDPOTQA-----QFRELKMD 413  
 QY 419 FYELFPMHREFLQLRNHTAGTPYLYRFPDSEETIIN--PYRIMRFGYKGVSHADE 474  
 Db 414 FMYVITA---LKAYQRSHAPVYEFEPHOSSFLKNKARSHYR-----ADHGDH 462  
 QY 475 LTVL-----FWNLISKRLPKESREYKTIEMVGIWTEFATGKPYNDIAGMELTWDPPIK 530  
 Db 463 VAFVFGSDFWGL--KIDLTEEKLKRMKMYWAFRHNPNNS-----EGLPYWPEL 513  
 QY 531 KSDDYKCLNTI-----GDELKVDLPEMDKI 556  
 Db 514 VHDQYLLKLDIOPAVGRALKSRKLHFWTKI 543

## RESULT 7

BAL\_BOVIN STANDARD; PRT; 597 AA.  
 ID BAL\_BOVIN STANDARD; PRT; 597 AA.  
 AC P30122;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Bile-salt-activated lipase precursor (EC 3.1.1.3) (EC 3.1.1.13) (BAL  
 DE (Bile-salt-stimulated lipase) (BSSL) (Carboxyl ester lipase) (Sterol  
 DE esterase) (Cholesterol esterase) (Pancreatic lysophospholipase)  
 DE (Frigmentl).  
 GN CEL.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 NC NCB1\_TaxID=9913;

RN [1] SEQUENCE FROM N.A.  
 RX MEDLINE-90073663; PubMed-2590203;  
 RA Kyger E.M., Wiegand R.C., Lange L.G.;  
 RT "Cloning of the bovine pancreatic cholesterol  
 esterase/lysophospholipase.";  
 RL Biochem. Biophys. Res. Commun. 164:1302-1309(1989).  
 RN [2]  
 RP SEQUENCE OF 19-40.  
 RC TISSUE-Pancreas;  
 RX MEDLINE-99238708; PubMed-10220579;  
 RA Tanaka H., Merlau I., Ito F.;  
 RT "Purification and characterization of bovine pancreatic bile salt-  
 activated lipase.";  
 RL J. Biochem. 125:883-890(1999).  
 RN [3]  
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 19-565, AND REVISION TO 45.  
 RX MEDLINE-97473004; PubMed-9331420;  
 RA Wang X., Wang C.S., Tang J., Dyda F., Zhang X.C.;  
 RT "The crystal structure of bovine bile salt activated lipase: insights  
 into the bile salt activation mechanism.";  
 RL Structure 5:1209-1218(1997).  
 RN [4]  
 RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS) OF 19-597.  
 RX MEDLINE-98215635; PubMed-9548741;  
 RA Chen J.C.-H., Miercke L.J.W., Krucinski J., Starr J.R., Saenz G.,  
 Wang X., Spilburg C.A., Lange L.G., Ellsworth J.L., Stroud R.M.;  
 RT "Structure of bovine pancreatic cholesterol esterase at 1.6 A: novel  
 structural features involved in lipase activation.";  
 RL Biochemistry 37:5107-5117(1998).  
 CC -1- FUNCTION: CATALYZES FAT AND VITAMIN ABSORPTION. ACTS IN CONCERT  
 WITH PANCREATIC LIPASE AND COLIPASE FOR THE COMPLETE DIGESTION  
 OF DIETARY TRIGLYCERIDES.  
 CC -1- CATALYTIC ACTIVITY: Triacylglycerol + H(2)O = diacylglycerol + a  
 fatty acid anion.  
 CC -1- CATALYTIC ACTIVITY: A sterol ester + H(2)O = a sterol + a fatty  
 acid.  
 CC -1- ENZYME REGULATION: ACTIVATED BY BILE SALTS CONTAINING A 7-HYDROXYL  
 GROUP IN THE INFANTS INTESTINE WHERE IT AIDS TO DIGEST MILK FATS.  
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL, M28402; AAA56788.1; -  
 DR PIR, A33668; A33668.  
 DR PDB, IAKN; 27-MAY-98.  
 DR PDB, IAOI; 05-AUG-98.  
 DR PDB, 2BCE; 23-MAR-99.  
 DR InterPro, IPR002018; Carboxylesterase.  
 DR InterPro, IPR000379; Ser\_Lestrn\_site.  
 DR Pfam, PF00135; Coesterase; 1.  
 DR PROSITE, PS00122; CARBOXYLESTERASE\_B\_1; 1.  
 DR PROSITE, PS00941; CARBOXYLESTERASE\_B\_2; 1.  
 KW Hydrolase; Serine esterase; Lipid degradation; Glycoprotein; Signal;  
 KW 3D-structure.  
 FT NON\_TER 1  
 FT SIGNAL <1 18  
 FT CHAIN 19 597  
 FT ACT\_SITE 212 212  
 FT ACT\_SITE 338 338  
 FT ACT\_SITE 455 455  
 FT DISULFID 82 98  
 FT DISULFID 264 275  
 FT CARBOHYD 205 205  
 FT CARBOHYD 379 379  
 FT CONFLICT 30 30  
 FT CONFLICT 45 45  
 FT I -> V (IN REF. 1).  
 FT N-LINKED (GLCNAC. . .)  
 FT F-LINKED (GLCNAC. . .)  
 FT P -> P (IN REF. 2).  
 FT I -> V (IN REF. 1).

SQ SEQUENCE 597 AA; 65161 MW; B23E7AED90EBFD1 CRC64;  
 Query Match 17.2%; Score 523; DB 1; Length 597;  
 Best Local Similarity 30.1%; Pred. No. 1e-37;  
 Matches 167; Conservative 67; Mismatches 211; Indels 109; Gaps 22;  
 QY 37 TEYGOIKGV-KRMVTYVDDSYSEFESIPYAKPVGELRFKAPORPYWEGVRCOCGPANS 95  
 DB 26 TEGGFVEGVNKKLSLSEGSIDIFKGIPIFAAPKA---LEKPEHNPQOSTLAKSPKRC 82  
 QY 96 VOTDFISGKPTSEDCLYNTVNDINPKR-----PVWPIFGDPIFE----- 142  
 DB 83 LQATLTQDSTYGENDCLYLNW---PQGRREVSHDLVMTIYGATLKAASOGANFL 138  
 QY 143 ANRMNFGPDYFKKPVYLTVOYRLGLVGLSLKSENLVNPGNAGLKDDVMAIWRVNSI 202  
 DB 139 SNLYIGEEIATRGVIVTFTNRVGPLFSLTGSNTL--PGNYGLMDHMLAWKRNI 196  
 QY 203 AIFGGDVNITVFGESAGASTHYMMITBOTQLFHRIGMSGNSMCSNASTECOSRALT 262  
 DB 197 EAFGDPDNITLFGESAGASVSIQTLSPYKGLIKRAISGSGVGLCPWA---IQDDPLF 253  
 QY 263 MAKR-----VGYGDENEKILFELMKANPYDLKEBPVLTFRMKNKYMPPGPT---- 314  
 DB 254 WAKRIAEKVGCVPDYSK--MAGCLKIT-----DPRALT--LAVKL--PLGSTERYK 299  
 QY 315 -----VEPYOTADCVVPKPIREWKSA-----WGSNIPILIGNSYEGL 353  
 DB 300 LHYLSFVPIIDDFIPDDPVNLYANADVDYIAGTNDMGHLFVGMDVAL--NSMKQDV 357  
 QY 354 LSKSAKQYR--EVKKELESC-----VNVPWELADSESAPELRAIYKKAHVDGET 406  
 DB 358 TEEDFEKLVSGLVITGGLGANATVEVTEPW---AODSSETR-----KKTWDLDT 407  
 QY 407 PRLDNFMELCSYFELFPMHRLQLRFNHTAGTPYLYFDEFESEIINPYRIMRGRGV 466  
 DB 408 DIL-----FLIPKRIAVAOHSHAKSANITYILFSPQSRNPITPKM----- 449  
 QY 467 KGVSHADELYLEWNLISRLPKRESREYKTERMGVWTEFATGKPYNSDIAGMENLW 526  
 DB 450 -GADHADLDQYVGRPFAPPLGVRADRTVSKAMIMVNTFATGDPNTHGSTVPAN--W 506  
 QY 527 DPKKSDVYKCN 540  
 DB 507 DPTLEDVDVLEIN 520  
 RESULT 8  
 CHIE HORSE  
 AC CHIE HORSE STANDARD; PRT: 574 AA.  
 AC P81908;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Cholinesterase (EC 3.1.1.8) (Acylcholine acylhydrolase) (Choline  
 esterase II) (Butyrylcholine esterase) (Pseudocholinesterase) (EO-  
 BChE).  
 GN GN  
 OS Equus caballus (Horse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
 OC NCBI\_TaxID=9796;  
 RN (1)  
 RP SEQUENCE.  
 RC TISSUE=Plasma;  
 RA Moorad D.R., Luo C., Garcia G.E., Doctor B.P.;  
 RT "Amino acid sequence of horse serum butyrylcholinesterase.";  
 RL (In) Doctor B.P., Taylor P., Quinn D.M., Kotundo R.L., Gentry M.K.  
 (eds.);  
 RL structure and function of cholinesterases and related proteins,  
 pp.145-146, Plenum Press, New York and London (1998).  
 CC -1- CATALYTIC ACTIVITY: An acylcholine + H(2)O = choline + a  
 carboxylic acid anion.



-1- SUBUNIT: HOMOTETRAMER. THE TETRAMER IS COMPOSED OF TWO DIMERS. THE TWO SUBUNITS IN A DIMER ARE LINKED BY A DISULFIDE BOND.  
 CC -1- TISSUE SPECIFICITY: PRESENT IN MOST CELLS EXCEPT ERYTHROCYTES.  
 CC -1- MISCELLANEOUS: CHOLINESTERASE IS HIGHLY REACTIVE WITH ORGANOPHOSPHATE ESTERS.  
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.  
 DR HSPSP, p21836; 1MAA.  
 DR InterPro: IPR002018; Carboxylesterase.  
 DR InterPro: IPR000997; Cholinesterase.  
 DR InterPro: IPR000379; Ser\_esterase.  
 DR Pfam: PF00135; Coesterase.1.  
 DR PRINTS: PR00878; CHOLINESTERASE.  
 DR PROSITE: PS00122; CARBOXYLESTERASE\_B.1; 1.  
 DR PROSITE: PS00941; CARBOXYLESTERASE\_B.2; 1.  
 KM Hydrolyase; Serine esterase; Glycoprotein.  
 FT ACT\_SITE 198 198 BY SIMILARITY.  
 FT ACT\_SITE 325 325 BY SIMILARITY.  
 FT ACT\_SITE 438 438 BY SIMILARITY.  
 FT DISULFID 65 92 BY SIMILARITY.  
 FT DISULFID 252 263 BY SIMILARITY.  
 FT DISULFID 400 519 BY SIMILARITY.  
 FT DISULFID 571 571 INTERCHAIN (BY SIMILARITY).  
 FT CARBOHYD 57 57 N-LINKED (GLCNAC. . .).  
 FT CARBOHYD 106 106 N-LINKED (GLCNAC. . .).  
 FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .).  
 FT CARBOHYD 256 256 N-LINKED (GLCNAC. . .).  
 FT CARBOHYD 341 341 N-LINKED (GLCNAC. . .).  
 FT CARBOHYD 455 455 N-LINKED (GLCNAC. . .).  
 FT CARBOHYD 481 481 N-LINKED (GLCNAC. . .).  
 FT CARBOHYD 486 486 N-LINKED (GLCNAC. . .).  
 SQ SEQUENCE 574 AA; 65641 MW; 07755E9FB9CB33E CMC64;

Query Match 17.1%; Score 520.5; DB 1; Length 574;  
 Best local similarity 29.9%; Pred. No. 1.5e-32;  
 Matches 165; Conservative 97; Mismatches 200; Indels 89; Gaps 24;

QY 31 ETOITDEYGOIKGVKRMVYDDSYTSPESIPYAKPVGELFKAPORPRVMEGVDCG 90  
 DB 2 EDIIITTKNKVGM-NLPLVGLGTVAFGIPLAPDLRLFKPKQSILTKMSNMWTK 60  
 QY 91 PANKSVQ-TD-----FISGKPTG-----SEDCLYLVNTYNDINPDKRPVWFIHGDFI 139  
 DB 61 YANSCTYNTQSPGFLGSEPMNPNTELSDDCYLVNWI.PAPKP-KNATVMTWYGGGGO 119  
 QY 140 FGEANRMWFGPDYFMK-KPVYLVTVQRIQVGLFSLKSENLVPCNAGLKDOVALRMV 198  
 DB 120 TGTSSLPVYDGKFLARVERIVVSMNRYVAGLGLAL-SENPEAPGNMGLFDQOLALOV 178  
 QY 199 KSNIAIFGSDVNTVTGESAGASTHYMTETQTRGLEFHRIIMSGNSKSNAST--E 255  
 DB 179 QKNIAAFGNGRSVTLGEGSAGASVSLHLSRSPQLFTRAILQSSNAPAVTSIYE 238  
 QY 256 COSPALTMARVYKGEKDNEKDLIEFLMKANPYDLIKEEQVUTLPERMONKVVFPFGPV 315  
 DB 239 ARNRTFLAKMGC-SRDNETEMIKLRDKDPOEIIINEVFVVPYDL--LSVNFQPTV 294  
 QY 316 EPIYQACVYKPIREWKASMGNSIPTLIGNTSYEGL-----LSKS-----VARQ 361  
 DB 295 D---GDFLTPMP-DTLIQLOQFKRTQIIVGNKDEGTAFLVYGAPFSKDNNSITRKE 349  
 QY 362 YPEVVKEL-----ESCV-NYVPELADSEKSAPELEKRAIVYKKAHVDDEFTLDV 411  
 DB 356 PQEGKIFPPVSEFGRESILFHYMDW-LDD-----QRAENVREALDD--VQCD 395  
 QY 412 FHELCSTYVLEFPMHRLQLRNHTAGPIYLYRFEDSEELINPYIMRFGKGVSH 471  
 DB 396 VYITCPALFE--TRKESL-----GNDAPFYFEHNSITLPPPEMW-----GYMH 438  
 QY 472 ADELTYLEFNNILSKRLPRESREYKTIERRVGIWTEPATGQPYNSDLAGEN--LTMDPI 529  
 DB 439 GYEIEVEVFLPERRVNTABEILSRIMKRWANFAKYNP-----NGTQNNSTAMPVF 493  
 QY 530 KKSDDVYKCLN 540

DB 494 KSTQKYLITLN 504  
 RESULT 9  
 CHLE\_HUMAN STANDARD; PRT; 602 AA.  
 ID CHLE\_HUMAN  
 AC P06276;  
 DT 01-JAN-1988 (Rel. 06, Created)  
 DT 01-AUG-1988 (Rel. 08, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Cholinesterase precursor (EC 3.1.1.8) (Acylcholine acylhydrolase)  
 DE (Choline esterase II) (Butyrylcholine esterase)  
 DE (Pseudocholinesterase).  
 GN BCHF OR CHEL  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 NCBI\_TaxID:9606;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90212557; PubMed=2322535;  
 RA Arpagaus M., Kolt M., Vatsis K.P., Bartels C.F., la Du B.N.,  
 RT "Structure of the gene for human butyrylcholinesterase. Evidence for  
 RT a single copy.";  
 RL Biochemistry 29:124-131(1990).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=87231856; PubMed=3035536;  
 RA Prod' C.A., Zevin-Sonkin D., Gnatt A., Goldberg O., Soreg H.,  
 RT "Isolation and characterization of full-length cDNA clones coding for  
 RT cholinesterase from fetal human tissues.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 84:3555-3559(1987).  
 [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=88016155; PubMed=3477799;  
 RA McTierman C., Adkins S., Chatonnet A., Vaughan T.A., Bartels C.F.,  
 RT Kolt M., Rosenberg T.L., la Du B.N., Lockridge O.,  
 RT "Brain cDNA clone for human cholinesterase.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 84:6682-6686(1987).  
 [4]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Skin;  
 RX Submitted (DEC-2001) to the EMBL/Genbank/DBJ databases.  
 [5]  
 RP SEQUENCE OF 29-602.  
 RC TISSUE=Plasma;  
 RX MEDLINE=87109144; PubMed=3542989;  
 RA Lockridge O., Bartels C.F., Vaughan T.A., Wong C.K., Norton S.E.,  
 RT Johnson L.L.;  
 RT "Complete amino acid sequence of human serum cholinesterase.";  
 RL J. Biol. Chem. 262:549-557(1987).  
 [6]  
 RP DISULFIDE BONDS.  
 RX MEDLINE=88007487; PubMed=3115973;  
 RA Lockridge O., Adkins S., la Du B.N.;  
 RT "Location of disulfide bonds within the sequence of human serum  
 RT cholinesterase.";  
 RL J. Biol. Chem. 262:12945-12952(1987).  
 [7]  
 RP REVIEW.  
 RX MEDLINE=89149758; PubMed=3067729;  
 RA Lockridge O.,  
 RT "Structure of human serum cholinesterase.";  
 RL Bioessays 9:125-128(1988).  
 [8]  
 RP VARIANT ATYPICAL GLY-98.  
 RX MEDLINE=89128896; PubMed=2915989;  
 RA McGuire M.C., Nogueira C.P., Bartels C.F., Lightstone H., Hajira A.,

[illegible]

Query Match	Best Local Similarity	Matches 175; Conservative 103; Mismatches 212; Indels 134; Gaps 31.
QY 6 QFIR-RLTKCKVNVKNTYRLSTNTQIILDEYQIKVKRMVYDYSSESIPYA 64	17.0%; Score 518; DB 1; Length 602;	N-LINKED (GLCNAC. . .)
Db 11 RFLWFLILLC--LIGK-----SHTEDDIIILAKKKNVRCM-NLFTGGTVAFLCIPYA 62	28.0%; Pred. No. 2,6e-32;	N-LINKED (GLCNAC. . .)
QY 65 KPVAGELRFKAPORPVWEGV-----RDCCGPANRSV-----QDFFISGRKT 106	103; Mismatches 212; Indels 134; Gaps 31.	N-LINKED (GLCNAC. . .)
Db 63 QPPLGRIRFKPKQSLTKWSDIMWATKYANSCCNIDQSPFGHSGMMNPNTDL----- 116		N-LINKED (GLCNAC. . .)
QY 107 GSEDCATLANYTYNDLMDPKRRPYMTIHGGDFJFEGANRNMFGPDYFMK-KPVLVTVQY 165		N-LINKED (GLCNAC. . .)
Db 117 -SEDCILNWTATPAPKPK-KNATVILVIYGGGQGTGSSLHVVDGKFLAVEREVIIVSMNY 174		N-LINKED (GLCNAC. . .)
QY 166 RLGVGLFLSKSBNLNVNPNAGLKDQVMAFLRWKSNIAJFGGDVNITVFGSAGASTH 225		N-LINKED (GLCNAC. . .)
Db 175 RVGALGFILAPG-NPEAPGNMGLFDQQLALQVQKNIAFGSNPKPSVYLFGESAGASVS 233		N-LINKED (GLCNAC. . .)
QY 226 YMTTEQGTGFLFRIGMGSNCSMAST---ECOSRALTMKRVYKGDENKDLLEFL 282		N-LINKED (GLCNAC. . .)
Db 234 LHLISPGSHSLFTRAILLOSGSFNAPAAVSLYEARNRRLINTLAKLTCGCSRE-NETFIKCL 292		N-LINKED (GLCNAC. . .)
QY 283 MKANPYDLTKKEPQV--TTPERMONKVFPPFGPVEPYQADCVAPKPIREMYKMSAGN 339		N-LINKED (GLCNAC. . .)
Db 293 RNKDPQELINLEAFVYPYGP-----LSVNGPFLVDGDFLTD-MPILILELQF---K 341		N-LINKED (GLCNAC. . .)
QY 340 STPLTIGNTSYGL-----LSKS-----VAKQPEVVKEL-----ESCV-NY 375		N-LINKED (GLCNAC. . .)
Db 342 KQIILVGVKKDGTGFLVYGAVGFGEKDNNSIITRKFEQGLKIPFGVSEGRKSILFHY 401		N-LINKED (GLCNAC. . .)
QY 376 VWEMLADSEPSAPETLERALVYKKAHVCGEPTLDNFE-----LCSTFYFLFPMHRLQL 431		N-LINKED (GLCNAC. . .)
Db 402 TWM-----VDDQRP--ENYREALGDVVGYNFTCPALFETTK- 435		N-LINKED (GLCNAC. . .)
QY 433 RNNHAGTPPIVLYRPDPESEELINPYRIMRGRGVKSGSHADELTLYFLWILSKRLPKES 491		N-LINKED (GLCNAC. . .)
Db 436 KFESEW-GNNAFYYVEHRSKSLPPEMK-----GVMGYELEEVF-----GLPLER 480		N-LINKED (GLCNAC. . .)
QY 492 RE-YTIER-----MGVITFEFATGKPYSDIAGMENLTWPIPKSDVYKCLINTGDEL 545		N-LINKED (GLCNAC. . .)
Db 491 KDNTKAEILSRISIVKWMANFAKYGPNDETQ--NNSTSMPEFKSTEQKYLTLNLT-EST 536		N-LINKED (GLCNAC. . .)
QY 546 KVMDLPEMDKIKQCASTFDKKKL 569		N-LINKED (GLCNAC. . .)
Db 537 RIMTKRAQCCRFWTSEFPKYLEM 560		N-LINKED (GLCNAC. . .)

DE Acetylcholinesterase precursor (EC 3.1.1.7) (ACHE).  
 GN ACHE.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID:10090;  
 RN [1]  
 RP MEDLINE=90380429; PubMed=2400605;  
 RA Rachinsky T.L., Camp S., Li Y., Ekstrom T.J., Newton M., Taylor P.;  
 RT "Molecular cloning of mouse acetylcholinesterase: tissue distribution  
 of alternatively spliced mRNA species.";  
 RN Neuron 5:317-327(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/SV;  
 RX MEDLINE=21138439; PubMed=11239002;  
 RA Wilson M.D., Riemer C., Martindale D.W., Schnupf P., Boright A.P.,  
 RA Cheung T.L., Hardy D.M., Schwartz S., Scherer S.W., Tsui L.-C.,  
 RA Miller W., Koop B.F.;  
 RT "Comparative analysis of the gene-dense ACHE/TFR2 region on human  
 chromosome 7q22 with the orthologous region on mouse chromosome 5.";  
 RN Nucleic Acids Res. 29:1352-1365(2001).  
 RN [3]  
 RP X-RAY CRYSTALLOGRAPHY (3.2 ANGSTROMS) OF COMPLEX WITH FASCICULIN.  
 RX MEDLINE=96067648; PubMed=8521480;  
 RA Bourne Y., Taylor P., Marchot P.;  
 RT "Acetylcholinesterase inhibition by fasciculin: crystal structure of  
 the complex.";  
 RN Cell 83:503-512(1995).  
 RN [4]  
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).  
 RX MEDLINE=99115643; PubMed=9915834;  
 RA Bourne Y., Taylor P., Bougis P.E., Marchot P.;  
 RT "Crystal structure of mouse acetylcholinesterase. A peripheral site-  
 occluding loop in a tetrameric assembly.";  
 RN J. Biol. Chem. 274:2963-2970(1999).  
 CC -1- FUNCTION: RAPIDLY HYDROLYZES CHOLINE RELEASED INTO THE SYNAPSE.  
 CC -1- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.  
 CC -1- SUBUNIT: ISOFORM H GENERATES GPI-ANCHORED DIMERS, DISULFIDE  
 LINKED. ISOFORM T GENERATES MULTIPLE STRUCTURES, RANGING FROM  
 MONOMERS AND DIMERS TO COLLAGEN-TAILED AND HYDROPHOBIC-TAILED  
 FORMS, IN WHICH CATALYTIC TETRAMERS ARE ASSOCIATED WITH ANCHORING  
 PROTEINS THAT ATTACH THEM TO THE BASAL LAMINA OR TO CELL  
 MEMBRANES. IN THE COLLAGEN-TAILED FORMS, ISOFORM T SUBUNITS ARE  
 ASSOCIATED WITH A SPECIFIC COLLAGEN COLO. WHICH TRIGGERS THE  
 FORMATION OF ISOFORM T TETRAMERS, FROM MONOMERS AND DIMERS (BY  
 SIMILARITY).  
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: H AND T (SHOWN HERE); MAY BE  
 PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- TISSUE SPECIFICITY: PREDOMINATES IN MOST EXPRESSING TISSUES  
 EXCEPT ERYTHROCYTES WHERE A GLYCOPHOSPHOLIPID-ATTACHED FORM OF  
 ACHE PREDOMINATES.  
 CC -1- MISCELLANEOUS: SYNAPSES USUALLY CONTAIN ASYMMETRIC MOLECULES OF  
 CHOLINESTERASE, WITH A COLLAGEN-LIKE PART DISULFIDE-BONDED TO THE  
 CATALYTIC PART. A DIFFERENT, GLOBULAR TYPE OF CHOLINESTERASE  
 OCCURS ON THE OUTER SURFACES OF CELL MEMBRANES, INCLUDING THOSE OF  
 ERYTHROCYTES.  
 CC -1- MISCELLANEOUS: THIS IS THE CATALYTIC SUBUNIT OF AN ASYMMETRIC OR  
 SOLUBLE FORM OF ACHE.  
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYL-ESTERASE/LIPASE FAMILY.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
 use by non-profit institutions as long as its content is in no way  
 modified and this statement is not removed. Usage by and for commercial  
 entities requires a license agreement (see <http://www.isb-sib.ch/announce/>  
 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC EMBL: X56518; CA939867.1; -  
 DR EMBL: AF312033; AKK28810.1; -  
 DR PIR: JH0314; JH0314.

DR PDB: 1MAH; 03-APR-96.  
 DR PDB: 1MAA; 20-APR-99.  
 DR MGD: MGI:87876; Ache.  
 DR InterPro: IPR002018; Carboxylase.  
 DR InterPro: IPR000997; Cholinesterase.  
 DR InterPro: IPR000379; Ser-estrs-site.  
 DR Pfam: PF00135; Coesterase; 1.  
 DR PRINTS: PR00878; CHOLINESTERASE.  
 DR PROSITE: PS00122; CARBOXYL-ESTERASE\_B\_1; 1.  
 DR PROSITE: PS00941; CARBOXYL-ESTERASE\_B\_2; 1.  
 DR Hydroxylase; Serine esterase; Synapse; Membrane; Nerve; Muscle; Signal;  
 KW Neurotransmitter degradation; Glycoprotein; Alternative splicing;  
 KW 3D-structure.  
 FT SIGNAL 1 31  
 FT CHAIN 32 614 ACETYLCHOLINESTERASE.  
 FT ACT\_SITE 234 234  
 FT ACT\_SITE 365 365  
 FT ACT\_SITE 478 478  
 FT DISULFID 100 127  
 FT DISULFID 288 303  
 FT DISULFID 440 560  
 FT DISULFID 611 611  
 FT CARBOHYD 266 266  
 FT CARBOHYD 381 381  
 FT CARBOHYD 495 495  
 FT SEQUENCE 614 AA; 68168 MW; 66E2512463C21172 CRC64;  
 SQ  
 Query Match 16.9%; Score 515.5; DB 1; Length 614;  
 Best Local Similarity 30.2%; Pred. No. 4,1e-32;  
 Matches 159; Conservative 81; Mismatches 236; Indels 51; Gaps 17;  
 40 GQIKGKRMVYDDSYSEFIPYAKPPVGLFKAPQRPVWEGVGDCCGPAKRSVQ-- 97  
 46 GQIRGI-RLKAPGPPVAFGLIPFAPVPSRREMPPEKPPKSGVLDATFONWCYIV 104  
 98 -----TDFISGKPTGSEDCILYVINDLPKRRPVMTFHGCGFGEARMMF 148  
 105 DTYLPGEGTEEMNPNNRESEDCILYVWVPPRPASPPVLTWITGGYSGAASLDVY 164  
 149 GPDYFMK-KPVVLTVOYRGLVGLFLSKSENLNVGNGALQDVVALRMVKSNIAPFG 207  
 165 DGRFLAOGAVLVSMYRVGTGFLALPSR-EARGNGVGLDRLALQVQENIAAPFG 223  
 208 DVDNITVFGSAGASTHYMTTEQRTGLFHRCIMSGNSGCSWAST--ECOSRLTMA 264  
 224 DPMVLTGFSAGASGMHILSPSRFLHRAVLQSGTFCNGVATVSGAEARRATLLA 283  
 265 KRVGK---GEDNKKLLEFLMKANPYDLKEBPVLTPERMKNKMPGPTVEPYQTA 321  
 284 RLVCGRPGAGGNDTELIACTRRPADLDVDEHNVLPQEST--FRFSVPVVD----G 336  
 322 DCVVPKPIREKVSAMNSIPTLIGNTSYGLLSKSAKQYPRVVELESCVNVPMELA 381  
 337 DFLSDTP-EALINTGPDQDQVLYGVYKDEG--SYFLVGVGVPFSKDNESLISRAQF-IA 392  
 382 DSESADETLERAILYKKAH---VDEETP--LDNMELCSFYFLFPHRRLOLRFNH 435  
 393 GVRIGVPOASDLAAEAVLVLTDMALHEDPTHLRDANSAVVGSHNVCPV---AQLAGRL 449  
 436 TA-GTPIYLVRFDESEIINPYRIMRFGVGVSHADELTVLFWNLTLSKRLPKSREY 494  
 450 AAGCARVAVYIEERASTLTWPLM-----GVPGYTEIEFTFGLPDPSLNTYTEER 501  
 495 KTIIRAVGIWTEFATGKPYSDIAGNEMLTWPIKSKSDVYKCLNT 541  
 502 IFARLIMKWTNFAFGTGP--NDPRDSKSPQMPYTTAAQOYVSLNL 546  
 RESULT 11  
 CHLE\_RABIT STANDARD; PRT; 581 AA.  
 ID CHLE\_RABIT  
 AC P21927;  
 DT 01-MAY-1991 (Rel. 18, Created)

Query Match 165; Score 512.5; DB: 1; Length 581; Best Local Similarity 29.0%; Pred. No. 6.5e-32; Matches 165; Conservative 92; Mismatches 198; Indels 113; Gaps 26;

FT	CAROHND	488	488	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CAROHND	492	492	N-LINKED (GLCNAC. . .) <td>(POTENTIAL)</td>	(POTENTIAL)
FT	CAROHND	493	493	N-LINKED (GLCNAC. . .) <td>(POTENTIAL)</td>	(POTENTIAL)
SO	SEQUENCE	581 AA;	66156 MW;	FE8B199EF7B32EB0A	CRC64;
QY	26	RUSTNETOIIDTEYGOIKGRMITYDDSYSSFESIPAKPVGELRKARQRPVMEGV	85		
DB	4	RSSTHEDYITTKNRIGI-NLPVGGTVAFLGIPAPOLGRKRPQSLTKMSDI	62		
QY	86	-----HDCGPANRSV-----QDFISGRTPGSEDCILVNVYINDLNPDKRR	127		
DB	63	WNAITYANSCCONIDQSPFGHSEMMNPNDL-----SEDCILVNWVLPTRPK-NNA	114		
QY	128	PVMEVIFHGDFLEFGANNMFGPDVFMK-KPVVLTVQYRGLVGLFSLKSENLVNPGNA	186		
DB	115	TYMIVITGGFQGTGSHSLQVYDGKRLTVEREYIVSMNYRGALGFLALPG-NPEAPGNM	173		
QY	187	GLKQVMAALRWKXSNIALFGGDVNNITYFGSAGASTHYMMITTEQTRGLFHRGIMSGN	246		
DB	174	GLFDQALQWVQKNIAAFGNGPNKRSVTLFGESAGAAVSJLHLSRSHPLPTRAILOSGS	233		
QY	247	SMCSW---ASTECOSRATLMKRVGYKEDENKDLLEFLMKANPYDLCKEPPVLTPERM	303		
DB	234	SNAPREVMSLHAKRKITLTKAPGCSIE-NETELIKLRKKDQOEILLNEVAVP---F	289		
QY	304	QNKVMEFGPTVEPYQTADCVVPR---IREWKSAMGNSIPTLIGNTSEGL----	353		
DB	290	DSLTSVNGSPVVD-----GDFLTMDPDTLLOGLQKLT-----QILGVNKEDETAFLVY	339		
QY	354	-----LSKS-----VAKQPEVYKEL-----ESCV-NVPEMLADSESAETLERA	394		
DB	340	GAPGSKDNTIITRKKEGELKTFEPGVSEFGKESILFHTDW-VDEOR--PENYREA	395		
QY	395	AIVKAAVHGETPLDNEFMELCSYFLEFPMHREPLQTFNHTAGTPYLVRFDPDESEII	454		
DB	437	WPEWM-----GVMHGELEFVFGLEPERVNTYKAEILLRSIMKRWANFAKYNP-	487		
QY	515	SNDIAGMEN--LTWDPITKSDVYKCLN	540		
DB	488	-----NGTQNNSTRWPFVKSTEQKYLTLN	511		

RESULT 12  
ACCS.ELEEL  
ID ACCS.ELEEL STANDARD; PRT; 633 AA.

DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Acetylcholinesterase precursor (EC 3.1.1.7) (ACHE).  
OS Acetylcholinesterase precursor (Electric eel).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
ACTinopterygii; Neopterygii; Teleostei; Ostariophysi; Gymnotiformes;  
OC Electrophorida; Electrophorus.  
OX NCBI\_TaxID=8005;  
RN [1]  
SEQUENCE FROM N.A.  
RX MEDLINE=98070504; PubMed=9407087;  
RA Simon S., Massoulié J.;  
RT "Cloning and expression of acetylcholinesterase from Electrophorus."  
RT Splitting pattern of the 3' exons in vivo and in transfected mammalian  
RT cells";  
RL J. Biol. Chem. 272:33045-33055(1997).  
CC -!- FUNCTION: RAPIDLY HYDROLYZES CHOLINE RELEASED INTO THE SYNAPSE.  
CC -!- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.







ID CHLE\_MOUSE STANDARD; PRT; 603 AA.  
AC 003311;  
DT 01-OCT-1993 (Rel. 27, Created)  
DT 01-OCT-1993 (Rel. 27, Last sequence update)  
DT 15-JUL-1998 (Rel. 36, Last annotation update)  
DE Cholinesterase precursor (EC 3.1.1.8) (Acetylcholine acylhydrolase)  
DE (Choline esterase II) (Butyrylcholine esterase)  
DE (Pseudochoolinesterase).  
GN BChE.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_Taxid=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=90380429; PubMed=2400605;  
RA Rachinsky T.L., Camp S., Li Y., Ekstrom T.J., Newton M., Taylor P.;  
RT "Molecular cloning of mouse acetylcholinesterase: tissue distribution  
of alternatively spliced mRNA species.";  
RL Neuron 5:317-327(1990).  
RN [2]  
RP SEQUENCE OF 97-237 FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=91201348; PubMed=2016308;  
RA Arpaegus M., Chatonnet A., Masson P., Newton M., Vaughan T.A.,  
RA Bartels C.F., Nogueira C.P., La Du B.N., Lockridge O.;  
RT "Use of the polymerase chain reaction for homology probing of  
butyrylcholinesterase from several vertebrates.";  
RL J. Biol. Chem. 266:6966-6974(1991).  
CC -1 CATALYTIC ACTIVITY: An acylcholine + H<sub>2</sub>O = choline + a  
CC carboxylic acid anion.  
CC -1 SUBUNIT: HOMOTETRAMER. THE TETRAMER IS COMPOSED OF TWO DIMERS. THE  
CC TWO SUBUNITS IN A DIMER ARE LINKED BY A DISULFIDE BOND.  
CC -1 TISSUE SPECIFICITY: PRESENT IN MOST CELLS (EXCEPT ERYTHROCYTES).  
CC -1 MISCELLANEOUS: CHOLINESTERASE IS HIGHLY REACTIVE WITH  
CC ORGANOPHOSPHATE ESTERS.  
CC -1 SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL: M99492; AAA37328.1; -;  
DR PIR: A39768; A39768.  
DR HSD; P21836; 1MAH.  
DR MGD; MGI:894278; Bche.  
DR InterPro: IPR002018; Carboxylesterase.  
DR InterPro: IPR000997; Cholinesterase.  
DR InterPro: IPR000379; Ser\_estrs\_site.  
DR Pfam: PF00135; Coesterase\_1.  
DR PRINTS; PR00878; CHOLINESTERASE.  
DR PROSITE; PS00122; CARBOXYLESTERASE\_B\_1; 1.  
DR PROSITE; PS00941; CARBOXYLESTERASE\_B\_2; 1.  
KW Hydrolyase; Serine esterase; Glycoprotein; Signal.  
FT CHAIN 1 29  
FT ACT\_SITE 30 603  
FT ACT\_SITE 227 227  
FT ACT\_SITE 354 354  
FT ACT\_SITE 467 467  
FT DISULFID 94 121  
FT DISULFID 281 292  
FT DISULFID 429 548  
FT DISULFID 600 600  
FT CARBOHYD 86 86  
FT CARBOHYD 135 135  
FT CARBOHYD 270 270  
FT CARBOHYD 370 370  
FT CARBOHYD 484 484  
FT CARBOHYD 510 510  
N-CHOLINESTERASE.  
BY SIMILARITY.  
BY SIMILARITY.  
BY SIMILARITY.  
BY SIMILARITY.  
BY SIMILARITY.  
BY SIMILARITY.  
BY SIMILARITY.  
INTERCHAIN (BY SIMILARITY).  
N-LINKED (GLCNAC. . .) (POTENTIAL).  
N-LINKED (GLCNAC. . .) (POTENTIAL).  
N-LINKED (GLCNAC. . .) (POTENTIAL).  
N-LINKED (GLCNAC. . .) (POTENTIAL).  
N-LINKED (GLCNAC. . .) (POTENTIAL).  
N-LINKED (GLCNAC. . .) (POTENTIAL).  
N-LINKED (GLCNAC. . .) (POTENTIAL).  
N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 515 515 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CONFLICT 129 129 R -> P (IN REF. 2).  
SQ SEQUENCE 603 AA; 68521 MW; 719B1B220D1E5567 CRC64;  
Query Match 16.7%; Score 508.5; DB 1; Length 603;  
Best Local Similarity 28.4%; Pred. No. 1,4e-31;  
Matches 165; Conservative 98; Mismatches 224; Indels 93; Gaps 22;  
QY 2 TELQFIFRLKLVCKVNVNRYNRYLSTNETQIIDEVQIKGVKMTYVDSYSPEST 61  
DB 6 TKYVQTHFLMLILLCMPEFGSK---TEEDFIITTKGVRLGS -MPVIGGVTAFLGI 60  
QY 62 PYAKPYGELRFRKAPQRPVMEGVRCOCGPANSVQ-----TDFISGKPGESD 110  
DB 61 PYAPQPLGSLRFRKQPLNKMPDILHNATQYANSCYONIDAPFGFSGSEMMNPTNLSID 120  
QY 111 CLYLVNTYNDLPDKRRPVVVFIFGDFEIGEANRMWFGPDYEMK -KPYLVTVVYRLGV 169  
DB 121 CLYLVNTVIRVPKP -KNATVWVWIIYGGGFQGTSSLPYDGKFLARERVIYVSMNRYGA 179  
QY 170 LGFSLKSENLVNPQNAGLKQYVALRWKSNIAIFGQVDNITVGEASGASTHYMMI 229  
DB 180 LGFLAFPG -MPDAPGNWGLFDQDLALQWQRIANAFGPNKSTITIGESAGAAVSGLHL 238  
QY 230 TEOTRGLFHRGIMSGNSMCWA---STEGOSRFLMAKRVGKGEDNEKDIIEFLMKAN 286  
DB 239 CPQSYPLFTAILLESSSNAPPAVKPBEARNITTLAFVGC -SKENMEMIKCLRSKD 297  
QY 287 PYDLKEEPQVLTPEKQNVKMPFGPTVEPYOTADCVKPIREM -VKSAMGNSIPVL 344  
DB 298 POELIRNERFVLPDSI---LSINFGPTVDGFLTD -MPHTLLQGVKKA-----QTL 347  
QY 345 IGMTSYEGLL---SKSAKVQPEVY--KELESCVN-----YVPWL 380  
DB 348 VGVNKBEGIAFLVYGAPGFSKDNDSLTTRKEQEGNMTFPGVSRGKEAVLYEYDV-- 405  
QY 381 ADSERSAPETTLERAIVKKAHVDEETPLDNFMELCSYFLEPMHREFQLRFNHTAGTP 440  
DB 406 --LGEOQSP-----VYRDALDDVIGDYNITCPALEF---TKKFALENN----- 444  
QY 441 ILYRRDPQSEELINRYLRMRGKGVKSHADELTLYFWNLKRLPRESREYTIIRM 500  
DB 445 AFYFPEHRSSKLPWEMW-----GVMAHYELEFVFGLEPLGRVYVTRAELIFRSRI 496  
QY 501 VGIWTEFATGKPKYSNDIAGMENLTWDPKRSDDVYKCN 540  
DB 497 MKTWANFAKYGHP--NGTGNSTW -WPEVTSDEQKYLILN 533

Search completed: April 4, 2003, 09:13:37  
Job time: 11.6371 secs



GenCore version 5.1.4-P5-4578  
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OM protein - protein search, using sw model

Run on: April 4, 2003, 09:09:58 ; Search time 56.8533 Seconds  
(without alignments)  
2065.788 Million cell updates/sec

Title: us-09-776-910-13

Perfect score: 3045  
Sequence: 1 MFELKQFIRLKLCKVCMWN.....PEMDKIKGASIFDKKELEF 570

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: SP-archaea:\*  
2: SP-bacteria:\*  
3: SP-fungi:\*  
4: SP-human:\*  
5: SP-invertebrate:\*  
6: SP-mammal:\*  
7: SP-mmc:\*  
8: SP-organellae:\*  
9: SP-phage:\*  
10: SP-plant:\*  
11: SP-rodent:\*  
12: SP-virus:\*  
13: SP-vertebrate:\*  
14: SP-unclassified:\*  
15: SP-rvirs:\*  
16: SP-bacteriap:\*  
17: SP-archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2945	96.7	570	5	09X270 musca domes
2	2348	77.1	570	5	025552 lucilia cup
3	2311	75.9	572	5	09U409 09v409 haematobia
4	1844.5	60.6	572	5	09V1B5 drosophila
5	1835.5	60.3	554	5	024201 drosophila
6	1330	43.7	554	5	09V1B0 drosophila
7	1312.5	43.1	555	5	09V1B0 drosophila
8	1311	43.1	572	5	09V1B1 drosophila
9	1299	42.7	572	5	024203 drosophila
10	1298.5	42.6	567	5	09V1B3 drosophila
11	1297.5	42.6	558	5	024202 drosophila
12	1281.5	42.1	554	5	09G1N0 drosophila
13	1277.5	42.0	554	5	09V1C2 drosophila
14	1267.5	41.6	554	5	09W243 drosophila
15	1264.5	41.5	554	5	024195 drosophila
16	1236.5	40.6	565	5	09V1C3 drosophila

17	1235	40.6	549	5	024204	024204 drosophila
18	1233.5	40.5	564	5	09V1E1	09v1e1 drosophila
19	1223.5	40.2	553	5	024194	024194 drosophila
20	1217	40.0	530	5	09V1L5	09v1l5 drosophila
21	1204	39.5	542	5	09V1B9	09v1b9 drosophila
22	1202	39.5	542	5	09V1B9	09v1b9 drosophila
23	1196	39.3	542	5	024198	024198 drosophila
24	1186	36.7	345	5	09V1E3	09v1e3 drosophila
25	1164	34.3	540	5	08W089	08w089 culix pipie
26	1036	34.0	540	5	P92025	P92025 culix quinq
27	1034	34.0	540	5	08W088	08w088 culix pipie
28	1031	33.9	540	5	023733	023733 culix quinq
29	1029	33.8	446	5	09V1E5	09v1e5 drosophila
30	994	32.6	551	5	09V1C1	09v1c1 drosophila
31	987.5	32.4	541	5	09V1E8	09v1e8 drosophila
32	987.5	32.4	541	5	08S2W5	08s2w5 drosophila
33	987.5	32.4	541	5	024196	024196 drosophila
34	977	32.1	540	5	09G0U5	09g0u5 culix trita
35	959.5	31.5	540	5	023734	023734 culix quinq
36	950.5	31.2	540	5	P91920	P91920 culix tarsa
37	948.5	31.1	541	5	024197	024197 drosophila
38	948.5	31.1	541	5	09V1C0	09v1c0 drosophila
39	943.5	31.1	568	5	023735	023735 culix quinq
40	899	29.5	544	5	09V1B6	09v1b6 drosophila
41	893	29.3	544	5	09V1E7	09v1e7 drosophila
42	886.5	29.1	467	5	P91597	P91597 culix pipie
43	884.5	29.0	467	5	P91598	P91598 culix pipie
44	881.5	28.9	467	5	P91596	P91596 culix pipie
45	878	28.8	401	5	09V1E0	09v1e0 drosophila

## ALIGNMENTS

RESULT 1  
ID 09X270 PRELIMINARY: PRT: 570 AA.

AC 09X270;  
DT 01-NOV-1999 (TREMBLrel. 12, Created)  
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)  
DT 01-NOV-2002 (TREMBLrel. 20, Last annotation update)  
DE Carboxylesterase Mdae7 (EC 3.1.1.1).  
GN MDAE7.  
OS Musca domestica (House fly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Muscidae; Muscidae; Musca.  
OX NCBI\_TaxID=7370;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=RUTGERS DIAZINON-R;  
RX MEDLINE=99361228; PubMed=10451921;  
RA Claudianos C., Russell R.J., Oakeshott J.G.;  
RT "The same amino acid substitution in orthologous esterases confers  
RT organophosphate resistance on the house fly and a blowfly."  
RL Insect Biochem. Mol. Biol. 29:675-686(1999).  
CC -!- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.  
DR EMBL: AF133341; AD29685.1; -.  
DR HSSP: P37967; IOE3  
DR InterPro: IPR002018; Carboxylesterase.  
DR InterPro: IPR000379; Ser\_estrs\_site.  
DR Pfam: PF00135; Coesterase; 1.  
KW PROSITE: PS00122; CARBOXYLESTERASE\_B\_1; 1.  
KW Hydrolyase.  
SQ SEQUENCE 570 AA; 65421 MW; 08AFEBEF284003BB CRC64;

Query Match 96.7%; Score 2945; DB 5; Length 570;  
Best Local Similarity 97.0%; Pred. No. 2.8e-226;  
Matches 553; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

QY 1 MFELKQFIRLKLCKVCMWNRYRLSTNETQIIDREYQIKVKRMYYDSDSYFS 60  
DB 1 MFELKQFIRLKLCKVCMWNRYRLSTNETQIIDREYQIKVKRMYYDSDSYFS 60

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QY 61 IPYAKPVGELRFKAPQRPVMEGVDRCCGPARNSVOTDFISGKNGSEDCILYNTND 120
Db 61 IPYAKPVGELRFKAPQRPVMEGVDRCCGPARNSVOTDFISGKNGSEDCILYNTND 120
QY 121 LNPDKRRPVAFTHGGDFIFGEANRNMFGDPYFMKKPVVLTVOYRLGVGLFSLKSEN 180
Db 121 LNPDKRRPVAFTHGGDFIFGEANRNMFGDPYFMKKPVVLTVOYRLGVGLFSLKSEN 180
QY 181 NVPGNAGLKDQVMAALRWKSNIAIFGGVDNITVFGESAGASTHYMMTEOTRGLFHRG 240
Db 181 NVPGNAGLKDQVMAALRWKSNIAIFGGVDNITVFGESAGASTHYMMTEOTRGLFHRG 240
QY 241 IMMSGNSMCWASTECOSRALYMAKRVYKGDENKDIIEFLMKANPYDLIKEEPOVLT 300
Db 241 IMMSGNSMCWASTECOSRALYMAKRVYKGDENKDIIEFLMKANPYDLIKEEPOVLT 300
QY 301 ERMQNKVMEFGPTVPEYOTADCVKPIREMYKSAMGNSIPTLIGNTSYEGLSKSVAK 360
Db 301 ERMQNKVMEFGPTVPEYOTADCVKPIREMYKSAMGNSIPTLIGNTSYEGLSKSVAK 360
QY 361 QYPEVVELSCVNYVWELADSESAPETLERAIVKKAHVDGEPPLDNFMELCSYFY 420
Db 361 QYPEVVELSCVNYVWELADSESAPETLERAIVKKAHVDGEPPLDNFMELCSYFY 420
QY 421 FLEPMHRLQLRNFHAGPIYLYRFPDSEELINPYRIMRGVKGVSADDELTYLFW 480
Db 421 FLEPMHRLQLRNFHAGPIYLYRFPDSEELINPYRIMRGVKGVSADDELTYLFW 480
QY 481 NILSKRLPKESREYKTIERNVGIWTEFATGKPYSDIAGMENLTWDPKKSDDVYKCLN 540
Db 481 NILSKRLPKESREYKTIERNVGIWTEFATGKPYSDIAGMENLTWDPKKSDDVYKCLN 540
QY 541 IGDELKVMIDLPEMDIKIKGASIFDKKLEF 570
Db 541 IGDELKVMIDLPEMDIKIKGASIFDKKLEF 570

RESULT 2
Q25252 PRELIMINARY: PRT: 570 AA.
AC 025252: 025247:
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Alpha esterase (LCAE7) (Carboxylesterase).
GN LCAE7.
OS Lucilia cuprina (Greenbottle fly) (Australian sheep blowfly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Oestriidae; Calliphoridae; Lucilia.
OX NCBI_TaxID=7375;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LS2;
RA Newcomb R.D., East P.D., Russell R.J., Oakeshott J.G.;
RL Insect Mol. Biol. 5:0-0(0).
RN [2]
RP SEQUENCE OF 70-181 FROM N.A.
RC STRAIN=LS2;
RA Newcomb R.D., East P.D., Russell R.J., Oakeshott J.G.;
RL Insect Mol. Biol. 0:0-0(0).
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL: U56636; AAB67728.1; -.
DR EMBL: U49421; AAA92012.1; -.
DR HSSP: P37967; IOE3.
DR InterPro: IPR002018; CarbesteraseB.
DR InterPro: IPR000379; Ser.estr._site.
DR Pfam: PF00135; Coesterase; 1.
DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
KW Hydrolase.
SQ SEQUENCE 570 AA; 65416 MW; 399D72B3A0F338FD CRC64;

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Query Match 77.1%; Score 2348; DB 5; Length 570;
Best Local Similarity 74.2%; Pred. No. 1.1e-178;
Matches 423; Conservative 73; Mismatches 74; Indels 0; Gaps 0;

QY 1 MTEFLKQIFRLKLCVKMKNYNTYRISTNETQIIDTEVGQIKGVKRMVYDSDYSFES 60
Db 1 MTEFLKQIFRLKLCVKMKNYNTYRISTNETQIIDTEVGQIKGVKRMVYDSDYSFES 60
QY 61 IPYAKPVGELRFKAPQRPVMEGVDRCCGPARNSVOTDFISGKNGSEDCILYNTND 120
Db 61 IPYAKPVGELRFKAPQRPVMEGVDRCCGPARNSVOTDFISGKNGSEDCILYNTND 120
QY 121 LNPDKRRPVAFTHGGDFIFGEANRNMFGDPYFMKKPVVLTVOYRLGVGLFSLKSEN 180
Db 121 LNPDKRRPVAFTHGGDFIFGEANRNMFGDPYFMKKPVVLTVOYRLGVGLFSLKSEN 180
QY 181 NVPGNAGLKDQVMAALRWKSNIAIFGGVDNITVFGESAGASTHYMMTEOTRGLFHRG 240
Db 181 NVPGNAGLKDQVMAALRWKSNIAIFGGVDNITVFGESAGASTHYMMTEOTRGLFHRG 240
QY 241 IMMSGNSMCWASTECOSRALYMAKRVYKGDENKDIIEFLMKANPYDLIKEEPOVLT 300
Db 241 IMMSGNSMCWASTECOSRALYMAKRVYKGDENKDIIEFLMKANPYDLIKEEPOVLT 300
QY 301 ERMQNKVMEFGPTVPEYOTADCVKPIREMYKSAMGNSIPTLIGNTSYEGLSKSVAK 360
Db 301 ERMQNKVMEFGPTVPEYOTADCVKPIREMYKSAMGNSIPTLIGNTSYEGLSKSVAK 360
QY 361 QYPEVVELSCVNYVWELADSESAPETLERAIVKKAHVDGEPPLDNFMELCSYFY 420
Db 361 QYPEVVELSCVNYVWELADSESAPETLERAIVKKAHVDGEPPLDNFMELCSYFY 420
QY 421 FLEPMHRLQLRNFHAGPIYLYRFPDSEELINPYRIMRGVKGVSADDELTYLFW 480
Db 421 FLEPMHRLQLRNFHAGPIYLYRFPDSEELINPYRIMRGVKGVSADDELTYLFW 480
QY 481 NILSKRLPKESREYKTIERNVGIWTEFATGKPYSDIAGMENLTWDPKKSDDVYKCLN 540
Db 481 NILSKRLPKESREYKTIERNVGIWTEFATGKPYSDIAGMENLTWDPKKSDDVYKCLN 540
QY 541 IGDELKVMIDLPEMDIKIKGASIFDKKLEF 570
Db 541 IGDELKVMIDLPEMDIKIKGASIFDKKLEF 570

RESULT 3
Q25409 PRELIMINARY: PRT: 570 AA.
AC 025409:
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Alpha E7 esterase.
GN AEF7.
OS Haematobia irritans irritans.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Muscidae; Muscidae; Haematobia.
OX NCBI_TaxID=75445;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CAMP COOLEY 4/97;
RA MEDLINE=20445807; PubMed=10989298;
RA Guerrero F.D.;
RT "Cloning of a horn fly cDNA, Hialpha7, encoding an esterase whose
RT transcript concentration is elevated in diazinon-resistant flies.";
RL Insect Biochem. Mol. Biol. 30:1107-1115(2000).
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL: AF139082; AAF1517.1; -.
DR HSSP: P37967; IOE3.
DR InterPro: IPR002018; CarbesteraseB.
DR InterPro: IPR000379; Ser.estr._site.
DR Pfam: PF00135; Coesterase; 1.

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RA Adams M.D., Colnicker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Vandal M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers V., H.-C., Blazer R.G., Champagne M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
RA Abrell J.F., Agbayan A.A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.T., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borokova D., Botchan M.R., Bouck J., Brooksstein P., Holtshaker S.,  
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Conway S., Dahlke S., Dahlen C., Davenport L.B., Davies P.,  
RA de Pablo S., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Kocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
RA Foster C., Gerdell L.A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Iyegyan C.,  
RA Jalali M., Kalusni F., Kapen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kung Y., Lai X.,  
RA Lasco P., Lei Y., Levitsky A.A., Li J., Li Z., Liang D., Lin X.,  
RA Liu X., Mettel B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclab J.M.,  
RA Palazzolo M., Peltman G.S., Pan S., Pollard J., Puri V., Reese M.G.,



09VIB1  
ID 09VIB1 PRELIMINARY: PRT: 572 AA.  
AC 09VIB1:  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
DE Alpha-EST9 protein.  
CN ALPHA-EST9 OR CG1128.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BERKELEY;  
RX MEDLINE=20196006; PubMed=10731132;  
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers J.H.C., Blazey R.G., Champe M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Bernier B.P., Bhandari D., Bolshakov S.,  
RA Borokov D., Botchan M.R., Bouck J., Brockstein P., Brotter P.,  
RA Burks K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K.J., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glöck A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Heiman J.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeagwam C.,  
RA Jaitani M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paule J.M.,  
RA Palazzolo M., Peltan G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reibert C., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spredling A.C., Stapleton M., Strong R., Sun E.,  
RA Svrtk R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of Drosophila melanogaster."  
RL Science 287:2185-2195(2000).  
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYL ESTERASE/LIPASE FAMILY.  
DR EMBL: AE003671; AAF54015.1; -  
DR HSSP: P37967; 1OE3.  
DR FLYBASE: FBgn0015577; alpha-Est9.  
DR InterPro: IPR002018; Carboxylesterase.  
DR InterPro: IPR000997; Cholinesterase.  
DR InterPro: IPR000379; Ser\_estrs\_site.  
DR Pfam: PF00135; Coesterase; 1.  
DR PRINTS: PR00878; CHOLINESTERASE.  
DR PROSITE: PS00122; CARBOXYL ESTERASE\_B\_1; 2.  
KW Hydrolase.  
SQ SEQUENCE 572 AA; 65767 MW; 9138FB95713D350 CRC64;

Query Match 43.1%; Score 1311; DB 5; Length 572;  
Best Local Similarity 46.1%; Pred. No. 5.7e-96;  
Matches 264; Conservative 95; Mismatches 184; Indels 30; Gaps 8;  
QY 21 KTYNRLSTNEIQIIDTEYGQIKGVKRMVYDDSYISFESIPAKPPVGLAFKAPQRPV 80

DB 5 KYOORRTTSEKTVASTYTGPIKGVKRSKISYGSYSFERRIFPAKPPVGLAFKAPQPE 64  
QY 81 PMEGVRDCCGPPANRSVQTPDISKPTGSEDCIYLYNTDLPNDKRPVWFGHGF 140  
DB 65 VMEVRSCTISQGRPKLQKHVFEMTDSDECLYNTKLYPTKPMVMWYGGGFGF 124  
QY 141 GEARNMFGDYPMKRVVLVTVQVRLGVY-----GFLSKSENLV 182  
DB 125 GEASRECYSDYLLREVVVISINRYLPGELTNDTWMKKHIFENISLPGLCLDDPELD 184  
QY 183 PGNAGLQDYVALRWKNSNIAITGVDNITVGEASGASTHYMMITQTLGRFRGTM 242  
DB 185 PGNAGLQDYVALRWKNSNIAITGVDNITVGEASGASTHYMMITQTLGRFRGTM 244  
QY 243 MSGNSMCSASTGOSRATLMARVKGKEDNEKDLIEFLMKANPDILKEEPOVLTPEP 302  
DB 245 MSGNTLSPMAVTVQRMPPYRLAVQAGTAGENNRDYMELKNAKSGEITKANCLDIDEE 304  
QY 303 MGNKMPFPGPTPEYOTADCVPKPIREWKSAWNSIPTLIGNTSYEGLLSKSVAKOY 362  
DB 305 KKERIGSFQPIEPIYTSCHVCPKPIEMRTAMSNIPILIGVSNGLLSETKTN 364  
QY 363 PEVVKELSCVNYVPELADSESAPELTERAIVKAVHGETPLD---NFMELCSYF 419  
DB 365 PKCLNELDRCFVYPIEL--WMDRESALCREYGDQRLQCYGGDTPLDTHLEHQLVSH 423  
QY 420 YELFPMRFLQLRNHNAGPIYLYRPDPSEETINPIRMRGVKGVSNADELTYLF 479  
DB 424 YFMPPIYRLVSLRQIARSAPTLYLRDPDSKA--FHLRLSLCKKVRGCHDDSLTYLF 482  
QY 480 WNLISKRLLPESREYKTIEMWGIWTEFATYTKRPSYNDIAGMENLTW---DPIKSDVY 536  
DB 483 YNLSARLKLKHTREYKCIERLVGLWTFHACGNP--NFDEQDLD--WQVPDAVAEKHOL 539  
QY 537 KCLNIGDELKVMDEPKDKIKGASTFDKKEL 569  
DB 540 KCLNISELKLVIDVPLDKLKLWSEFP--RDEL 571  
RESULT 9  
QY 024203 PRELIMINARY: PRT: 572 AA.  
AC 024203:  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
DE Alpha esterase.  
CN ALPHA-EST9 OR AE9 OR CG1128.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC Robin C., Medveczky K.M., Russell R.J., Oakeshott J.G.;  
RA J. Mol. Evol. 0:0-0(0).  
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYL ESTERASE/LIPASE FAMILY.  
DR EMBL: U51053; AAB01152.1; -  
DR HSSP: P37967; 1OE3.  
DR FLYBASE: FBgn0015577; alpha-Est9.  
DR InterPro: IPR002018; Carboxylesterase.  
DR InterPro: IPR000379; Ser\_estrs\_site.  
DR Pfam: PF00135; Coesterase; 1.  
DR PROSITE: PS00122; CARBOXYL ESTERASE\_B\_1; 1.  
KW Hydrolase.  
SQ SEQUENCE 572 AA; 65680 MW; 37F144078FAD2BD8 CRC64;

Query Match 42.7%; Score 1299; DB 5; Length 572;  
Best Local Similarity 45.7%; Pred. No. 5.2e-95;  
Matches 262; Conservative 96; Mismatches 185; Indels 30; Gaps 8;

[illegible]

Db 487 EFKTKRLVSMVYHFAISGDPNIPMVOCDEKQBPGRGAMLPISKDKKVCGLNSHDVHYI 546  
 QY 549 DLEPMKIKOGASIFDKK 566  
 Db 547 DLPEAKRLMLMDCIYDRE 564

## RESULT 11

Q24202 PRELIMINARY; PRT; 558 AA.

AC Q24202  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)  
 DE ALPHA-EST8 OR CG1121.  
 GN ALPHA-EST8 OR CG1121.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 CC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 CC Ephydroidea; Drosophilidae; Drosophila.  
 NCBI\_TaxId=7227;

SEQUENCE FROM N.A.  
 RA Robin C., Medveczky K.M., Russell R.J., Oakeshott J.G.;  
 RL J. Mol. Evol. 0:0-0(0).  
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.  
 DR EMBL: U51052; AAB01151.1; .  
 DR HSP: P37967; 10E3.  
 DR FlyBase: FBgn0015576; alpha-Est8.  
 DR InterPro: IPR002018; Carboxylesterase.  
 DR InterPro: IPR000379; Ser\_esterase.  
 DR Pfam: PF00135; Coesterase; 1.  
 DR PROSITE: PS00122; CARBOXYLESTERASE\_B\_1; 1.  
 DR PROSITE: PS00941; CARBOXYLESTERASE\_B\_2; 1.  
 KM Hydrolyase.  
 FT NON\_TER  
 SQ SEQUENCE 558 AA; 63916 MW; BF6P62C8FF212720 CRC64;

Query Match 42.6%; Score 1297.5; DB 5; Length 556;  
 Best Local Similarity 46.6%; Pred. No. 6 6e-95;

Matches 260; Conservative 92; Mismatches 187; Indels 19; Gaps 7;

QY 21 KYNYRLSTNEIOITTEYGQIKGVKRMVYDDSYSEFISIPAKPPVGLFKAPQRPV 80  
 Db 5 KYNQQRKRSNDKVIADTVYGVKGVKWSIYGNYSFEGIFAPKPPVGLFKAPVDEE 64  
 QY 81 PWEGVDCGCPANRSVQTFISGKPTGSEDCLYLNYTMDLPDKRRPYWVTHGGDTF 140  
 Db 65 HNSDVAKRCHVNAKPCQVNVIVLKQVGSDECLYLVYTRHLPVLYVWYGGGQ 124  
 QY 141 GEANRMFGPDYFMKKPVVLYTVYRLGYLGLSLKSENLANPGNAGLKDQVMAIRWYS 200  
 Db 125 GASRDLVSPDYIMEHVLYLVISYRLGALGLSLADELDVPGNAGLKDQVMAIRWYR 184  
 QY 201 NTAIFGVDNITVFGESAGSTHYMMITBQTRGLFHRGIMSGNSMCMASTECQ-SR 259  
 Db 185 NQGFPGSDNITVFGESAGSTHYMMITBQTRGLFHRGIMSGNSMCMASTECQ-SR 259  
 QY 260 ALTKARVYKGEDEKDLFELKMANPYDLIKEPQVLT-PERQONVMPFPGTVPY 318  
 Db 245 PYRLQAQGYTGANDRDIFALHKCKKASMLKVAEDLITMEERQRLTMSFGPTLPY 304  
 QY 319 QTADCVVPKPREMVKSAWNSIPTLIGNTSYEGILSKSVAKQYPEVVKELSECVNYVPW 378  
 Db 305 LTPHCYIKSPLEMRDQWNSIPVYIGNSFEGILMPEVANKPELLCQLGDCENLAPQ 364  
 QY 379 ELADSESAPELTERAAIVKKA---HYDGEPP---TLDNELCSYFYFLFPMARFQLR 432  
 Db 365 DAHDEQ-----QRKAFGKVVRELTYGDRTPGKRTLLSESDLSYKRYFMHGIRTLISR 418  
 QY 433 FNNHAGPIIYVRPDESEELINPYRIMRFGVGVSHADELYLFWNLLSKRLPEESR 492

Db 419 AHNAPLAPTELYRPFDSKH-FNIMRIITGCRKRYGTCHADLSLYFYNAAKKLKRRTA 477  
 QY 493 EYKTIERNVGIWTEFATGKP---YSDNLAGHENTLWIDIKKSDVYKCLNIGDELKYM 548  
 Db 478 EFKTKRLVSMVYHFAISGDPNIPMVOCDEKQBPGRGAMLPISKDKKVCGLNSHDVHYI 537  
 QY 549 DLEPMKIKOGASIFDKK 566  
 Db 538 DLPEAKRLMLMDCIYDRE 555

## RESULT 12

Q961N0 PRELIMINARY; PRT; 566 AA.

AC Q961N0  
 DT 01-DEC-2001 (TREMblrel. 19, Created)  
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)  
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)  
 DE GH15053p.  
 GN ALPHA-EST2 OR CG2505.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 CC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 CC Ephydroidea; Drosophilidae; Drosophila.  
 NCBI\_TaxId=7227;

SEQUENCE FROM N.A.  
 RC STRAIN-BERKELEY;  
 RA Stapleton M., Brocksstein P., Hong L., Aghayani A., Carlson J.,  
 RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,  
 RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,  
 RA Nuno J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,  
 RA Yu C., Lewis S.E., Rubin G.M., Celnikier S.;  
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.  
 DR EMBL: AY051497; AAK92921.1; .  
 DR FlyBase: FBgn0015570; alpha-Est2.  
 DR InterPro: IPR002018; Carboxylesterase.  
 DR InterPro: IPR000379; Ser\_esterase.  
 DR Pfam: PF00135; Coesterase; 1.  
 KM Hydrolyase.  
 SQ SEQUENCE 566 AA; 64664 MW; 84C4FFA3CC0CF312 CRC64;

Query Match 42.1%; Score 1281.5; DB 5; Length 566;  
 Best Local Similarity 45.6%; Pred. No. 1.3e-93;

Matches 251; Conservative 110; Mismatches 174; Indels 15; Gaps 9;

QY 11 LKLCVCKVKNKYNTVRLSTNEIOITTEYGQIKGVKRMVYDDSYSEFISIPAKPPV 69  
 Db 11 IKMGALVGHVQOYRLSTGHTVLDTKYQVKGRLQKRTYDKEPYFAFGIYAKPPV 70  
 QY 70 ELARKAPQRPVWEGVDCGCPANRSVQTFISGKPTGSEDCLYLNYTMDLPDKRRPY 129  
 Db 71 DLRFAPQRPVWEGVDCGCPANRSVQTFISGKPTGSEDCLYLNYTMDLPDKRRPY 130  
 QY 130 MVEFHGDLTFGEANRMFGPDYFMKKPVVLYTVYRLGYLGLSLKSENLANPGNAGL 189  
 Db 131 IWTYGGGFGGASRDLVSPDYIMEHVLYLVISYRLGALGLSLADELDVPGNAGL 190  
 QY 190 DQVMAIRWYSNIAIFGVDNITVFGESAGSTHYMMITBQTRGLFHRGIMSGNSMC 249  
 Db 191 DQVMAIRWYSNIAIFGVDNITVFGESAGSTHYMMITBQTRGLFHRGIMSGNSMC 250  
 QY 250 SMASTECQSAALTKARVYKGEDEKDLFELKMANPYDLIKEPQVLT-PERQONVMPF 309  
 Db 251 EWESPDNMAFRLAONLGYKGEKEDADVLSFKCARQIAIDQVYINDEVASFLLF 310  
 QY 310 PEGPTVEPYOTADCVVPKPREMVKSAWNSIPTLIGNTSYEGILSKSVAKQYPEVVKEL 369  
 Db 311 AEGPVATEPEYTDHCYVKKHKLDSLSEAWGNDIPVYIGNSFEGILSYDLVVRDKPALNF 370  
 QY 370 ESCVNVVPELAD-SERSAPELTERAAIVKKAHYGGE-TPTLDNF---MELCSYFYFLFPM 425



DB 371 H--NIIIPREVETSSLEGODLVR--LKOLYFNNEQESMEMEALNIFSHQIWHDT 425  
 QY 426 HRFQLQFNHTAGTPTLYLRFDFDSEELINPRIMRGVGVKSHADELTLYFNNILSK 485  
 DB 426 HRFQLQFNHTAGTPTLYLRFDFDSEELINPRIMRGVGVKSHADELTLYFNNILSK 484  
 QY 486 RLPEKSERYTIERMGIWTEPATGPKYPSNDIAGMENITWDPK-KSDVYKCLNIGDE 544  
 DB 485 KLDKSSMEYKTIERMVGMWTSFSSGNNPCNELGSAK---WEAVOLKENAVEKCFNISHD 541  
 QY 545 LKXVMDLPEMD 554  
 DB 542 LEMKDLPESD 551  
 RESULT 13  
 ID 09VTC2 PRELIMINARY; PRT; 554 AA.  
 AC 09VTC2;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Alpha-EST2 protein.  
 GN ALPHA-EST2 OR CG2505.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 NC NCBITaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BERKELEY;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers J.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abril J.F., Aghayani A., An H.-J., Andrews-Frankoch C., Baldwin D.,  
 RA Baller R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,  
 RA Burks K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson R., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin R.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Foster C., Gabriellian A.E., Gary N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegami C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclab J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhou M., Zhou G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster.";  
 RL Science 287:2185-2195(2000).  
 CC -I- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYL ESTERASE/LIPASE FAMILY.  
 DB EMBL; AE003671; AAF54003.1; -

DR HSP; P37967; 10E3.  
 DR Flyase; FBgn015570; alpha-est2.  
 DR Interpro; IPR002018; Carboxylase.  
 DR Interpro; IPR009997; Cholinesterase.  
 DR Interpro; IPR003799; Ser-estrase.  
 DR Pfam; PF00135; Coesterase; 1.  
 DR PRINTS; PR00878; CHOLINESTRASE.  
 KW Hydrolyase.  
 SQ SEQUENCE 554 AA; 63254 MW; 6E4AC221A45B02D CRC64;  
 Query Match 42.0%; Score 1277.5; DB 5; Length 554;  
 Best Local Similarity 46.2%; Fred. No. 2.6e-93;  
 Matches 250; Conservative 106; Mismatches 170; Indels 15; Gaps 9;  
 QY 20 NKTYNRLSTNQTQIIDEYGOIKGVKRTVYD-DSYSFESIPYAKPPVGLRKAPQR 78  
 DB 8 HKVQYRLSTGHTVILDTKYGVGRLOKRTYDYKPYFAFEGIPYAKPPVGLRRAQRP 67  
 QY 79 PVWEGVRDCCGPNRANKSVQTFDFISGRPTGSEDCILYNTDNLNPKRRPVWFLHGGDF 138  
 DB 68 PEPWGVNLCTNRKSPMQRMNLLGIVESDCILYNTVYALKSEKPLPVYVWLYGGGF 127  
 QY 139 TGEANRNMFGPDYFPAKPPVLYVQYRLGVGLSLKSENLNPGNAGLKDQVWALRW 198  
 DB 128 QKGASRDYSPDYFPAKPPVLYVQYRLGVGLSLKSENLNPGNAGLKDQVWALRW 187  
 QY 199 KSNIAIFGGDVNTVFECSAGASTHYMMITTEQRLGFEHGIIMSGSMCSMASTEQS 258  
 DB 188 SONIAHFNGDPNNITLMDGSASASVHVMYTEQRLGFEHGIIMSGSMCSMASTEQS 247  
 QY 259 RALTMARVYKGEDENEKDLFEELKAMPYDLIKEEPOVLPERRQNVMPFPGTVEPY 318  
 DB 248 WAFRLAQNLNGYGDGKADVLSFLSKVCAQRLAIDQVINDVRSPLTFAFGVIEPY 307  
 QY 319 QTADEVKPEPIEMKWSANGSIPTLIGNTSTEGILSSVAKQPEVYKLESCVNYPW 378  
 DB 308 ETDHCVPRHRHDLSEAMGNDIPVIVGNSPFGFLSYQLVAKPFWALKNPH--NIIIP 364  
 QY 379 ELAD-SERAPETLRALVAKAHVDS-TPRLDNF--MELCSYVFLFPMHRLQLRPN 434  
 DB 365 EYRETSLEGGDLVR--LKOLYFNNEQESMEMEALNIFSHQIWHDTFRFLAROS 422  
 QY 435 HPGAGTPLYLRFDFDSEELINPRIMRGVGVKSHADELTLYFNNILSKRLPRESREY 494  
 DB 423 YAPKPTPTLYLRFDFDSEELINPRIMRGVGVKSHADELTLYFNNILSKRLPRESREY 481  
 QY 495 KTIERNVGIWTEPATGPKYPSNDIAGMENITWDPK-KSDVYKCLNIGDELKXVMDLPEM 553  
 DB 482 KTIERNVGMWTSFSSGNNPCNELGSAK---WEAVOLKENAVEKCFNISHDLEMDLPES 538  
 QY 554 D 554  
 DB 539 D 539  
 RESULT 14  
 ID 09W243 PRELIMINARY; PRT; 566 AA.  
 AC 09W243;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE CG6018 protein.  
 GN CG6018  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 NC NCBITaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BERKELEY;  
 RX MEDLINE=20196006; PubMed=10731132;





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OM protein - protein search, using sw model

Run on: April 4, 2003, 09:10:57 ; Search time 15.7722 Seconds  
(Without alignments)  
1063.331 Million cell updates/sec

Title: US-09-776-910-13

Perfect score: 3045

Sequence: 1 MFLLKQFIFRLKLCVCMVN.....PEMDKIKGASIFDKKELF 570

Scoring table: BLOSUM62

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Issued\_Patents\_AA:\*  
1: /cgn2\_6/prodata/1/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/prodata/1/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/prodata/1/1aa/5A\_COMB.pep:\*  
4: /cgn2\_6/prodata/1/1aa/5B\_COMB.pep:\*  
5: /cgn2\_6/prodata/1/1aa/5A\_COMB.pep:\*  
6: /cgn2\_6/prodata/1/1aa/5B\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	3045	100.0	570	4	US-09-068-960-13 Sequence 13, Appl
2	2348	77.1	570	4	US-09-068-960-8 Sequence 8, Appl
3	2342	76.9	570	2	US-08-669-524-3 Sequence 3, Appl
4	2335	76.7	570	4	US-09-068-960-2 Sequence 2, Appl
5	2335	76.7	570	4	US-09-068-960-4 Sequence 4, Appl
6	2335	76.7	570	4	US-09-068-960-6 Sequence 6, Appl
7	2335	76.7	570	4	US-09-068-960-10 Sequence 10, Appl
8	2330	76.5	570	2	US-08-669-524-4 Sequence 4, Appl
9	1847.5	60.7	572	2	US-08-669-524-8 Sequence 8, Appl
10	1062	34.9	207	4	US-09-068-960-15 Sequence 15, Appl
11	819	26.9	528	3	US-08-747-221B-37 Sequence 37, Appl
12	795	26.1	528	3	US-09-005-051-37 Sequence 37, Appl
13	795	26.1	528	3	US-08-747-221B-19 Sequence 19, Appl
14	735.5	24.2	550	3	US-08-747-221B-58 Sequence 58, Appl
15	735.5	24.2	550	3	US-09-005-051-58 Sequence 58, Appl
16	735.5	24.2	550	4	US-09-005-051-19 Sequence 19, Appl
17	735.5	24.2	550	4	US-09-005-051-58 Sequence 58, Appl
18	733.5	24.1	530	3	US-08-747-221B-53 Sequence 53, Appl
19	733.5	24.1	530	3	US-09-005-051-53 Sequence 53, Appl
20	723.5	23.8	505	3	US-08-747-221B-14 Sequence 14, Appl
21	723.5	23.8	505	4	US-09-005-051-14 Sequence 14, Appl
22	624	20.5	570	3	US-08-747-221B-55 Sequence 55, Appl
23	624	20.5	570	3	US-09-005-051-55 Sequence 55, Appl
24	624	20.5	595	3	US-08-747-221B-31 Sequence 31, Appl
25	624	20.5	595	4	US-09-005-051-31 Sequence 31, Appl
26	609	20.0	570	3	US-08-747-221B-54 Sequence 54, Appl
27	609	20.0	570	4	US-09-005-051-54 Sequence 54, Appl

28	609	20.0	596	3	US-08-747-221B-25 Sequence 25, Appl
29	609	20.0	596	4	US-09-005-051-25 Sequence 25, Appl
30	574	18.9	489	1	US-08-589-893-14 Sequence 14, Appl
31	574	18.9	489	2	US-09-020-991-14 Sequence 14, Appl
32	574	18.9	489	2	US-09-062-890-14 Sequence 14, Appl
33	573	18.8	489	1	US-08-589-893-4 Sequence 4, Appl
34	573	18.8	489	1	US-08-589-893-6 Sequence 6, Appl
35	573	18.8	489	2	US-09-020-991-16 Sequence 16, Appl
36	573	18.8	489	2	US-09-062-890-6 Sequence 6, Appl
37	573	18.8	489	2	US-09-062-890-4 Sequence 4, Appl
38	573	18.8	489	2	US-09-062-890-6 Sequence 6, Appl
39	573	18.8	489	1	US-09-062-890-32 Sequence 32, Appl
40	572	18.8	489	1	US-08-124-674-2 Sequence 2, Appl
41	572	18.8	489	1	US-08-589-893-16 Sequence 16, Appl
42	572	18.8	489	2	US-09-020-991-16 Sequence 16, Appl
43	572	18.8	489	2	US-09-062-890-16 Sequence 16, Appl
44	572	18.8	489	2	US-09-062-890-30 Sequence 30, Appl
45	571	18.8	489	1	US-08-589-893-8 Sequence 8, Appl

#### ALIGNMENTS

RESULT 1  
US-09-068-960-13  
Sequence 13, Application US/09068960A  
Patent No. 6235515  
GENERAL INFORMATION:  
APPLICANT: Commonwealth Scientific and Industrial Rerch. Org.  
TITLE OF INVENTION: MALATION CARBOXYL ESTERASE  
FILE REFERENCE: Attorney Docket No. 6235515 50179-051  
CURRENT APPLICATION NUMBER: US/09/068,960A  
CURRENT FILING DATE: 1998-05-20  
EARLIER APPLICATION NUMBER: PCT/AU96/00746  
EARLIER FILING DATE: 1996-11-22  
EARLIER APPLICATION NUMBER: AU 6751  
NUMBER OF SEQ ID NOS: 43  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 13  
LENGTH: 570  
TYPE: PRT  
ORGANISM: Musca domestica  
US-09-068-960-13

Query Match	100.0%	Score 3045	DB 4	Length 570
Best Local Similarity	100.0%	Pred. No. 3.6e-296		
Matches 570	Conservative	0	Mismatches 0	Indels 0
Gaps				
0				
QY	1	MFLLKQFIFRLKLCVCMVNRYTNRSLSTNEQIIDTEYGQIKGVRMTVYDSSYSES	60	
DB	1	MFLLKQFIFRLKLCVCMVNRYTNRSLSTNEQIIDTEYGQIKGVRMTVYDSSYSES	60	
QY	61	IPYAPKPVGELPFKAPQRPVPEWGVDCGPPANRSVQDFISGKPTGSEDCLYLVNTND	120	
DB	61	IPYAPKPVGELPFKAPQRPVPEWGVDCGPPANRSVQDFISGKPTGSEDCLYLVNTND	120	
QY	121	LPDQRPRPMTVTHGDFIFEGANRNRWGPDPFMKPPVLYVYVQRLVGLFLSKSNL	180	
DB	121	LPDQRPRPMTVTHGDFIFEGANRNRWGPDPFMKPPVLYVYVQRLVGLFLSKSNL	180	
QY	181	NVPGNAGLQDQYMALRWVSNIAIFGVDNITTVGESAGASTHYMMITDTRGLFPRG	240	
DB	181	NVPGNAGLQDQYMALRWVSNIAIFGVDNITTVGESAGASTHYMMITDTRGLFPRG	240	
QY	241	IMSGNSMCMASTECQSRALTMARVGVKGDNEKDIIEFLMKANPYDLIKEPQVLTLP	300	
DB	241	IMSGNSMCMASTECQSRALTMARVGVKGDNEKDIIEFLMKANPYDLIKEPQVLTLP	300	
QY	301	ERMOKRVMPFPPYEPYOTACVVPKPIREKVKSKANGSIPTLIGNTSYGLLSKSVAK	360	
DB	301	ERMOKRVMPFPPYEPYOTACVVPKPIREKVKSKANGSIPTLIGNTSYGLLSKSVAK	360	

QY 361 QYEVVKELESQVNVYVWELADSEKSAPELLEKRAIVYKKAHVDEGPTLNDNFMELCSFY 420  
 DB 361 QYEVVKELESQVNVYVWELADSEKSAPELLEKRAIVYKKAHVDEGPTLNDNFMELCSFY 420  
 QY 421 FLFPMHRLQJLRFNHTAGTPIYLYRFDPDSEIINPYRIMFGRGVKGVSHADELYLFW 480  
 DB 421 FLFPMHRLQJLRFNHTAGTPIYLYRFDPDSEIINPYRIMFGRGVKGVSHADELYLFW 480  
 QY 481 NILSKRLPKRESREKTYTERMWGIGWTEFATGTGKPSNDIAGMENLTPDIKSDVYKCLN 540  
 DB 481 NILSKRLPKRESREKTYTERMWGIGWTEFATGTGKPSNDIAGMENLTPDIKSDVYKCLN 540  
 QY 541 IGDELKVMIDPEMDKIKOGASIFDKKKELF 570  
 DB 541 IGDELKVMIDPEMDKIKOGASIFDKKKELF 570

## RESULT 2

US-09-068-960-8  
 ; Sequence 8, Application US/09068960A  
 ; Patent No. 6235515  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Commonwealth Scientific and Industrial Resrch. Org.  
 ; TITLE OF INVENTION: MALATHION CARBOXYL ESTERASE  
 ; FILE REFERENCE: Attorney Docket No. 6235515 50179-051  
 ; CURRENT APPLICATION NUMBER: US/09/068, 960A  
 ; CURRENT FILING DATE: 1998-05-20  
 ; EARLIER APPLICATION NUMBER: PCT/AU96/00746  
 ; EARLIER FILING DATE: 1996-11-22  
 ; EARLIER APPLICATION NUMBER: AU 6751  
 ; EARLIER FILING DATE: 1995-11-23  
 ; NUMBER OF SEQ ID NOS: 43  
 ; SOFTWARE: Patent In Ver. 2.0  
 ; SEQ ID NO 8  
 ; LENGTH: 570  
 ; TYPE: PRT  
 ; ORGANISM: Lucilia cuprina  
 ; US-09-068-960-8

Query Match 77.1%; Score 2348; DB 4; Length 570;

Best Local Similarity 74.2%; Pred. No. 2.4e-226;  
 Matches 423; Conservative 73; Mismatches 74; Indels 0; Gaps 0;

QY 1 MTFLEKQIFRLKLCVCKVANKYTNRLSTNETQIIDTEYQIGVKRMVYDSDYSSES 60  
 DB 1 MTFLEKQIFRLKLCVCKVANKYTNRLSTNETQIIDTEYQIGVKRMVYDSDYSSES 60  
 QY 61 IPYAKPPVGLERFAPQRPVMEGVRDCCGPARNSVQDFISGKPTGSEDCLYLWVYTN 120  
 DB 61 IPYAKPPVGLERFAPQRPVMEGVRDCCGPARNSVQDFISGKPTGSEDCLYLWVYTN 120  
 QY 121 LNPDKRPVWVFIFHGDFIFGEANRMFEGPDYFMKKPVLVTVQYRLGVGLFLSKSEN 180  
 DB 121 LNPDKRPVWVFIFHGDFIFGEANRMFEGPDYFMKKPVLVTVQYRLGVGLFLSKSEN 180  
 QY 181 NVPGNAGLKDQVYALRWKNSNATIFGQDVNITVFGESAGASTHYMMITTEQTRCLFHRG 240  
 DB 181 NVPGNAGLKDQVYALRWKNSNATIFGQDVNITVFGESAGASTHYMMITTEQTRCLFHRG 240  
 QY 241 IMMSGAGMKSMASTECOSALMAKRVGKGDNEKDIPEFLMKRNPDLIKKEEVOVLP 300  
 DB 241 IMMSGAGMKSMASTECOSALMAKRVGKGDNEKDIPEFLMKRNPDLIKKEEVOVLP 300  
 QY 301 ERMQNVMPFPGPTVEPYOTADCVVKKPIRENVKSAWNSIPTLIGNSYEGILSKSVAK 360  
 DB 301 ERMQNVMPFPGPTVEPYOTADCVVKKPIRENVKSAWNSIPTLIGNSYEGILSKSVAK 360  
 QY 361 QYEVVKELESQVNVYVWELADSEKSAPELLEKRAIVYKKAHVDEGPTLNDNFMELCSFY 420  
 DB 361 QYEVVKELESQVNVYVWELADSEKSAPELLEKRAIVYKKAHVDEGPTLNDNFMELCSFY 420  
 QY 421 FLFPMHRLQJLRFNHTAGTPIYLYRFDPDSEIINPYRIMFGRGVKGVSHADELYLFW 480  
 DB 421 FLFPMHRLQJLRFNHTAGTPIYLYRFDPDSEIINPYRIMFGRGVKGVSHADELYLFW 480

DB 421 FWPMMHRLQJLRFNHTAGTPIYLYRFDPDSEIINPYRIMFGRGVKGVSHADELYLFW 480  
 QY 481 NILSKRLPKRESREKTYTERMWGIGWTEFATGTGKPSNDIAGMENLTPDIKSDVYKCLN 540  
 DB 481 NILSKRLPKRESREKTYTERMWGIGWTEFATGTGKPSNDIAGMENLTPDIKSDVYKCLN 540  
 QY 541 IGDELKVMIDPEMDKIKOGASIFDKKKELF 570  
 DB 541 IGDELKVMIDPEMDKIKOGASIFDKKKELF 570

## RESULT 3

US-08-669-524-3  
 ; Sequence 3, Application US/08669524  
 ; Patent No. 5843758  
 ; GENERAL INFORMATION:  
 ; APPLICANT: RUSSELL, Robyn J.  
 ; APPLICANT: NEWCOMB, Richard D.  
 ; APPLICANT: ROBIN, Geoffrey C.  
 ; APPLICANT: BOYCE, Thomas M.  
 ; APPLICANT: CAMPBELL, Peter M.  
 ; APPLICANT: PARKER, Anthony G.  
 ; APPLICANT: OAKSHOTT, John G.  
 ; APPLICANT: SMITH, Kertie A.  
 ; TITLE OF INVENTION: ENZYME BASED BIOMEDIATION  
 ; NUMBER OF SEQUENCES: 22  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Lowe Price Leblanc & Becker  
 ; STREET: 99 Canal Center Plaza, Suite 300  
 ; CITY: Alexandria  
 ; STATE: Virginia  
 ; COUNTRY: USA  
 ; ZIP: 22314  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: IBM PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/669,524  
 ; FILING DATE:  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Price, Robert L.  
 ; REGISTRATION NUMBER: 22,685  
 ; REFERENCE/DOCKET NUMBER: 1451-021  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 703-684-1111  
 ; TELEFAX: 703-684-1124  
 ; INFORMATION FOR SEQ ID NO: 3:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 570 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; US-08-669-524-3

Query Match 76.9%; Score 2342; DB 2; Length 570;

Best Local Similarity 73.9%; Pred. No. 9.7e-226;  
 Matches 421; Conservative 75; Mismatches 74; Indels 0; Gaps 0;

QY 1 MTFLEKQIFRLKLCVCKVANKYTNRLSTNETQIIDTEYQIGVKRMVYDSDYSSES 60  
 DB 1 MTFLEKQIFRLKLCVCKVANKYTNRLSTNETQIIDTEYQIGVKRMVYDSDYSSES 60  
 QY 61 IPYAKPPVGLERFAPQRPVMEGVRDCCGPARNSVQDFISGKPTGSEDCLYLWVYTN 120  
 DB 61 IPYAKPPVGLERFAPQRPVMEGVRDCCGPARNSVQDFISGKPTGSEDCLYLWVYTN 120  
 QY 121 LNPDKRPVWVFIFHGDFIFGEANRMFEGPDYFMKKPVLVTVQYRLGVGLFLSKSEN 180  
 DB 121 LNPDKRPVWVFIFHGDFIFGEANRMFEGPDYFMKKPVLVTVQYRLGVGLFLSKSEN 180







100

Best Local Similarity 60.1%; Pred. No. 3,4e-176;  
Matches 339; Conservative 92; Mismatches 132; Indels 1; Gaps 1;

```

OY 7 FIRRLKVCYKWNKTYNRLSTNEQIIDTEGQIKYKRMVDDSYSESIIPYAKP 66
   1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   7 FVERLRKRLKTIHKVOYQROSTNETVADTEGOVGRGIRLSLYDVPFSEEGIYAPQ 66
OY 67 PVGELFKAPQRPVPEWEGVDDCCGPARNSVQTDIFISGPTGSEDCLYLVNVTNDINPKR 126
   1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   67 PVGELFKAPQRPVPEWEGVDDCCGPARNSVQTDIFISGPTGSEDCLYLVNVTNDINPKR 126
OY 127 RPVMVTHGGDFIFPGANMWECPDYEMKPVVLYTVQYRLGVLGFLSKSENLVWPGA 186
   1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   127 RPVMVTHGGDFIFPGANMWECPDYEMKPVVLYTVQYRLGVLGFLSKSENLVWPGA 186
OY 127 RPVMVTHGGDFIFPGANMWECPDYEMKPVVLYTVQYRLGVLGFLSKSENLVWPGA 186
   1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   127 RPVMVTHGGDFIFPGANMWECPDYEMKPVVLYTVQYRLGVLGFLSKSENLVWPGA 186
OY 187 GLKDOVALRWKNSNIAIFGSDVDNITVFGSAGASTHYMITEBOTGLFHRGIMSGN 246
   1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   187 GLKDOVALRWKNSNIAIFGSDVDNITVFGSAGASTHYMITEBOTGLFHRGIMSGN 246
OY 247 SMCSSA-STECOSRALTMKARYKGENEDILEFLKAMPYDIKEEPOVLTPERMQN 305
   1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   247 SMCSSA-STECOSRALTMKARYKGENEDILEFLKAMPYDIKEEPOVLTPERMQN 305
OY 247 AICPMAVYGDITTHNPYRIAKLVGKGDNDKDVLEFONVAKADLIRVENVYLTLEERN 306
   1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   247 AICPMAVYGDITTHNPYRIAKLVGKGDNDKDVLEFONVAKADLIRVENVYLTLEERN 306
OY 306 KVPMPGPTVEYQYADCVVPKPIREMYKSAWNSIPTLIGNTSEGLSKSVAKOYPEV 365
   1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   306 KVPMPGPTVEYQYADCVVPKPIREMYKSAWNSIPTLIGNTSEGLSKSVAKOYPEV 365
OY 307 KIMFFGSPLEPSTPECVISKPKKEMMKITAMNSIPFIGNTSEGLLVPEVKLPQV 366
   1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   307 KIMFFGSPLEPSTPECVISKPKKEMMKITAMNSIPFIGNTSEGLLVPEVKLPQV 366
OY 366 VKELSCVNYVPWELADSEKAPETLERALVYKAHVDGETPPLDNEMELCSEYFPLPM 425
   1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   366 VKELSCVNYVPWELADSEKAPETLERALVYKAHVDGETPPLDNEMELCSEYFPLPM 425
OY 367 LQOJDAGPPLPKELLATEPSKRLDSMSAQIRDVHRTGSESTPDNYMDLCISYFVFA 426
   1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   367 LQOJDAGPPLPKELLATEPSKRLDSMSAQIRDVHRTGSESTPDNYMDLCISYFVFA 426
OY 426 HRFLQLRNHTAGTPIYLYRDFDSEETINPYRIMRFGKGVSHADDELTYFWNLK 485
   1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   426 HRFLQLRNHTAGTPIYLYRDFDSEETINPYRIMRFGKGVSHADDELTYFWNLK 485
OY 427 LRVYSHRVAAGAAYFYRDPSEELIFPYRIMRGRGVSHADDELTYFSSLLAR 486
   1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   427 LRVYSHRVAAGAAYFYRDPSEELIFPYRIMRGRGVSHADDELTYFSSLLAR 486
OY 486 RLPESESEYTIEMVGIWEPATTKGPRYSNDIAGMENLWDPYKSDVYKCLNIGDEL 545
   1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   486 RLPESESEYTIEMVGIWEPATTKGPRYSNDIAGMENLWDPYKSDVYKCLNIGDEL 545
OY 487 RLPESESEYTIEMVGIWEPATTKGPRYSNDIAGMENLWDPYKSDVYKCLNIGDEL 546
   1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   487 RLPESESEYTIEMVGIWEPATTKGPRYSNDIAGMENLWDPYKSDVYKCLNIGDEL 546
OY 546 KVMDLPEMDKIKOGASFDDKKEL 569
   1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   546 KVMDLPEMDKIKOGASFDDKKEL 569
OY 547 KFTDLPEMKIKWESLIDNKKDL 570
   1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   547 KFTDLPEMKIKWESLIDNKKDL 570

```

Query Match 34.9%; Score 1062; DB 4; Length 207;  
Best Local Similarity 97.1%; Pred. No. 3e-98; Indels 0; Gaps 0;  
Matches 201; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

```

OY 97 QTDIFSGPTGSEDCLYLVNVTNDINPKRPPVVFTHGGDFIFGEANRNMFGPDYMK 156
   1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   1 QTDIFSGPTGSEDCLYLVNVTNDINPKRPPVVFTHGGDFIFGEANRNMFGPDYMK 156

```

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OY 157 PVVLTVQYRLGVLGFLSKSENLVWPGNAGLKQOVVALRWKNSNIAIFGSDVDNITVFG 216
   1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   61 PVVLTVQYRLGVLGFLSKSENLVWPGNAGLKQOVVALRWKNSNIAIFGSDVDNITVFG 120
OY 217 ESAGASTHYMITEQTRGLFHRGIMSGNSMCSMASTECOSRALTMKARYKKGEDNEK 276
   1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   121 ESAGASTHYMITEQTRGLFHRGIMSGNSMCSMASTECOSRALTMKARYKKGEDNEK 180
OY 277 DILEFLKAMPYDIKEEPOVLTPERM 303
   1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   181 DILEFLKAMPYDIKEEPOVLTPERM 207

```

RESULT 11  
US-09-068-960-43  
Sequence 43, Application us/09068960A  
Patent No. 6235515  
GENERAL INFORMATION:  
APPLICANT: Commonwealth Scientific and Industrial Rsrch. Org.  
TITLE OF INVENTION: MALATHION CARBOXYLESTERASE  
FILE REFERENCE: Attorney Docket No. 6235515 50179-051  
CURRENT FILING DATE: 1998-05-20  
EARLIER APPLICATION NUMBER: US/09/068,960A  
EARLIER FILING DATE: 1996-11-22  
EARLIER APPLICATION NUMBER: AU 6751  
NUMBER OF SEQ ID NOS: 43  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 43  
LENGTH: 207  
TYPE: PRT  
ORGANISM: Lucilia cuprina  
US-09-068-960-43

Query Match 26.9%; Score 819; DB 4; Length 207;  
Best Local Similarity 73.7%; Pred. No. 6,7e-74;  
Matches 151; Conservative 27; Mismatches 27; Indels 0; Gaps 0;

```

OY 97 QTDIFSGPTGSEDCLYLVNVTNDINPKRPPVVFTHGGDFIFGEANRNMFGPDYMK 156
   1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   1 QVDFITGVVCSSEDCLYLVNVTNNLNPETKRPVLYIHGGGFLIGENHBDWYGPDIYKK 60
OY 157 PVVLTVQYRLGVLGFLSKSENLVWPGNAGLKQOVVALRWKNSNIAIFGSDVDNITVFG 216
   1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   61 DVVLINIGYRLGALGFLSLNSEDNLVWPGNAGLKQOVVALRWKNSNIAIFGSDVDNITVFG 120
OY 217 ESAGASTHYMITEQTRGLFHRGIMSGNSMCSMASTECOSRALTMKARYKKGEDNEK 276
   1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   121 ESAGASTHYMITEQTRGLFHRGIMSGNACPLANTOCOHRAFLAKLAGYKGEDNDK 180
OY 277 DILEFLKAMPYDIKEEPOVLTPERM 301
   1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   181 DVLEFLKAKRQDIKLEKVTILE 205

```

RESULT 12  
US-08-747-221B-37  
Sequence 37, Application us/08747221B  
Patent No. 6063610  
GENERAL INFORMATION:  
APPLICANT: Silver, Gary W.  
APPLICANT: Wisniewski, Nancy  
TITLE OF INVENTION: No. 6063610e1 Carboxylesterase Nucleic Acid  
TITLE OF INVENTION: Molecules, Proteins and Uses Thereof  
NUMBER OF SEQUENCES: 66  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Carol Talkington Verser, Ph.D.  
ADDRESSEE: Heska Corporation  
STREET: 1825 Sharp Point Drive  
CITY: Fort Collins  
STATE: Colorado

```

COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Wordperfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/747,221B
FILING DATE: No. 6063610ember 12, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: FC-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 528 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-747-221B-37

Query Match      26.1%; Score 795; DB 3; Length 528;
Best Local Similarity 35.6%; Pred. No. 8.3e-71;
Matches 190; Conservative 105; Mismatches 202; Indels 36; Gaps 15;

QY 40 GOIKGVKMTYVDSDSYSEFSPYAKPPVGLRFAAPRPVPEWEGVDCGPNRNSVQTD 99
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 11 GLTKKEQISEKGNVHSHSYGIPYAKPPVGLRFAAPRPVPEWEGVDCGPNRNSVH 70
QY 100 FISGKPTGSEDCILYLVNTYNDLNPDKRRPVYVFIHGDFIFGEANRNWFGPDYEMKRPV 159
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 71 FIKKIKVGAEDCLYLVNTYVPTSEKSLPVVWVHIGGFGFMSGSDMYGPEYIMDYGI 130
QY 160 LVTVOYRGLVGLFSLKSENLVPGNAGLKDOVMALRWKSNIAIFGGDVNITVFEESA 219
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Db 131 LVTENRRLVGLGLNLGIE--EAPGNVGLMDQVEALKWKNNINASFSGDPNNVTIFGESA 188
QY 220 GGAATHYMMITEOTRGLFHRGIMSGNSMCNASTECOSR--ALTMARVGYKGEDNEKD 277
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Db 189 GGAATHYMLSDLSKGLFKHKAISOSGSAFNPWALQHDNNKKNARFCKLLGHP--VDNETE 247
QY 278 ILEFLMKANPYDLIKEBPVLTPERMQNKVMPFPGTVP--YQTADCVVPRKIREMWSA 336
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 248 ALKILRQAPIDDLI--DNRIKPKDKGQLIIDYPLPTIEKRYQNEPFLDQSPLSKMSG 305
QY 337 WGNSTPLTIGNTSYEGILSKSAKQYPEVVKEL--CVNYVPMELADSENSAPETLERAA 395
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Db 306 NPTKVPFICGYNASAEGLILGMDPKDDPNIFKFEADFEFVVDLNLTLRS--KESKILAE 364
QY 396 IYKAAHVDEPTLDN---FMELCSYFYLFPFMRFLQLRNFHAGTPIYLYRPFDP--- 449
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 365 EMKRFYQDEPVSSDNKEKFEVSIQDTPWFLRGINKTARYIIHSS--EPLLYLVYSFDDFG 423
QY 450 --SEIINPYIRMRGRGVKGVSHADELYTLF--WNILSKRLPKESREKYTEIRMGIV 504
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 424 FLKLVLVLDP-----NIEGAHGDDELGYLFKMSFTEFPDLS---AVYNNRRLQLW 472
QY 505 TEFTFTGKPYSDIAGMENLWTDPIKSDVYKCLNIGDELKAVMDPEMDKIK 557
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Db 473 TNFAKTGNP--TPELNDVITTKWD--KATEEKSMDMDIDNLRMLPDDAKRLR 522

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```

APPLICANT: Wisniewski, Nancy
TITLE OF INVENTION: No. 6291222a1 Carboxyltransferase Nucleic Acid
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESSEE: Hesk Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Wordperfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,051
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/747,221
FILING DATE: No. 6291222ember 12, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: FC-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 528 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-005-051-37

Query Match      26.1%; Score 795; DB 4; Length 528;
Best Local Similarity 35.6%; Pred. No. 8.3e-71;
Matches 190; Conservative 105; Mismatches 202; Indels 36; Gaps 15;

QY 40 GOIKGVKMTYVDSDSYSEFSPYAKPPVGLRFAAPRPVPEWEGVDCGPNRNSVQTD 99
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Db 11 GLTKKEQISEKGNVHSHSYGIPYAKPPVGLRFAAPRPVPEWEGVDCGPNRNSVH 70
QY 100 FISGKPTGSEDCILYLVNTYNDLNPDKRRPVYVFIHGDFIFGEANRNWFGPDYEMKRPV 159
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 71 FIKKIKVGAEDCLYLVNTYVPTSEKSLPVVWVHIGGFGFMSGSDMYGPEYIMDYGI 130
QY 160 LVTVOYRGLVGLFSLKSENLVPGNAGLKDOVMALRWKSNIAIFGGDVNITVFEESA 219
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 131 LVTENRRLVGLGLNLGIE--EAPGNVGLMDQVEALKWKNNINASFSGDPNNVTIFGESA 188
QY 220 GGAATHYMMITEOTRGLFHRGIMSGNSMCNASTECOSR--ALTMARVGYKGEDNEKD 277
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 189 GGAATHYMLSDLSKGLFKHKAISOSGSAFNPWALQHDNNKKNARFCKLLGHP--VDNETE 247
QY 278 ILEFLMKANPYDLIKEBPVLTPERMQNKVMPFPGTVP--YQTADCVVPRKIREMWSA 336
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 248 ALKILRQAPIDDLI--DNRIKPKDKGQLIIDYPLPTIEKRYQNEPFLDQSPLSKMSG 305
QY 337 WGNSTPLTIGNTSYEGILSKSAKQYPEVVKEL--CVNYVPMELADSENSAPETLERAA 395
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 306 NPTKVPFICGYNASAEGLILGMDPKDDPNIFKFEADFEFVVDLNLTLRS--KESKILAE 364
QY 396 IYKAAHVDEPTLDN---FMELCSYFYLFPFMRFLQLRNFHAGTPIYLYRPFDP--- 449
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 365 EMKRFYQDEPVSSDNKEKFEVSIQDTPWFLRGINKTARYIIHSS--EPLLYLVYSFDDFG 423
QY 450 --SEIINPYIRMRGRGVKGVSHADELYTLF--WNILSKRLPKESREKYTEIRMGIV 504
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

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Db 424 ELKVLVDP-----NIEGAHDELGLVLFKMSFTEPKDLPSS---AVVNERELQW 472

QY 505 TEFATGKPYSDIAGMENLTWPIKSDVYKCLNIGDLKYMDELPMKIK 557

Db 473 TNEAKTGNP--TPEINDVITTKWD--KATEBKSDHMDIDNLRMLPDDAKRLR 522

RESULT 14

US-08-747-221B-19

; Sequence 19, Application US/08/47221B

; Patent No. 6063610

GENERAL INFORMATION:

APPLICANT: Silver, Gary W.

APPLICANT: Wisniewski, Nancy

TITLE OF INVENTION: No. 6063610el Carboxylesterase Nucleic Acid

NUMBER OF SEQUENCES: 66

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Haska Corporation

STREET: 1825 Sharp Point Drive

CITY: Fort Collins

STATE: Colorado

COUNTRY: USA

ZIP: 80525

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: Windows 95

SOFTWARE: WordPerfect for Windows, Version 7.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/747,221B

FILING DATE: No. 6063610ember 12, 1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Verser, Carol Talkington

REGISTRATION NUMBER: 37,459

REFERENCE/DOCKET NUMBER: FC-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 970/493-7272

TELEFAX: 970/484-9505

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:

LENGTH: 550 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-747-221B-19

Query Match 24.2%; Score 735.5; DB 3; Length 550;

Best Local Similarity 32.8%; Pred. No. 8.1e-65;

Matches 188; Conservative 89; Mismatches 233; Indels 63; Gaps 16;

QY 3 FLKQIFRLKLCVCKMKNKTYRSLSTNETQIIDTEYQIKGVKRMVYDSDYSSESIP 62

Db 11 FLESENF-----IKC-----DPTVTLPGDELVGKALTNENKKEVSYTGVP 52

QY 63 YAKPVGELRFKAPORPVMEGVRCDCGPANRSVQTDIFISGKPTGSEDCILVNYTNDLN 122

Db 53 YAKPVGELRFKAPORPVMEGVRCDCGPANRSVQTDIFISGKPTGSEDCILVNYTNDLN 112

QY 123 PDKRRVAVYVTHGDFIFGEANRNMFPGDYEMKRPVVLVYQYRLGVIGFLSLKSENIN 182

Db 113 SOKKLPVFFVHVGSGFVTSNLEFQSPDYLVNVDVIEVTENYRLGFLNLELE--GA 170

QY 183 PENAGLQOVMALRWKXSIALFFGSDVNITVFGESAGASHYVMITEQTFGLHRTIM 242

Db 171 PENAGLQOVMALRWKXSIALFFGSDVNITVFGESAGASHYVMITEQTFGLHRTIM 230

QY 243 MGNNSMCSWA--STECOSRALTMKRVGYKGEDEKEDILEFLKANRPYDLIKEEPOVLPE 301

Db 231 QSGSALNMPAFORHVPKRSLOLAELIGHP--TNTQDLEFLQKAVDSDLTCKMPAETGE 289

QY 302 RMQNVMEP---FGPTVEPYQTADCVVPKPIREKVSAGMNSIPTLIGNTSYGLSKS 357

Db 290 IIEFEVYSIEKVPSPHPF-----LEESPLAR-KSGSFNKVPLLVGFNSAGGLYKF 343

QY 358 VAKQPEVYKELSCVNVYPMELADESAP-----ETTERAIVKKAHVDGETP 407

Db 344 FMKEKPEMLNQA-----ADFERLVPAEFPLANGSESKKLAKIKKFFFD-DKP 392

QY 408 TLDN---FMELCSYFELFPMHFRFLQRFNMHTAGTPIVLYREDPDEEIIINPYRMRGR 464

Db 393 VEENKQKFDLDGLDMFTGTIDKHVLSV-EKQDEPYYVEYSFSES--HPAKGTGDH 448

QY 465 GVKGVSHADELYLFWNLKRLPKESREYKTIEMKGIWIEFATGPGYSDIAGMENL 524

Db 449 NLTGACHGELVNLFEVEMKLEKDKPVLVLTGKDRVLAAMNFIKGNP--TPEYELLVP 507

QY 525 TWDPIKSDVYKCLNIGDLKYMDELPMKIK 557

Db 508 KMEPAVK--DKLNYINDATVLTGTPNETRYK 538

RESULT 15

US-08-747-221B-58

; Sequence 38, Application US/08/47221B

; Patent No. 6063610

GENERAL INFORMATION:

APPLICANT: Silver, Gary W.

APPLICANT: Wisniewski, Nancy

TITLE OF INVENTION: No. 6063610el Carboxylesterase Nucleic Acid

NUMBER OF SEQUENCES: 66

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Carol Talkington Verser, Ph.D.

STREET: 1825 Sharp Point Drive

CITY: Fort Collins

STATE: Colorado

COUNTRY: USA

ZIP: 80525

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: Windows 95

SOFTWARE: WordPerfect for Windows, Version 7.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/747,221B

FILING DATE: No. 6063610ember 12, 1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Verser, Carol Talkington

REGISTRATION NUMBER: 37,459

REFERENCE/DOCKET NUMBER: FC-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 970/493-7272

TELEFAX: 970/484-9505

INFORMATION FOR SEQ ID NO: 58:

SEQUENCE CHARACTERISTICS:

LENGTH: 550 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-747-221B-58

Query Match 24.2%; Score 735.5; DB 3; Length 550;

Best Local Similarity 32.8%; Pred. No. 8.1e-65;

Matches 188; Conservative 91; Mismatches 231; Indels 63; Gaps 16;

QY 3 FLKQIFRLKLCVCKMKNKTYRSLSTNETQIIDTEYQIKGVKRMVYDSDYSSESIP 62

Db 11 FLESENF-----IKC-----DPTVTLPGDELVGKALTNENKKEVSYTGVP 52

QY 63 YAKPVGELRFKAPORPVMEGVRCDCGPANRSVQTDIFISGKPTGSEDCILVNYTNDLN 122

Db 53 YAKPPVGELEFKPPQKAEPMQGVNATLYGNVCKSLNFIKLTIGDEDCLVNVVAPKPT 112

QY 123 PDKRRPVMEFIHSGDETFEGEANNMVEGPDYEMKKPVVLTVOYRGLGVGLSLKSENLV 182

Db 113 SDKKLPEFVFWHGGFVYTGSGNLEFOSPDYLVBEVDVLEFVFNRYRLGPGFLNLELE--GA 170

QY 183 PGNAGLDQVMALRWVKSNAIFGGVDVNTVGESAGASTHYMMTEQTRGLFHRGIM 242

Db 171 PGNGGLDDQVAALKWTEKENLEKFGDPENITIGVSAGASVHLLSHTTGGLKRAIA 230

QY 243 MSGNSMCSMA-STECOSRALTMKRVGKGEDEKDIIEFLMKANPYDLIKEEPOVLTP 301

Db 231 QSSSAFNPMAFQRRPVKRSQJLAELIGHP--TNNTQDALFEFLQKAPVDSILKKMPAEETGE 289

QY 302 RMQNKVMEP---FGPTVEPYQTADCVVPPKPIREMKVSANGNSIPTLIGNTSTEGLSKS 357

Db 290 IIEEFVFPVPSIEKVPESHOPF---LEESPLARM-KSGSFNKVPPLLVGENSAEGLLFKF 343

QY 358 VAKQYPEVVKELSCVNVVPMELADSEPSAP-----ETLERAIYKKAHVDETP 407

Db 344 FMKEKPEMLNQA-----ADFERLYPAEPELVHGSSESKKLAKTRKEFTD-DKP 392

QY 408 TLDN---FMELCSYFYLEFPMHRLQLEFNHTAGTPILYXREDFDSEELINPYRIMRGR 464

Db 393 VPENQKFIIDLIGDIWFRGVDKHVKLSV--EKODEPYYYEYSESES---HPAKGTFGDH 448

QY 465 GYKGVSHADELTLYFMNLSKRLPKESREYKTIERMGVWTEFATGKPYSDIAGMENL 524

Db 449 NLTGACHGEELVNLFEKVEMKLEKDPVLLTKDRVLAMMTNFIKNGNP--TPEVTELLPV 507

QY 525 TWDPYKSDVYKCLINIGDELKVMDLPEMDKIK 557

Db 508 KMEPATK--DKLNYLNIDATITLGTNPEANRYK 538

Search completed: April 4, 2003, 09:18:08  
Job time : 17.7722 secs



GenCore version 5.1.4.p5\_4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 4, 2003, 09:16:33 ; Search time 24.5753 Seconds

(without alignments)  
1417.991 Million cell updates/sec

Title: US-09-776-910-13

Perfect score: 3045

Sequence: 1 MTFUKQIFRKLCKVCMVN.....PEMDKIKQASIFDKKELF 570

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 248812 seqs, 61136040 residues

Total number of hits satisfying chosen parameters: 248812

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA: \*

- 1: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCY\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
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- 9: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep.\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	642	21.1	612	9 US-09-875-353-4	Sequence 4, App1
2	640.5	21.0	574	9 US-10-023-515-4	Sequence 4, App1
3	630	20.7	585	10 US-09-934-323-4	Sequence 4, App1
4	520.5	17.1	574	10 US-09-748-739A-21	Sequence 21, App1
5	518	17.0	602	10 US-09-748-739A-2	Sequence 2, App1
6	514	16.9	574	10 US-09-748-739A-6	Sequence 6, App1
7	514	16.9	574	10 US-09-748-739A-17	Sequence 17, App1
8	514	16.9	574	10 US-09-748-739A-20	Sequence 20, App1
9	513	16.8	574	10 US-09-748-739A-4	Sequence 4, App1
10	513	16.8	574	10 US-09-748-739A-18	Sequence 18, App1
11	511	16.8	574	10 US-09-748-739A-8	Sequence 8, App1
12	509	16.7	574	10 US-09-748-739A-23	Sequence 23, App1
13	508.5	16.7	574	10 US-09-748-739A-19	Sequence 19, App1
14	501.5	16.5	549	9 US-10-102-806-689	Sequence 22, App1
15	500	16.4	549	9 US-10-102-806-689	Sequence 689, App1
16	498.5	16.4	554	10 US-09-895-860-5	Sequence 5, App1
17	488	16.0	554	10 US-09-895-860-4	Sequence 4, App1
18	485	15.9	816	9 US-09-978-295A-375	Sequence 375, App1
19	485	15.9	816	9 US-09-978-697-375	Sequence 375, App1

20	485	15.9	816	9 US-09-978-192A-375	Sequence 375, App1
21	485	15.9	816	9 US-09-999-832A-375	Sequence 375, App1
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27	485	15.9	816	9 US-09-978-585A-375	Sequence 375, App1
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29	485	15.9	816	9 US-09-978-824-375	Sequence 375, App1
30	485	15.9	816	9 US-09-981-915A-375	Sequence 375, App1
31	485	15.9	816	9 US-09-999-833A-375	Sequence 375, App1
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33	485	15.9	816	9 US-09-918-585A-375	Sequence 375, App1
34	484.5	15.9	816	9 US-09-934-323-5	Sequence 2, App1
35	484.5	15.9	816	9 US-09-934-323-2	Sequence 5, App1
36	481.5	15.8	835	10 US-09-925-301-1177	Sequence 2, App1
37	479.5	15.7	583	10 US-09-925-301-1177	Sequence 1177, App1
38	476.5	15.6	547	10 US-09-895-860-2	Sequence 23, App1
39	476.5	15.6	571	9 US-10-036-041-23	Sequence 542, App1
40	476.5	15.6	571	9 US-10-028-072-542	Sequence 23, App1
41	476.5	15.6	571	9 US-10-035-855-23	Sequence 542, App1
42	476.5	15.6	571	9 US-10-123-049-542	Sequence 542, App1
43	476.5	15.6	571	9 US-10-123-904-542	Sequence 542, App1
44	476.5	15.6	571	9 US-10-140-470-542	Sequence 542, App1
45	476.5	15.6	571	9 US-09-931-836-23	Sequence 23, App1

## ALIGNMENTS

RESULT 1  
US-09-875-353-4  
Sequence 4, Application US/09875353  
Patent No. US20020168713A1  
GENERAL INFORMATION:  
APPLICANT: Curtiss, Roy A. J.  
TITLE OF INVENTION: 46960, A NOVEL HUMAN NEUROLIGIN FAMILY  
FILE REFERENCE: 10448-058001  
CURRENT APPLICATION NUMBER: US/09/875,353  
CURRENT FILING DATE: 2001-06-06  
PRIOR APPLICATION NUMBER: US 60/209,949  
PRIOR FILING DATE: 2000-06-06  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 4  
LENGTH: 612  
TYPE: PRT  
FEATURE:  
ORGANISM: Artificial Sequence  
OTHER INFORMATION: consensus sequence  
US-09-875-353-4

Query Match 21.1%, Score 642, DB 9; Length 612;  
Best Local Similarity 30.3%, Pred. No. 4.7e-51;  
Matches 187; Conservative 95; Mismatches 252; Indels 84; Gaps 22;  
1 MTFUKQIFRKLCKVCMVNKTNTSTNETQIIDRE--YGOIKGVKRTVY-DPSY 56  
1 MULLFLFLLLTLLTAAVAAA---KASPEDEPLLVATNNVLCKVRGVNKRKTGDEGSY 56  
57 SPESIPYAKPPVGGELRFAPO-RPVPMGVDRDCGPNRSVQDFIS----- 102  
57 SFLGIPVAPPEPVGNRFAAPQPEKPSMDVADATKYPSCLODDDFGFSLSLKLKML 116  
103 -----GKPLG---SEDCLYLNVY-NDLNPDKRPVWVFHIGDFIFGEAN----RWMPG 150  
117 SLGMNKLGLKLSKCYLANYTPTKNTKPLVWVWVHIGGFMGSGSLPLSLYDDE 176  
151 DYFMKKPVLTVOYRGVIGFSLKSENLVNPGNAGLKQVVALKWKVSNIAIFGDDV 210  
177 SLARGNVIVYSIKRGLPGLFSTGDDKLPKSGNGLDQRLALWKVODNIAAFGDDN 236

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Db      181 IALKWVONDIAAFGSDNASTLIFGEBSGAAVSLILLSNGDNPSPSKGLFHHRAISOGS 240
QY      247 SMCWSA--STEGCSRALYAKRHYGKGEDNEKDILFEFLMKANPYDIKEEPVYLPERH 303
Db      241 ALSPMAIDSESNARGAKKELARILGCG-NETSSSELLDCIRKSAEBELLEATRSFLLEY 299
QY      304 QAKWAF-FEGTIVPERYQACVYKPIREYVWSAMGNSIPTLIGNTSYEG---ILSKS 357
Db      300 PLPLFLFAGPVWDDDAPEFLFEDPEBELIKGKRAQVPLILGVTKDEGSGYFAAMLINA 359
QY      358 VAKOYPEVWKELESCVNVYVW-----ELADSRKAPETLER-AAIVYKAH 401
Db      360 SSKGEDELKKEKNPNV----WLELDIKYLFEYSEALINIKMDLADKYLEKPGDVDFGS 415
QY      402 VDGEPITLDNMELOSYEFLEFPHNRFLOLRFNHTAGTPIYLLRPFDSSEITNPIRYMR 461
Db      416 VERKRP--NLODMITDLLEKCPFRVAADHANH-GGSPVUYAVVDHPSAFGICQFLAKR 471
QY      462 FGRGVKGVSHADELYLFWM--ILSKRLPK--ESREKTKITERRWVGWITEPATYTGKYSNDI 518
Db      472 VDPEFGAAGHGEIEFVFGNPLKEOLYKKTETEEBESSKTYMANTYANFAKTGNPNOTS 531
QY      519 AGMENLTWPIKKSDDVYKCLNI-----QDELKMYD 549
Db      532 NGL--VWMEKYSDEOKSLILITLTTPYAKLKARD 565

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RESULT 3
US-09-934-323-4
; Sequence 4, Application US/09934323
; Patient No. US20020150910A1
GENERAL INFORMATION:
APPLICANT: Curtiss, RORY A. J.
TITLE OF INVENTION: 33410, A NOVEL HUMAN CARBOXYLSTERASE
TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF
FILE REFERENCE: 10448-081001
CURRENT APPLICATION NUMBER: US/09/934,323
CURRENT FILING DATE: 2001-08-21
PRIORITY APPLICATION NUMBER: US 60/226,774
PRIORITY FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 585
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Consensus sequence
US-09-934-323-4

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Query Match	20.7%	Score 630;	DB 10;	Length 585;
Best Local Similarity	31.2%	Pred. No. 5,7e-50;		
Matches 180;	Conservative	88;	Mismatches 231;	Indels 78; Gaps 21;

QY	40	GOLKGVKRMIVY--DQSYSPESIPYAKPVGELRKAPO--RPVMEGVRCOCGPANRSW	97
Db	11	GKRVGVNEKTDNGEQSVYFSLGIPAEPPVGLTRAKAPQPYKEEWSVLDATYTRPSCLD	70
QY	98	TDFIS-----GKPLG---SEDCLYLNVYT--NDLNPDKRRRPVWFIHGG	136
Db	71	DDDFGSLSLDKALKMLSLGNKKLVGLKLSBDCLYLVNVPKTKPKNSKLPVWVWHGG	130
QY	137	DLTFEGEAN---RNWFGPDYFMAKKRPVLYVTOYRLGVGFSLKSENLYVGNAG--LKQD	191
Db	131	GFMGSGSHSLPLSLYDGESEIARGNATIVSYNRIGPLGFLSTGDDKRLPGSGNNGLLDQ	190
QY	192	VMAIRVWKSINAIIFGVDVNTITVEFGSAGASTHYMITE-----QTRGLFHGIMSG	245
Db	191	RLALKWQVDNLIAFGGSPNSVTTFEGESAAASYSLLLSNGDNPSSKGLFHAISQSG	250
QY	246	NSMCKSA---STEOGSAITMAKRVYKGEDEKNDLIEFLMKANPYDLIKKEEPVLTPEER	302







```

US-09-748-739A-20
; Sequence 20, Application US/09748739A
; Patent No. US20020119489A1
; GENERAL INFORMATION:
; APPLICANT: Lockridge, Oksana
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: Butyrylcholinesterase Variants and
; FILE REFERENCE: P-IX 4143
; CURRENT APPLICATION NUMBER: US/09/748,739A
; CURRENT FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 574
; TYPE: PRN
; ORGANISM: Homo sapiens
US-09-748-739A-20

```

```

Query Match      16.9%; Score 514; DB 10; Length 574;
Best Local Similarity 28.2%; Pred. No. 3,4e-39;
Matches 168; Conservative 97; Mismatches 204; Indels 126; Gaps 28;

```

```

QY 34 IIDPEYQIKGVKMTVYDDSYSPESIPYAKPPVGLRFRKAPQRPVMEGV-----R 86
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 5 IIAIKNGKVRGM-NLTVFGGTVAFLGIPYAQPLRLRFRKQPSLTKMSDINNAIKYAN 63
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 87 DCCGPRANRSV-----QTFDISGKPTGSEDCLYLNVYTNIDLPDKRRPVWFIHG 135
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 64 SCCQNIQSPFGHSGEMMNPNTDL-----SEDCLYLNVWIPAKRP-KNATVLTWIMG 115
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 136 GDFIFGEANRMWFGPDYFMK-KPVVLTVOYRLGVLGFLSLKSENLVNPGNAGLKDOYMA 194
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 116 GGFQGTGSSLHYVDGKFLARVERIYVSMNRGALGFLAPG-NPEAGNMGFLDQOLA 174
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 195 LRWVKSNTAIFGGVDNITVFGESAGASTHYMMITEQTRGLFHRGIMSGNSMCSMAST 254
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 175 LQWVOKNTAIAAGNPKSVTLFGESAGAAVSLLHLSPGSHLFTRAILQSGSFNAPMAVT 234
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 255 ---ECOSRALTMARKRVGKGDNEKDLIEFLMKANPYDLIKEEPOVL--TPERMQNKVM 308
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 235 SLYEARKNTLNLAKLTGCSRE-NETELIKLRNKDQOELLNFAVVPYGLVN-----LS 287
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 309 FPGPPTVEPYQTADCVYPKPIREMVKSAMGNSIPTLIGNTSYEGL-----LSKS-- 357
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 288 VNFPGTYVDGFLTD--MPDILLELGOF--KKTQILVGNKDEGTAFVLVGAPGFSKDN 342
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 358 ---VAKOYPEVVKEL-----ESCV-NYVPWELADSESAPETLERAAIYKKAHVDG 404
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 343 SIIRKREFQEGKLTFFPGVSEFGKESILFHYTDW-----VDD 379
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 405 EPTPLDNFME---LCSYFELFPMHRLQLRNHTAGTPILYLRPDSEELINPYRIM 460
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 380 QRP--ENYREALGDVVGDNFICPALEFTK-KFSEW-GNNAFFYFHRSSSKLPWPEWM- 434
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 461 RFGGVGVSHADELTLYLFWNLSKRLPKESRE-YKTIER-----MVGITFEATGKPY 514
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 435 -----GVWNGYEIEFV-----GLPLERNYTKAEILLRSYKRWANFAKYGNPN 481
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 515 SNDIAGMENTLWDPRIKSDVYKCLINIGDELKVMDLPEMDKIKOGASIFDKKEL 569
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 482 ETQ---NNSTSMVPFKSTEQKYLTLNT-ESTRIKTLRAQOOCRFMTSFFPKVLEM 532
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

```

```

RESULT 9
US-09-748-739A-4
; Sequence 4, Application US/09748739A
; Patent No. US20020119489A1
; GENERAL INFORMATION:
; APPLICANT: Lockridge, Oksana
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: Butyrylcholinesterase Variants and
; TITLE OF INVENTION: Methods of Use

```

```

; FILE REFERENCE: P-IX 4143
; CURRENT APPLICATION NUMBER: US/09/748,739A
; CURRENT FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 574
; TYPE: PRN
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human Butyrylcholinesterase variant
US-09-748-739A-4

```

```

Query Match      16.8%; Score 513; DB 10; Length 574;
Best Local Similarity 28.2%; Pred. No. 4.2e-39;
Matches 168; Conservative 97; Mismatches 204; Indels 126; Gaps 28;

```

```

QY 34 IIDPEYQIKGVKMTVYDDSYSPESIPYAKPPVGLRFRKAPQRPVMEGV-----R 86
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 5 IIAIKNGKVRGM-NLTVFGGTVAFLGIPYAQPLRLRFRKQPSLTKMSDINNAIKYAN 63
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 87 DCCGPRANRSV-----QTFDISGKPTGSEDCLYLNVYTNIDLPDKRRPVWFIHG 135
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 64 SCCQNIQSPFGHSGEMMNPNTDL-----SEDCLYLNVWIPAKRP-KNATVLTWIMG 115
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 136 GDFIFGEANRMWFGPDYFMK-KPVVLTVOYRLGVLGFLSLKSENLVNPGNAGLKDOYMA 194
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 116 GGFQGTGSSLHYVDGKFLARVERIYVSMNRGALGFLAPG-NPEAGNMGFLDQOLA 174
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 195 LRWVKSNTAIFGGVDNITVFGESAGASTHYMMITEQTRGLFHRGIMSGNSMCSMAST 254
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 175 LQWVOKNTAIAAGNPKSVTLFGESAGAAVSLLHLSPGSHLFTRAILQSGSFNAPMAVT 234
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 255 ---ECOSRALTMARKRVGKGDNEKDLIEFLMKANPYDLIKEEPOVL--TPERMQNKVM 308
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 235 SLYEARKNTLNLAKLTGCSRE-NETELIKLRNKDQOELLNFAVVPYGLVN-----LS 289
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 309 FPGPPTVEPYQTADCVYPKPIREMVKSAMGNSIPTLIGNTSYEGL-----LSKS-- 357
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 290 --FGPVTVDGFLTD--MPDILLELGOF--KKTQILVGNKDEGTAFVLVGAPGFSKDN 342
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 358 ---VAKOYPEVVKEL-----ESCV-NYVPWELADSESAPETLERAAIYKKAHVDG 404
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 343 SIIRKREFQEGKLTFFPGVSEFGKESILFHYTDW-----VDD 379
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 405 EPTPLDNFME---LCSYFELFPMHRLQLRNHTAGTPILYLRPDSEELINPYRIM 460
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 380 QRP--ENYREALGDVVGDNFICPALEFTK-KFSEW-GNNAFFYFHRSSSKLPWPEWM- 434
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 461 RFGGVGVSHADELTLYLFWNLSKRLPKESRE-YKTIER-----MVGITFEATGKPY 514
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 435 -----GVWNGYEIEFV-----GLPLERNYTKAEILLRSYKRWANFAKYGNPN 481
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 515 SNDIAGMENTLWDPRIKSDVYKCLINIGDELKVMDLPEMDKIKOGASIFDKKEL 569
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 482 ETQ---NNSTSMVPFKSTEQKYLTLNT-ESTRIKTLRAQOOCRFMTSFFPKVLEM 532
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

```

```

RESULT 10
US-09-748-739A-18
; Sequence 18, Application US/09748739A
; Patent No. US20020119489A1
; GENERAL INFORMATION:
; APPLICANT: Lockridge, Oksana
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: Butyrylcholinesterase Variants and
; FILE REFERENCE: P-IX 4143
; CURRENT APPLICATION NUMBER: US/09/748,739A
; CURRENT FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18

```

```

; LENGTH: 574
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-748-739A-18

```

Query Match	16.8%	Score 513	DB 10	Length 574	
Best Local Similarity	28.2%	Pred No 4	2e-39		
Matches 168	Conservative 96	Mismatches 205	Indels 126	Gaps 28	

```

0Y 34 IIDEYGOIKGVKMMYVDDSDYSEFESIPAKPVGELKRAQORVPYMGV-----R 86
Db 5 IIAIKNGVVRBM-MLYPEGVITVAFELGIPAAQPPILGRKKKQOSLTKWSDIMNAIKRYAN 63
QY 87 DCCGPNRBSV-----QDTFISGKPTGSEDCLYLVNTYNDLPDKRBPVNFHG 135
Db 64 SCCQNIQGSFPGFHGSEMMNNTDL-----SEDCILYVNWJIPAPKP-KNATVLLIWIYG 115
QY 136 GDFIFGEENRMMFEGDPYFMK-KPVLVLYQYRGLVGGLFSLKSBNLNVPGNACLKQOYMA 194
Db 116 GGFQGTGSSLHYVDOGKFLARERVIYVSMNRGVALGFLALPG-NPEAPGNMGLJFDQOLA 174
QY 195 LRMVXSNTAIFGSDVDNTTVEGASGASTHYMTIQTGTLFPRGIMGSMGMSWAST 254
Db 175 LQWQKNTAAAGGNKSYTLTEGASGASYSLLHLSGSHSLTRAILQSGSFENAPMAT 234
QY 255 ---ECOSRALIMARKVYGKGDENKDLLEFLMKANPDLKKEEPOVY---TPERMONKVM 308
Db 235 SLYEKRNTTLMNAKTGCSRE-NETEITIKCLRNDDPEILLNEFVVPYGT-----LS 287
QY 309 FPFGEYVERPYOTADCVBPKPIREMYKKSAMGNSIPTLIGNTSYBGL-----LSKS-- 357
Db 288 VNFGEYVGDLELTD-MEDLILELGOE---KKTQILGVNKNDEGTAFUYGAGFGFSDDN 342
QY 358 ---VAKQYREYVKEL-----ESCV-NVYPEWELADSEBSAETLEBRAIYKKAHVGD 404
Db 343 SLITRKEFOEGSLKTFPGVSESGESILFHTDN-----VDD 379
QY 405 ETPTLDNME---LCSYFVLFPMHRELOLFMHTAGTPILYLRFPDSEELINPYRIM 460
Db 380 QNR--ENVRREALGDVGVGNICFALPETK-KFSDM-GNNAFFYFHEBRSSKILPWEPM- 434
QY 461 RFGRCVKGVSNADELTYLFWMILSKRLPKRE-YKILER-----MVCINTERATTIKPY 514
Db 435 -----GVMHQYLEIEFYF-----GLPLERDRNVTAEELLSRSIYKRNANFEKYGPN 481
QY 515 SNDIAGMENTLMDPIKKSDDVYKCLINDELDKVLWDPEMDKIKOGASIFDCKEL 569
Db 482 ETQ---NNSTSPVYKSTEQKTYLLNT-ESRIRMTKRLAQOGRWTSFEPKYLEM 532

```

```

RESULT 11
US-09-748-739A-8
: Sequence 8, Application US/09748739A
: Patent No. US20020119489A1
:
GENERAL INFORMATION:
:
APPLICANT: Lockridge, Oksena
:
APPLICANT: Watkins, Jeffrey D.
:
TITLE OF INVENTION: Butyrylcholinesterase Variants and
:
FILE REFERENCE: P-IX 4143
:
CURRENT APPLICATION NUMBER: US/09/748,739A
:
CURRENT FILING DATE: 2000-12-06
:
NUMBER OF SEQ ID NOS: 31
:
SOFTWARE: fastseq for Windows Version 4.0
:
SEQ ID NO 8
:
LENGTH: 574
:
TYPE: PRT
:
ORGANISM: Artificial Sequence
:
FEATURE:
:
OTHER INFORMATION: Human Butyrylcholinesterase variant
US-09-748-739A-8

```

Best Local Similarity 28.0%; Pred. No. 6.5e-39;  
Matches 166; Conservative 97; Mismatches 209; Indels 120; Gaps 27;

```

OY 34 IIDFEYQIKVKKMYADSDSYSFESIIPAKPVPVGLERKAFORVPMEGV-----R 86
Db 5 IIAIKNGKVRQM-NLIVYFGGTVAFLGIPYAPORPLRLGRKKRQOSLTKMSDLMNATKAN 63
OY 87 DCCGPANRSY-----QTFDISGRPTGSEDCLYLVNTYNDLNPDKRRPYVFI 135
Db 64 SCCONIDQSPFGHGFSEMMNPNDL-----SEDCGLYLWVWIPAPKP-KNATVLIWIG 115
OY 136 GDFLIFGEANRWBPDXFMK-KPVVLTVYORLGVGLFSKSENLNVGSGNAGLKQOYWA 194
Db 116 GGFOTGTSILVHYGKFLARERYIVVSMKIRGALGFLALPG-NPEARQNGMLFPQOLA 174
OY 195 LRWKSNIAIFGQDVNITVYFGEBSAGASTHYMIMITEQTRGLPHRGIMNSGMSMAST 254
Db 175 LQWVQKNIAAGGNPKSVTLFEGESAGAAVSLHLLSPGSHSLFTRALDQGSFNAPAVT 234
OY 255 --ECQSALTMARVYKGGEDNEKDLLEFLMKANPYDLIKEEPQVLTPERMOKKMYFP 311
Db 235 SLYEARNRITLAKLTGCSRE-NETEELIKLRNKDPQELILNAFAFVP--YQTSLSVNF 290
OY 312 GPVPEPYTACVCPKPIRENVKAMGNSIPTLLIGNSYEGL-----LSKS----- 357
Db 291 GPVYDGDFLTP-MPDLILLELQGF--KTQIILVGNKDDGTAFPLYVYAGBGSFKNDSII 345
OY 358 VAKQPEPVVKEL-----ESCV-NYVWELADSERAPETLERAAIVKKAHVDGETP 407
Db 346 TRKEPQDEBLKTFPFGVSEFQGESLILPHYTDW-----YDQSRP 382
OY 408 TLDNME---LCSFYFLPMMHFFLQRENNHAGPIYILRPDPDSEELINPYRIMRGG 463
Db 383 --ENYREALGDVVDYNNICPALEFTK-KFSEW-GNNAFYYEFEHRSKLPMPEMM---- 434
OY 464 RGVGVSHADDELTYLFWMLSKRLPKRSRE-YKTIER----WVGITFEATGKRPYND 517
Db 435 ---GVMGTLELYF-----GLPLERDRYTAEBELLSRSIVKRRANAKKGNINETO 484
OY 518 IAGMENLITWDEPIKRSDDVYKCLNIGDELKYMDLPENDKIKOGASIEDKKEL 569
Db 485 ---NNSTSWPVFKSTPEOKYLTILNP-ESTRIIMTKLRAAOCCRFMTSFFPKVLEM 532

RESULT 12
US-09-748-739A-19
: Sequence 19, Application US/09748739A
: Patent No. US20020119489A1
: GENERAL INFORMATION:
: APPLICANT: Lockridge, Oksana
: APPLICANT: Watkins, Jeffrey D.
: TITLE OF INVENTION: Butyrylcholinesterase Variants and
: TITLE OF INVENTION: Methods of use
: FILE REFERENCE: P-IX 4143
: CURRENT APPLICATION NUMBER: US/09/748,739A
: CURRENT FILING DATE: 2000-12-06
: NUMBER OF SEQ ID NOS: 31
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 19
: LENGTH: 574
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-748-739A-19

```

```

RESULT 12
US-09-748-739A-19
; Sequence 19, Application US/09748739A
; Patent No. US00020119489A1
; GENERAL INFORMATION:
; APPLICANT: Lockridge, Oksana
; APPLICANT: Watkins, Jeffry D.
; TITLE OF INVENTION: Butyrylcholinesterase Variants and
; TITLE OF INVENTION: Methods of Use
; FILE REFERENCE: P-IX 4143
; CURRENT APPLICATION NUMBER: US/09/748,739A
; CURRENT FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 574
; TYPE: prt
; ORGANISM: Homo sapiens
US-09-748-739A-19

```

```

Qy      87 DCCGPAHSV-----QTDFISKPPGSGEDCLYNTYDMLDPKRRPMPVFIHG 135
Db      5 IATNGKVRGH-NLTVEGTYATLGIPIYAPPLGLRFRFKPGSLRKWSDIMNMTKYAN 63
Qy      34 IIDTSGOIKGKRMRTYYDDSYSPESIPYAKPVGELFRFAPORVPVMEGV-----R 86
          ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Best Local Similarity 28.2%; Score No. 1e-38; DB 10; Length 574;
Query Match 16.7%; Score 509; Mismatches 205; Indels 126; Gaps
Matches 168; Conservative 96;

```

```

Db      64  SCCQNTDQSPGPGHSEMMNPNTDL-----SEDCLYLNTVTPAKP- KNAITVIMWIG 115
Qy      136  GDFIEGEANRMWGPDPYEMK-KPVVLVTVQYRLVGLFSLKSENLNVNGAGLQDVYA 194
      116  GGGTQTSLSLHYDDGFLARVERIVVSMNYRGALGFLALPG-NPEARGNMGLEPDOLA 174
Qy      195  LRMVKSNTIAFEGGDVNTIVFGESAGASTHYMMITEQRLGFHRGIMMSGMSKMAST 254
      175  LQWVQKNIAFAGNPKSVTLFGESAGASVSLHLSPGHSLFTRAILLOSGSFMAWAVT 234
Qy      255  ---ECOSRALTMARKVYSGEDNEKIDLEFLMKANPYDLKEEPVYL---TPERMQNKYM 308
      235  SLYEANRRLNLAKLTGCSRE-NETETIKCLRKPQDELLNEAFVYPTG-LS 287
Qy      309  FPGPTVEPYQTADCVVPRKIREMVSAMGNSIPTLIGNTSYEGL-----LSKS-- 357
      288  VNFPGPTVDGFLTD-MPDLLELGOF---KKTOLLVGNKDEGTAFLVYGAPGFSKDN 342
Qy      358  ---VAKOYPEVVKEL-----ESCV-NYVPWELADERSAPETLERAIYKKAHVDG 404
      343  SITTRKREFDGLKIFPPGVSEKESILFHYTD-----VDD 379
Qy      405  EPTPLDNFME---LCSYEFILPMHRFLOLRFNHTAGTPILYLRPDESEIINDYRIM 460
      380  QRP--ENYREALGDVYGDVNFICPALEFTR-KPSEW-GNNAFPYFPHRSSKLPMEEM- 434
Qy      461  RFGRGVKGVSADLELYLLENILSKRLPKESRE-YKTIER---VVGWTEPATITGKPY 514
      435  ---GVNHGEIEFV---GLPLERRDNYTRAELIISRSIVKRAKNAKYGNN 481
Qy      515  SNDIAGMENTWPIKSDVYKCLNIGDELKWDPEMDKIKOGASIEDKKEL'569
      482  ETQ---NNSISWVFKSTVQKYLTLNT-ESTRIMTKLRQOQCFMWSFFPKVLEM 532

```

```

RESULT 13
US-09-748-739A-23
; Sequence 23, Application US/09748739A
; Patent No. US20020119489A1
; GENERAL INFORMATION:
; APPLICANT: Lockridge, Oksana
; TITLE OF INVENTION: Butyrylcholinesterase Variants and
; FILE REFERENCE: P-IX 4143
; CURRENT APPLICATION NUMBER: US/09/748,739A
; CURRENT FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Rattus sp.
US-09-748-739A-23

```

```

Query Match      16.7%; Score 508.5; DB 10; Length 574;
Best Local Similarity 28.9%; Pred. No. 1,1e-38;
Matches 159; Conservative 97; Mismatches 206; Indels 89; Gaps 23;

```

```

Qy      31  ETQIIDTEYGOIKGVKRMVYDDSYSESIYKAPPVGELREKAPORPVWEGVRDCG 90
      111  : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      2  EDVITITTKGVRGLS-MPIIGTVAFLGIPYAQPLGRLFKKPOPLNKMPDYNAIK 60
Qy      91  PANSVQ-----TDFISKRPFGSDCLYLTNDLNPKRRPVWFIHGDFI 139
      111  : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      61  YANSCYQNDQSPGPGHSEMMNPNTDLSEDCLYLNTVTPAKP-KNAITVIMWIGGDF 119
Qy      140  FGEANRMWGPDPYEMK-KPVVLVTVQYRLVGLFSLKSENLNVNGAGLQDVYA 198
      120  TGTSSLPYDDGFLARVERIVVSMNYRGALGFLALPG-NSEARGNMGLEPDOLA 178
Qy      199  KSNIAIFEGGDVNTIVFGESAGASTHYMMITEQRLGFHRGIMMSGMSMA---STE 255

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      239  ARNRITLAKFIGC-SKENETIITCLSKDPQELINELKVLPSDSIRS--INFGPTV 294
Qy      316  EPYQTADCVVPRKIREMVSAMGNSIPTLIGNTSYEGL-----SKSAKQYPEV- 366
      295  DGDFLTD-MHTLLOLQKVT-----QLVGNKDEGTAFLVYGAPGFSKDNLSLTR 347
Qy      367  KELESCVN-----YVPWELADERSAPETLERAIYKKAHVDGEPITL 409
      348  REFQGLNMWPPGVSSLGKEALILEYVDW-LGD---QTPPE---YREAFFD---II 393
Qy      410  DNFMELCSYFFELPMHRFLOLRFNHTAGTPILYLRPDESEIINDYRIMRFGVGYK 469
      394  GYNTICPALE-TRKFALEIN-----AFIYFPHRSSKLPMEEM-----GV 436
Qy      470  SHADELYLFWNLISKRLPKESREYKTIERNVGIWTEPATITGKPYSDIAGMENLWDP 529
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Qy      530  KKSDDVYKCLN 540
      494  TSTEQKYLTLN 504

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RESULT 14
US-09-748-739A-22
; Sequence 22, Application US/09748739A
; Patent No. US20020119489A1
; GENERAL INFORMATION:
; APPLICANT: Lockridge, Oksana
; TITLE OF INVENTION: Butyrylcholinesterase Variants and
; FILE REFERENCE: P-IX 4143
; CURRENT APPLICATION NUMBER: US/09/748,739A
; CURRENT FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Felis catus
US-09-748-739A-22

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Best Local Similarity 27.9%; Pred. No. 5e-38;
Matches 153; Conservative 99; Mismatches 212; Indels 85; Gaps 21;

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      111  : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      61  YANSCYQNDQSPGPGHSEMMNPNTDLSEDCLYLNTVTPAKP-KNAITVIMWIGGDF 119
Qy      140  FGEANRMWGPDPYEMK-KPVVLVTVQYRLVGLFSLKSENLNVNGAGLQDVYA 198
      120  TGTSSLPYDDGFLARVERIVVSMNYRGALGFLALPG-NSEARGNMGLEPDOLA 178
Qy      199  KSNIAIFEGGDVNTIVFGESAGASTHYMMITEQRLGFHRGIMMSGMSMA---STE 255
      179  QKNIAAFGNGPKSVTLFGESAGASVSLHLSPRQPLFTRAILLOSGSNAPAWAVIDE 238
Qy      256  COSRALTMARKVYSGEDNEKIDLEFLMKANPYDLKEEPVYLTPERMQNKYMPPGPTV 315
      239  AKNRITLAKFIGC-SKENDTEIICLRKNDPQELINELNLVVPDITL---LSVNFQPV 294
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Db 295 D-----GDFLTDMF-DTLLQLGQFKKTQILVGVNKKDEGTAFLVYGAGFGFKNDNSITRKE 349
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Db 350 FQEGKITYFPGVSEFGREALEFYVDLDDORA-----EKYREALDDVLDGDN 397
QY 414 ELCSYFELFPMHREFLQLRNFHTAGTPILYLRFPDSEELINPYRIMRGVGVSHAD 473
Db 398 IICPLALEF---TTKSEL-----GNAFFYTFEHRSSQLPPEWM-----GYMHCY 440
QY 474 ELTYLFWNLISRLPKRESREYKTIERMGWTEFATGKPYNDIAGMEN--LTWDPICK 531
Db 441 ELTFEFGJLERRVYVTRAEEILSRIMYMANFAKYNP-----NGTQNNSTRMPEAFRS 495
QY 532 SDDVYKCLN 540
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## RESULT 15

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US-10-102-806-689
: Sequence 689, Application US/10102806
: Publication No. US20030054421A1
: GENERAL INFORMATION:
: APPLICANT: Rosen et al.
: TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
: FILE REFERENCE: PA103P1C1
: CURRENT APPLICATION NUMBER: US/10/102,806
: CURRENT FILING DATE: 2002-03-22
: PRIOR APPLICATION NUMBER: 09/925,298
: PRIOR FILING DATE: 2001-08-10
: PRIOR APPLICATION NUMBER: PCT/US00/05881
: PRIOR FILING DATE: 2000-03-08
: PRIOR APPLICATION NUMBER: 60/124,270
: PRIOR FILING DATE: 1999-03-12
: NUMBER OF SEQ.ID NOS: 846
: SOFTWARE: PatentIn Ver. 2.0
: SEQ.ID NO 689
: LENGTH: 549
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: SITE
: LOCATION: (1)
: OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
: NAME/KEY: SITE
: LOCATION: (7)
: OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
US-10-102-806-689

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Query Match 16.4%; Score 500; DB 9; Length 549;
Best Local Similarity 29.1%; Pred. No. 6,4e-38;
Matches 161; Conservative 88; Mismatches 203; Indels 102; Gaps 22;

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Db 86 LQDLTAVESSEFLSQFNMTPSDSMSSEDLVLYSTTPAHSHGSLNPVWVWTHGGLVPGM 145
QY 143 ANRMWPGPDYFMKKPVLYVQYRLGYGLSLKSENINPQANGLKQDVNALLRWKSN 202
Db 146 ASL-YDGSMLAALENVVYVYIQRIGVIGFPPS--TGDKHATGNMGYLDQVAALRWQONI 202
QY 203 AIFGADVNTIVFGEAGASTHYMITEOTRGLEFHGIMSGMCSW-----251
Db 203 AHFGGNDRYTIRESAGGTSVSLVSPISQGLFHGAINESGVALDGLTIASSADVI 262
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QY 364 EYVKELESCVNYVPMELADSESAPELTERAAIVKAAH--DGETPTLD-NPELECSYFY 420
Db 348 DTQKEMDREASQAALQKMLTLMLPPTF--GDILREYTGDNQDPQTLOAQFOEMWADSM 405
QY 421 FLFPMHREFLQLRNFHTAGTPILYLRFPDSEELIN--PYRIMRGVGVSHADELY 477
Db 406 FVIPA--LQVAHFQCSRAPVYFEEQHPMSLKNIRPH-----MKADHGDELPE 453
QY 478 LFWNLISRLPKRESREYKTIER-AVGWTEFATGKPYNDIAGMENLTWDPICKSDVY 536
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QY 537 KCLN-----IGDELK 546
Db 508 LQNLQPAVGRALK 521

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Search completed: April 4, 2003, 09:34:03
Job time : 25.5753 secs

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GenCore version 5.1.4.p5\_4578  
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OM nucleic - nucleic search, using sw model

Run on: April 10, 2003, 22:59:47 ; Search time 2938.87 Seconds

(without alignments) 16933.650 Million cell updates/sec

Title: US-09-776-910-14

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Sequence: 1 atgacttcctgaagcaatt.....ataaagaaggaattgttt 1710

Scoring table:

IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:\*  
1: gb\_da:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
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6: gb\_pat:\*  
7: gb\_ph:\*  
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10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*  
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17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
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22: em\_ov:\*  
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24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_sts:\*  
28: em\_un:\*  
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37: em\_htg\_vrt:\*  
38: em\_sy:\*  
39: em\_htgo\_hum:\*  
40: em\_htgo\_mus:\*  
41: em\_htgo\_other:\*

Score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	1657.4	96.9	2160	3	ARI133341
3	956.6	55.9	1713	6	AR062837
4	956.6	55.9	1713	6	ARI53438
5	956.6	55.9	1713	6	ARI53441
6	956.6	55.9	1713	6	ARI53442
7	956.6	55.9	2240	3	LCU56636
8	955	55.8	1713	6	ARI53439
9	953.4	55.8	2175	3	AF139082
10	952.2	55.7	1713	6	AR062838
11	951.8	55.7	1713	6	ARI53440
12	646.6	37.8	2017	3	AY051473
13	353.2	20.7	2122	3	AY058637
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16	349.4	20.4	57335	2	AC015272
17	349.4	20.4	188459	3	AC008312
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19	349.4	20.4	309023	3	AE003671
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## ALIGNMENTS

RESULT 1  
LOCUS ARI53445  
DEFINITION Sequence 14 from patent US 6235515.  
ACCESSION ARI53445  
VERSION ARI53445.1 GI:15120977  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 1710)  
AUTHORS Russell, R. Joyce., Newcomb, R. David., Campbell, P. Malcolm.,  
Robin, G. Charlesde, Queterville., Claudianos, C., Smyth, K. A.,  
Boyce, T. Mark., Oakeshott, J. Graham. and Brownlie, J. Colin.  
TITLE Malathion carboxylesterase

Pred. No. is the number of results predicted by chance to have a







QY	584	TGAGATGGGTCAAAGATATATGGCATTTTCGGGGGAGATGACAAATATTACGCTC	643
Db	584	TGCGTGGATTAAANATATATGGCCAACTTTGGGGCAATCCGATATTTACACTC	643
QY	644	TGCGCAAAAGTCTGTGGGGCTTCAACCCATTACATGATATTAACGACAGCCGCTG	703
Db	644	TTGGTGAAGTCCGGTGGCTGCTTACCACATGATGATTTTAACGAAACAACTCGC	703
QY	704	GTATTATTCATGCTGTATCATGATGTCGGTAATTGCATGTGCTCATGGGCTCTACG	763
Db	704	GTCTTTTCATGTGTATCTAATTAATGTCGGTAATGCTATTTTGTCATGGGCTAATACC	763
QY	764	AATGCCAAAGTGTGCGCTCACATATGGCCAAACGCTGTGGCTATTAAGAGAGACATG	823
Db	764	AATGTCAACATGTGCTCTTCACTACCTTAAGCAATTTGGCCGCTAATAAGGTGAGATATG	823
QY	824	AAAAAGATATCTGGAATTCCTAATGAAGCAATCCCTATGATTTGATCAAGAGAGAGC	883
Db	824	ATTAAGAGATGTTTGGAAATTTCTTATGAAGGCCAAGCCACAGATTTTAATAAACTTGAG	883
QY	884	CACAGTTTTCACCCGCAAGAAATGCAAAATTAAGTATGATTTCCCTTTGGACCACTG	943
Db	884	AAAAAGTTTAACTGTAGAAGAGCGTACAAATTAAGTCAATGTTTCTTTGGTCCACTG	943
QY	944	TAGAACCATTACCAGACAGCCGACTGTGTGTGTAACCCAAACCAATCAGAGAAATGTGAGA	1000
Db	944	TTGAGCCATATCAGACCCGCTATTTGTGCTTACCACAAACATCTCGGGAAATGTGTAAA	1000
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Db	1004	CTGCTTGGGGTAATTCGATACCACACTATGATGGGTAACACTTATATGAGGGCTATTTT	1060
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QY	1124	ATGAGCCTTGGGAGTTGGCTGACAGTAAACGCACTGCCCGGAACCTGTGAGAGGGCTG	1180
Db	1124	TTTGCCCAAGTAATGGCTGATGCTGTAAACGACCGCCGACGAGACCTTGGAATGGGTG	1180
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QY	1364	ACCCTATCGTATATGCGTTTTGGCCGCGCTTTAAAGGTGAAGCCATGCGCATGAGC	1420
Db	1364	ATCCCTATCGAATTAATGCGTAGTGACGAGCGGTGTTAAGGTGTTATGCTATGATAT	1420
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QY	1484	AAACCAATTAAGCATATGACGTATGATATGATATGATATTTGGCACCCTGTAATCTTATTA	1540
Db	1484	AAACCAATTAAGCATATGACGTATATGATATGATATTTGGCACCCTGTAATCTTATTA	1540
QY	1544	GCAATGATATAGCCGCGATGAAAAACCTCACCTGGGATTCCTAATAAAATATCCATGATG	1600
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Db	1124	TTGTGCTCAAGTAATTTGGGTGATGTTGAAGCAAGCAAGCGCCCAAGAACCTTGAAATGGGTG	1183
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Db	1364	AACCTATCGTATTTATGCGTATGGAACGGTGGTAAAGGTATGTCATGTCGATGAAT	1423
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QY	1484	AAACCATTTGAACGATGTTGGCATTTTGAGCGGAATTCGCCACCAACCGGCAAAACATACA	1543
Db	1484	AAACCATTTGAAGATGTAATGCTGTAATATGATTCATATTTCCACCTCGTATACCTTTATA	1543
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JOURNAL Insect Mol. Biol. 5 (3), 211-216 (1996)  
 MEDLINE 96392952  
 PUBMED 8799740  
 REFERENCE 2 (bases 1 to 2240)  
 AUTHORS Newcomb, R.D., Campbell, P.M., Russell, R.J. and Oakeshott, J.G.  
 TITLE cDNA cloning, baculovirus-expression and kinetic properties of the esterase, E3, involved in organophosphorus resistance in *Lucilia cuprina*

JOURNAL Insect Biochem. Mol. Biol. 27 (1), 15-25 (1997)  
 MEDLINE 97215578  
 PUBMED 9061925  
 REFERENCE 3 (bases 1 to 2240)  
 AUTHORS Newcomb, R.D., Campbell, P.M., Ollis, D.L., Cheah, E., Russell, R.J. and Oakeshott, J.G.  
 TITLE A single amino acid substitution converts a carboxylesterase to an organophosphorus hydrolase and confers insecticide resistance on a blowfly

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 94 (14), 7464-7468 (1997)  
 MEDLINE 97352821  
 PUBMED 9207114  
 REFERENCE 4 (bases 1 to 2240)  
 AUTHORS Campbell, P.M., Newcomb, R.D., Russell, R.J. and Oakeshott, J.G.  
 TITLE Two different amino acid substitutions in the allele-esterase, E3, confer alternative types of organophosphorus insecticide resistance in the sheep blowfly

JOURNAL Unpublished  
 REFERENCE 5 (bases 1 to 2240)  
 AUTHORS Newcomb, R.D., Campbell, P.M., Russell, R.J. and Oakeshott, J.G.  
 TITLE Direct Submission  
 JOURNAL Submitted (24-Apr-1996) Richard D. Newcomb, Molecular Genetics, HortResearch, Private Bag 92 169, Auckland, New Zealand

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 809..1369  
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BASE COUNT 740 a 357 c 417 g 726 t

ORIGIN

Query Match 55.9%; Score 956.6; DB 3; Length 2240;  
 Best Local Similarity 73.4%; Pred. No. 3..9e-270;  
 Matches 1223; Conservative 0; Mismatches 444; Indels 0; Gaps 0;

QY 44 TTAATGCGATGCGCAATAAATACCAACATACCGTGTGATACAAATGAACCAATATA 103  
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 Db 341 TTAATGCGATGCAAAATAGCTTTTAACTATGCTTAACCTACCAATGAACGGGTGAG 400

QY 104 TCGATGATGATATGACAAATTAAGGCTGTTAAGCAATGACCGTCTACGATATCTT 163  
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 Db 401 CTGAAGTGAATATGCAAAAGTGAAGCGCTTAAGCTTAACCTGATGATGATGATTCCT 460

QY 164 ACTACGTTTCGAGATATACCTGATGATGATGATGATGATGATGATGATGATGATGAT 223  
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 Db 461 ACTACGTTTGAAGGATATACCGTACCGCCACCGCGAGGCTGAGCTGAGCTGATTAAG 520

QY 224 CACCCGAGCGCGCTGCAACATGAGGAGGTGATGATGATGATGATGATGATGATGATGAT 283  
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QY 344 ATGCTGTACCATGATGATTAACCCAGCAAAAGCGCTCTGTTATGCTTATCATCATG 403  
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 Db 641 GTGCTATGAGAAATTAATCTAAATCCGAAATCAAGCTCCGCTTTATGATATCATCAAG 700

QY 404 GCGGAGATTTTATTTTGGGGAAGCAAAATGCTAAGTGTGCTGCTCCGCACTACTTATGA 463  
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 Db 701 GTGCTGTTTATTTATGCGTGAAGAAATCATGCTATATGATGCTGCTGATTTATTA 760

QY 464 AGAAACCCGTGCTTGTGTAACCGTGAATGTTTGGGTGTGTTGCTTCCCTAGCC 523  
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QY 644 TCGGCGAAGTGTGCTGCGGCTCAACCATTAATGATGATGATGATGATGATGATGATGAT 703  
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 Db 1001 GTCTTTCAATGCTGATATCATATGTCCTGCTGATATTCATATGCTGATGCTGCTGAT 1060

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QY 824 AAAAGATTCCTGATATCTAATGAAGCAATCCCTGATGATGATGATGATGATGATGATGAT 883  
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 Db 1121 ATAAAGATGTTTGAATTTCTTATGAAGCAAGCAAGATGATTAATAAATCTTGAAG 1180

QY 884 CACAAGTTTGAACCCGAAGATCAAAATTAAGTATGTTTCTTCTTCTTCTTCTTCTTCTTCT 943  
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 Db 1901 TCTATTAATGTTTAAATTCGCGATGATGAAAGTATGATGATGATGATGATGATG 1960  
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 Db 1961 AGATTAACATTTGGCAATGATGATGATGATGATGATGATGATGATGATGATGATG 2007

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 LOCUS AR153439  
 DEFINITION Sequence 3 from patent US 6235515.  
 ACCESSION AR153439  
 VERSION AR153439.1 GI:15120971  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 1713)  
 AUTHORS Russell, R. Joyce, Newcomb, R. David, Campbell, P. Malcolim, Robin, G. Charlesde, Queteville, Claudianos, C., Smyth, K. A., Boyce, T. Mark, Oakeshott, J. Graham, and Brownlie, J. Colin.  
 TITLE JOURNAL Malation carboxylesterase  
 FEATURES Patent: US 6235515-A 3 22-MAY-2001;  
 Location/Qualifiers  
 1..1713

BASE COUNT 515 a 306 c 370 g 522 t  
 ORIGIN  
 Query Match 55.8%; Score 955; DB 6; Length 1713;  
 Best Local Similarity 73.3%; Pred. No. 1.1e-269;  
 Matches 1222; Conservative 0; Mismatches 445; Indels 0; Gaps 0;

Oy 44 TTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 103  
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RESULT 9
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DEFINITION cds.
ACCESSION AF139082
VERSION AF139082.1 GI:6502938
KEYWORDS
SOURCE
ORGANISM Haematobia irritans irritans.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Muscoidea; Muscidae; Haematobia.
REFERENCE
1 (bases 1 to 2175)
AUTHORS Guerrero, F.D.
TITLE Cloning of a horn fly cDNA, Halpnae7, encoding an esterase whose
transcript concentration is elevated in diazinon-resistant flies
JOURNAL Insect Biochem. Mol. Biol. 30 (11), 1107-1115 (2000)
MEDLINE 20445807
PUBMED 10989298
REFERENCE
2 (bases 1 to 2175)
AUTHORS Guerrero, F.D.
TITLE Direct Submission
JOURNAL Submitted (30-MAR-1999) USDA-ARS, Knippling-Bushland U.S. Livestock
Insects Research Laboratory, 2700 Fredericksburg Rd., Kerrville, TX

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282..1994
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BASE COUNT 690 a 365 c 435 g 685 t
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Query Match 55.8%; Score 953.4; DB 3; Length 2175;
Best Local Similarity 73.2%; Pred. No. 3.4e-269;
Matches 1221; Conservative 0; Mismatches 446; Indels 0; Gaps 0:
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Db 325 TTAAGTGTGTAATAATTAATTTAAACCTATTAACCAAGAAACCAATATG 384
Oy 104 TCGATACGATATGAGCAATTTAAGGTTGTAAGCAATGACCGTACGATGATCTT 163
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Oy 164 ACTACAGTTTGGAGATATACCTATGCTTAAGCCTCGAGTGGTGAATTCAGT 223
Db 445 TCTACAGTTTGGAGATATACCTATGCTTAAGCCTCGAGTGGTGAATTCAGT 504
Oy 224 CACCCAGCGGCTGTACATGGAGGCTGACGTGATTTGCTGTGGCCAGCCACAGAT 283
Db 505 CTCCACAAACGTCCTGCTTGGATGAGTGAAGATTTGTTCATGATGCTCCCGT 564
Oy 284 CGGTACAGAGATTTTCAATTAAGTGGCAACCCACAGATTCGAGATTTCTATACCT 343
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Oy 344 ATGTGATACCAATGACTTGAACCCAGACAAAGCGCTGTTATGCTTCAATCATG 403
Db 625 ATGTGATACCAATGACTTGAATTAATTAATGATACCAACGCTCCGTTTGTTCATG 684
Oy 404 GCGAGATTTTATTTTGGCGCAACCAATGCTAATGTTTGTTCGCGACCTACTTGA 463
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Oy 464 AGAATCCGCTGCTTGGTACCTGCAATTCCTTTGGGTGTGTGGTTTCTTATGCC 523
Db 745 AGAAGAGCTTGTCTTCAATCTGCAATTCCTTTAGGGGTGTGTGGTTTCTTATG 804
Oy 524 TGAATCGAAATCTCAATGCTCCCGCAACGCTGACCTTCAGATCAAGTATGCGCT 583
Db 805 TAAATTCGAAATCTCAATGCTGATGCTGCTTAAAGATCAAGTATGCGCT 864

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Unit	Score	Query Match	Length	DB	ID	Description
1	1095	100.0	570	18	AAW17768	Malathion carboxy
2	1090	99.5	570	18	AAW17766	Malathion carboxy
3	1089	99.5	570	16	AAW81812	Op-sensitive ester
4	1089	99.5	570	18	AAW17765	l $\alpha$ -lpha-E7 malath
5	819	74.8	570	18	AAW17767	Drosophila melano
6	812.5	74.2	572	22	ABBS7850	Drosophila melano
7	653.5	59.7	567	22	ABBS7857	Drosophila melano
8	610	55.7	552	22	ABBS7866	Drosophila melano
9	591	54.0	572	22	ABBS7867	Drosophila melano
10	590	53.9	530	22	ABBS7868	Drosophila melano

11	578	52.8	555	22	ABB57746	Drosophila melano
12	573	52.3	554	22	ABB59161	Drosophila melano
13	561	51.2	542	22	ABB57790	Drosophila melano
14	546.5	49.9	566	22	ABB61983	Drosophila melano
15	530.5	48.4	602	23	AAAM47598	Drosophila cell c
16	499.5	45.6	541	22	ABB57789	Drosophila melano
17	498	45.5	568	22	ABB57831	Drosophila melano
18	496.5	45.3	513	19	AAAM57863	C. felis esteraze
19	466.5	45.3	528	19	AAAM57862	C. felis esteraze
20	466.5	45.3	528	22	AAE12916	Ctenocephalides f
21	470	42.9	551	22	AAE12911	Drosophila melano
22	434	39.6	551	22	AAAM57788	C. felis esteraze
23	434	39.6	530	19	AAAM57866	C. felis esteraze
24	432	39.5	495	19	AAAM57869	C. felis esteraze
25	432	39.5	530	19	AAAM57855	C. felis esteraze
26	432	39.5	530	19	AAAM57877	Ctenocephalides f
27	432	39.5	530	22	AAE12911	Ctenocephalides f
28	432	39.5	550	22	AAAM57853	C. felis esteraze
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34	429	39.2	550	19	AAAM57864	Ctenocephalides f
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37	426.5	38.9	527	22	AAE12923	Ctenocephalides f
38	413.5	37.8	527	22	AAE12923	Ctenocephalides f
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40	397.5	36.3	555	23	ABAB64915	Drosophila melano
41	393.5	35.9	584	23	ABAB64708	Drosophila melano
42	391.5	35.8	570	19	AAAM78676	C. felis esteraze
43	391.5	35.8	570	19	AAAM78677	C. felis esteraze
44	391.5	35.8	570	22	AAAM78678	Ctenocephalides f
45	391.5	35.8	570	22	AAE12913	C. felis esteraze
			596	19	AAAM78656	C. felis esteraze

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RESULT 1
AAW17768
ID AAW17768 standard; Protein; 570 AA
YY

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DT	08-AUG-1997	(first entry)
XX		
DE	Malathion carboxylesterase RM8Con.	
XX		
KW	Malathion carboxylesterase; organophosphate; insecticide;	
KW	pesticide; remediation; bioremediation; decontamination; est	
KW	Lucilia cuprina.	
XX		
OS	Lucilia cuprina.	
XX		
PN	WO9719176-A1.	
XX		
PD	29-MAY-1997.	
XX		
PF	22-NOV-1996; 96WO-AU00746.	
XX		
PR	23-NOV-1995; 95AU-0006751.	
XX		
PA	(CSTR ) COMMONWEALTH SCI & IND RES ORG.	
XX		
PI	Boyce T, Brownlie JC, Campbell PM, Ciaudianos C;	
PI	Newcomb RD, Oakeshott JG, Robin GC, Russell RJ, Smyth K;	
DR	WPI: 1997-298113/27.	
XX		
PT	DNA encoding enzyme that degrades organophosphate pesticides .	
PT	useful for decontamination of soil, water, food etc	

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XX
PS Claim 6; Fig 1; 52bp; English.
CC A malathion carboxylesterase (AAW17768), designated RM-8Con, differs
CC from the esterase (AAW17765) of a malathion susceptible clone of
CC Lucilia cuprina by a substn. of the tryptophan residue at amino
CC acid position 251 by a leucine residue. This mutation from the active
CC site of the active site gorge, 6.5 Angstroms from the active
CC site serine. The RM8Con amino acid sequence is a consensus deduced
CC from the DNA sequences of 3 resistant clones (RM8 A-C) and their
CC comparison to the reference susceptible clone Lc743 (AA168596) of
CC Lc-alpha-E7. The enzyme is capable of hydrolysing carboxylester
CC and/or dimethylloxon organophosphates and can be formulated for use
CC in bioremediation strategies for treatment of soil or water.
XX
SQ Sequence 570 AA;
XX
Query Match 100.0%; Score 1095; DB 18; Length 570;
Best Local Similarity 100.0%; Pred. No. 1.2e-116; Indels 0; Gaps 0;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 QVDFITGKVGSEDCILSVYTNLNPETKRPVLYIHGGFTIGENHRDMYGPDYFIKK 60
DB 97 QVDFITGKVGSEDCILSVYTNLNPETKRPVLYIHGGFTIGENHRDMYGPDYFIKK 156
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DB 157 DVLINIOYRLGALGFLSLNSEDLVNPGNAGLKQOVALRWIKNNCANFGNPDNITVFG 216
OY 121 ESAGASTHYMMLTEQRTGFLHRIILMSGNAICPLANTQCOHRAFTLAKLAGYGEDNDK 180
DB 217 ESAGASTHYMMLTEQRTGFLHRIILMSGNAICPLANTQCOHRAFTLAKLAGYGEDNDK 276
OY 181 DYLEFLMKAKPDLIKLEKVTLEER 207
DB 277 DYLEFLMKAKPDLIKLEKVTLEER 303
XX
RESULT 2
AAW17766
ID AAW17766 standard; Protein; 570 AA.
XX
AC AAW17766;
XX
DT 08-AUG-1997 (first entry)
XX
DE Malathion carboxylesterase.
XX
KW Malathion carboxylesterase; organophosphate; insecticide;
KW pesticide; remediation; bioremediation; decontamination; esterase;
KW Lucilia cuprina.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT MISC-difference 251 /label= Leu, Ser, Ala, Ile, Val, Thr, Cys, Met, Gly
ET /note= "pref. Leu or Ser."
XX
XX WO9719176-A1.
XX
XX 29-MAY-1997.
XX
XX 22-NOV-1996; 96WO-AU00746.
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XX 23-NOV-1995; 95AU-0006751.
XX
XX (CSIR ) COMMONWEALTH SCI & IND RES ORG.
XX
XX Boyce T, Brownlie JC, Campbell PM, Claudianos C;
XX Newcomb RD, Oakeshott JG, Robin GC, Russell RJ, Smyth K;
XX WPI, 1997-298113/27.
XX

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XX
PS DNA encoding enzyme that degrades organophosphate pesticides -
XX useful for decontamination of soil, water, food etc
XX
XX Claim 1; Fig 1; 52bp; English.
CC A malathion carboxylesterase (AAW17766) differs from the esterase
CC (AAW17765) of a malathion susceptible clone of Lucilia cuprina by
CC a substn. of the tryptophan residue at amino acid position 251.
CC The enzyme is capable of hydrolysing carboxylester and/or
CC dimethylloxon organophosphates and can be formulated for use in
CC bioremediation strategies for treating soil or water.
XX
SQ Sequence 570 AA;
XX
Query Match 99.5%; Score 1090; DB 18; Length 570;
Best Local Similarity 99.5%; Pred. No. 4.4e-116; Indels 1; Gaps 0;
Matches 206; Conservative 0; Mismatches 1; Indels 1; Gaps 0;
OY 1 QVDFITGKVGSEDCILSVYTNLNPETKRPVLYIHGGFTIGENHRDMYGPDYFIKK 60
DB 97 QVDFITGKVGSEDCILSVYTNLNPETKRPVLYIHGGFTIGENHRDMYGPDYFIKK 156
OY 61 DVLINIOYRLGALGFLSLNSEDLVNPGNAGLKQOVALRWIKNNCANFGNPDNITVFG 120
DB 157 DVLINIOYRLGALGFLSLNSEDLVNPGNAGLKQOVALRWIKNNCANFGNPDNITVFG 216
OY 121 ESAGASTHYMMLTEQRTGFLHRIILMSGNAICPLANTQCOHRAFTLAKLAGYGEDNDK 180
DB 217 ESAGASTHYMMLTEQRTGFLHRIILMSGNAICPXANTQCOHRAFTLAKLAGYGEDNDK 276
OY 181 DYLEFLMKAKPDLIKLEKVTLEER 207
DB 277 DYLEFLMKAKPDLIKLEKVTLEER 303
XX
RESULT 3
AAR78142
ID AAR78142 standard; Protein; 570 AA.
XX
AC AAR78142;
XX
DT 22-DEC-1995 (first entry)
XX
DE OP-sensitive esterase E3.
XX
KW Esterase; E3; bioremediation; organophosphate; carbamate;
KW insecticide; pesticide; water decontamination; meat decontamination.
XX
OS Lucilia cuprina.
XX
XX WO9519440-A1.
XX
XX 20-JUL-1995.
XX
XX 13-JAN-1995; 95WO-AU00016.
XX
XX 13-JAN-1994; 94AU-0003347.
XX
XX (CSIR ) COMMONWEALTH SCI & IND RES ORG.
XX
XX Boyce TM, Campbell PM, Newcomb RD, Oakeshott JG;
XX Parker AG, Robin GC, Russell RJ, Smyth K;
XX WPI, 1995-263870/34.
XX
XX N-P-SDB; AAQ91561.
XX
XX Pure E3 esterase from Lucilia cuprina and related DNA - used to
XX eliminate residues of organo:phosphate and carbamate pesticides from
XX water, meat etc.
XX
XX Example 3; Page 12-17; 38pp; English.
XX

```

CC cDNA from organophosphate (OP)-sensitive *L. cuprina* pupa cDNA  
 CC library was amplified using cluster-specific esterase primers.  
 CC Isolated clone Lc743, a probable full-length cDNA, was expressed  
 CC using a baculovirus vector in insect cells and shown to encode  
 CC an OP-susceptible E3 esterase useful in bioremediation.

XX Sequence 570 AA:

Query Match 99.5%; Score 1089; DB 16; Length 570;  
 Best Local Similarity 99.5%; Pred. No. 5, 7e-116;  
 Matches 206; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QVPEITGKVGSEDCILSYVTNNLNPETRKPYLYIHGGFIIIGENHDMGPDYFIKK 60  
 DB 97 QVPEITGKVGSEDCILSYVTNNLNPETRKPYLYIHGGFIIIGENHDMGPDYFIKK 156  
 QY 61 DVLINIQYRIGALGFLSLNSEDLPNGANGKDOYMAIRKNNCANFGNPDNITVFG 120  
 DB 157 DVLINIQYRIGALGFLSLNSEDLPNGANGKDOYMAIRKNNCANFGNPDNITVFG 216  
 QY 121 ESAGASTHYWMLTEQRTGLFHRGILMSGNAICPLANTOCOHRAFTLAKLAGYKGEDNDK 180  
 DB 217 ESAGASTHYWMLTEQRTGLFHRGILMSGNAICPMANTOCOHRAFTLAKLAGYKGEDNDK 276  
 QY 181 DVEFLMKAKPQDLIKLEKVLTEER 207  
 DB 277 DVEFLMKAKPQDLIKLEKVLTEER 303

RESULT 4  
 AAM17765  
 ID AAM17765 standard; Protein: 570 AA.

XX AAM17765;

DT 08-AUG-1997 (first entry)

DE Lc-alpha-E7 malathion susceptible clone Lc743 esterase E3.

KW Malathion carboxylesterase; organophosphate; insecticide;

XX pesticide; remediation; bioremediation; decontamination; esterase.

OS *Lucilia cuprina*.

XX Key Location/Qualifiers

FT Misc-difference 251 /note= "amino acid 251 is Leu in resistant

FT mutants"

XX WO9719176-A1.

XX 29-MAY-1997.

XX 22-NOV-1996; 96WO-AU00746.

XX 23-NOV-1995; 95AU-0006751.

XX (CSIR ) COMMONWEALTH SCI & IND RES ORG.

XX Boyce T, Brownlie JC, Campbell PM, Claudianos C; Smyth K;

XX Newcomb RD, Oakeshott JG, Robin GC, Russell RJ, Smyth K;

XX WPI: 1997-298113/27.

XX N-PSDB; AAT68596.

XX DNA encoding enzyme that degrades organophosphate pesticides -

XX useful for decontamination of soil, water, food etc

XX Disclosure; Fig 1; 52pp; English.

XX Esterase E3 (AAM17765) from a malathion susceptible strain of

XX *Lucilia cuprina* differs from an esterase enzyme (see also

XX AAM17768) from malathion resistant RM8 strains by a Trp for Leu

CC substn. at amino acid position 251, owing to a mutation in the  
 CC encoding DNA sequence (see also AAT68596). The resistant enzyme,  
 CC termed malathion carboxylesterase, can be formulated for use in  
 CC degrading environmental carboxylester or dimethyl general  
 CC organophosphates.

XX Sequence 570 AA:

Query Match 99.5%; Score 1089; DB 18; Length 570;  
 Best Local Similarity 99.5%; Pred. No. 5, 7e-116;  
 Matches 206; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QVPEITGKVGSEDCILSYVTNNLNPETRKPYLYIHGGFIIIGENHDMGPDYFIKK 60  
 DB 97 QVPEITGKVGSEDCILSYVTNNLNPETRKPYLYIHGGFIIIGENHDMGPDYFIKK 156  
 QY 61 DVLINIQYRIGALGFLSLNSEDLPNGANGKDOYMAIRKNNCANFGNPDNITVFG 120  
 DB 157 DVLINIQYRIGALGFLSLNSEDLPNGANGKDOYMAIRKNNCANFGNPDNITVFG 216  
 QY 121 ESAGASTHYWMLTEQRTGLFHRGILMSGNAICPLANTOCOHRAFTLAKLAGYKGEDNDK 180  
 DB 217 ESAGASTHYWMLTEQRTGLFHRGILMSGNAICPMANTOCOHRAFTLAKLAGYKGEDNDK 276  
 QY 181 DVEFLMKAKPQDLIKLEKVLTEER 207  
 DB 277 DVEFLMKAKPQDLIKLEKVLTEER 303

RESULT 5  
 AAM17767  
 ID AAM17767 standard; Protein: 570 AA.

XX AAM17767;

DT 08-AUG-1997 (first entry)

DE Md-alpha-E7 malathion resistant mutant.

KW Malathion carboxylesterase; organophosphate; insecticide;

XX pesticide; remediation; bioremediation; decontamination.

OS *Musca domestica* Rutgers strain.

XX Key Location/Qualifiers

FT Misc-difference 251 /note= "Ser-251 is tryptophan in the susceptible

FT allele expression product"

XX WO9719176-A1.

XX 29-MAY-1997.

XX 22-NOV-1996; 96WO-AU00746.

XX 23-NOV-1995; 95AU-0006751.

XX (CSIR ) COMMONWEALTH SCI & IND RES ORG.

XX Boyce T, Brownlie JC, Campbell PM, Claudianos C; Smyth K;

XX Newcomb RD, Oakeshott JG, Robin GC, Russell RJ, Smyth K;

XX WPI: 1997-298113/27.

XX N-PSDB; AAT68597.

XX DNA encoding enzyme that degrades organophosphate pesticides -

XX useful for decontamination of soil, water, food etc

XX Disclosure; Fig 3; 52pp; English.

XX A polypeptide (AAM17767) is the expression product of a malathion

XX resistant allele of the *Musca domestica* Md-alpha-E7 gene, and

XX contains a Ser for Trp substn. at amino acid position 251. The

CC enzyme is capable of hydrolysing carboxylester and/or  
CC dimethylloxon organophosphates and can be formulated for use  
CC in bioremediation strategies for treatment of soil or water  
XX  
SQ Sequence 570 AA;

Query Match	74.8%;	Score 819;	DB 18;	Length 570;
Best Local Similarity	73.7%;	Pred. No. 6.1e-85;		
Matches 151;	Conservative 27;	Mismatches 27;	Indels 0;	Gaps 0;

QY	1	QVDFINQKCGSDECDLTYSVTNNLNEPTRLRPVLVYTHGGGFLIGNHMDMTGPDYFTKK	60
		: : : : :   : : : : :   : : : : :   : : : : :   : : : : :	
Db	97	QIDFISGKRTGSGEDDLTANVTINDLNDPKRRPVPWVFHGGDFIFGEANFMNMGPDYFMKK	156
QY	61	DVVLINIOYRIGALGATLSINSEDLNTPGNGAGLKDQWALRMKRNKNCANFGGPDITVFG	120
		: : : : :   : : : : :   : : : : :   : : : : :   : : : : :	
Db	157	PVVLVYQYRGLGVLGSLTSKSENLTNPVGNGAGLKDQWALRMKRNKNAIFGGVNDITVFG	216
QY	121	ESAGGASTHYMMLTBQTRGLFHRGILMSGNAICPLANTOCQHRAPFTLKLAKYGGEDNDK	180
		: : : : :   : : : : :   : : : : :   : : : : :   : : : : :	
Db	217	ESAGGASTHYMMITBQTRGLFHRGILMSGNSMCSASTECQSRALTLMKRNRYGGEDNEK	276
QY	181	DVLEFLMKRAKPDILKLEEKVLTE	205
		: : : : :   : : : : :   : : : : :	
Db	277	DILFEFLMKANPYDLKKEPVLVPE	301

RESULT 6  
ABB57850

ABBS/850 standard; Protein; 572 AA.

AC ABB57850;

26-MAR-2002 (first entry)

Protophila melanogaster polypeptide SEQ ID NO 342.

pharmaceutical.

*Drosophila melanogaster*.

PN WO200171042-A2

PD 27-SEP-2001.

23-MAR-2001; 2001WO-US09231

PR 23-MAR-2000; 2000US-191637P,  
11-TUE-2000 6:11PM

11-JUL-2000; 200000S-0614150.  
PK  
XY

(PEKE) PE CORP NY.

Venter JC, Adams M, Li PWD, Myers EW;

DR: WPL; 2001-656860/75.  
DB: N-DCDD; 2001-656860/75.

DK N-PSDB; ABL01953.  
XX

genes from *Drosophila* and for elucidating cell signalling and cell-cell interactions -

Disclosure; SEQ ID NO 342; 21pp + Sequence Listing; English.

The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from *Drosophila*. The invention is useful in experimental biology and in elucidating cell signaling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (AB116175-AB110511), expressed DNA sequences (AB101840-AB116175) and the encoded proteins (AB057737-AB072072).

CC specification, but was obtained in electronic format directly from WIPO  
CC at [ftp.wipo.int/pub/published\\_pct\\_sequences](http://wipo.int/pub/published_pct_sequences).  
XX

Query Match	74.28;	Score 812.5;	DB 23;	Length 572;
Best Local Similarity	73.18;	Pred. No. 3.4e-84;		
Matches 152;	Conservative 26;	Mismatches 29;	Indels 1;	Gaps 1;

[illegible]

RESULT 7  
ABB57857

ABBB/83/ standard; 567 AA.

AC ABB57857

DI 20-MAR-2002 (first entry)  
XX

XX  
XX

Protophila metallinogaster polypeptide seq ID NO 363

pharmaceutical.

*Drosophila melanogaster*.

PN WO200171042-A2  
XY

27-SEP-2001

23-MAR-2001; 2001WO-US09231.

23-MAR-2000; 200005-191637P.  
11-MAR-2000; 200005-191415P.  
BR

11-JUL-2000; 2000005-0614150.

(FENE) PE CORP NY

venlter uc, adams m, li pmd, myers ew;

WFL; 2001-656860/15;  
N-PSDB: APT 019650

IN FOLD; ABLVLT900

genes from *Drosophila* and for elucidating cell signalling and cell-cell interactions -

disclosure; SEQ ID NO 363; ZIPP + Sequence Listing; English.

The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from *Drosophila*. The invention is useful in developmental biology and in elucidating cell signaling and cellular interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (AB161576-AB130511), expressed DNA (AB57725-AB57728) and the encoded proteins (the *serpin* and *ABP*2072).







Query Match	49.9%	Score 546.5;	DB 22;	Length 566;
Best Local Similarity	50.5%;	Pred. No. 1.2e-53;		
Matches 105; Conservative	36;	Mismatches 66;	Indels 1;	Gaps 1

The present invention relates to *Drosophila* cell cycle progression proteins (AAW47572-AAW47608) and their coding sequences (AB90366-AB90520). The coding sequences and proteins are useful for identifying a substance capable of affecting the function of the corresponding gene, a substance capable of inhibiting the cell division cycle, or capable of inhibiting mitosis and/or meiosis. They can also be used in a method for treating a tumour or proliferative disorder, cardiovascular disorders (such as restenosis and cardiomyopathy), autoimmune disorders such as (glomerulonephritis and rheumatoid arthritis), dermatological disorders (such as psoriasis), antinflammatory, antifungal and antiparasitic disorders (such as malaria).

Query Match	48.48;	Score 530.5;	DB 23;	Length 602;
Best Local Similarity	49.58;	Pred. No. 9.3e-52;		
Matches 99;	Conservative 38;	Mismatches 54;	Indels 9;	Gaps 1

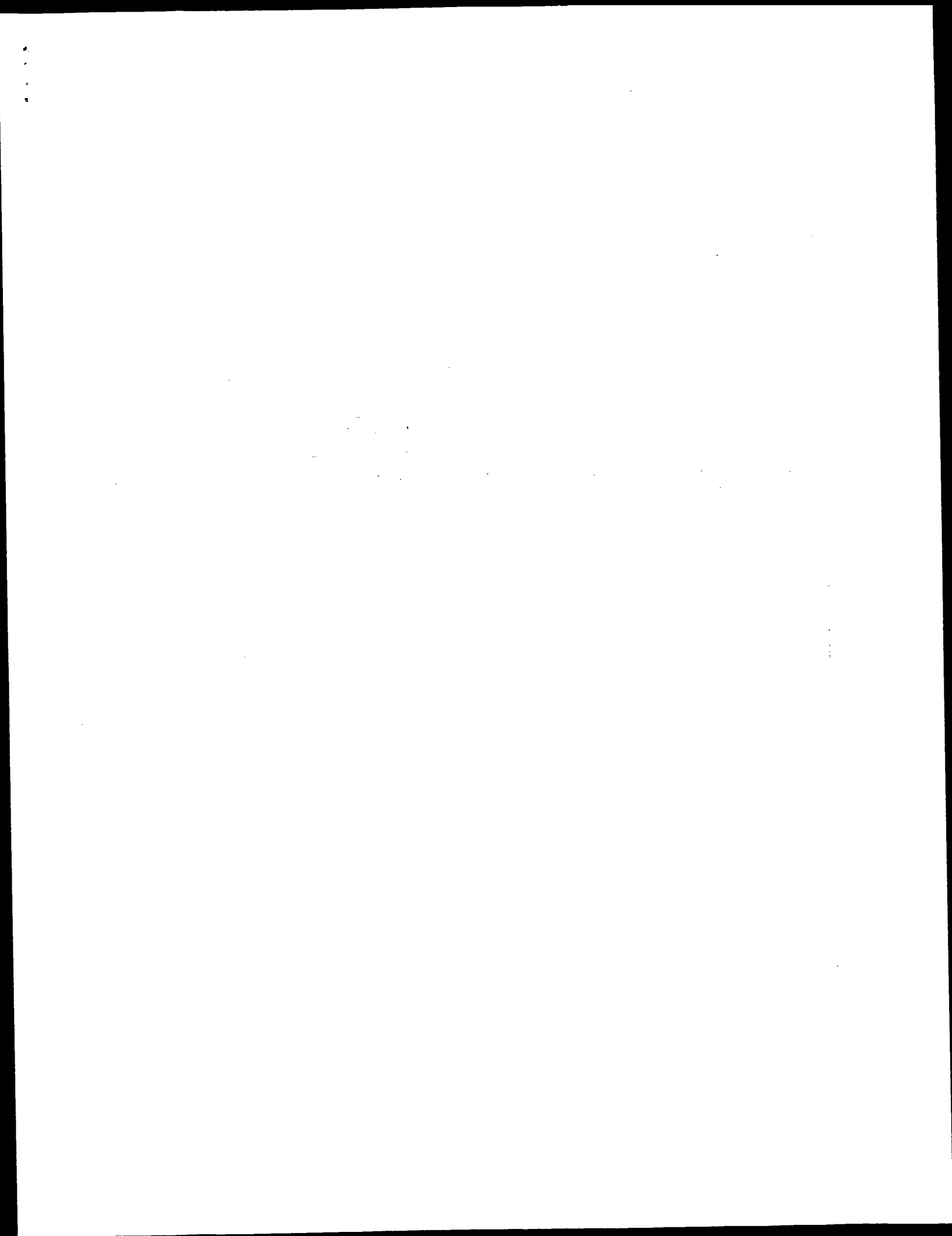


```

OY      8 KVGSEDCIYLSVYTNLNPETKRPVLYYIHGGFTIGENHRDMGPDYFIKKDVLINI 67
Db      150 KYAGSEDCIYLVYKVDLPDKLRPVWMIYGGGYOVGEASRGL-----DVIYTV 200
OY      68 QYRLGALGFLSUNSEDLNVPNGAGLKDQYVALRWIKNNCANFGNPDNITVFGESAGAAS 127
Db      201 AYRLGALGFLSLDDPOLNVPNGAGLKDQIMALRWYQONIEAFGDSNNTITLFGESAGAS 260
OY      128 THVMMLTEOTRGIFHRGILMSGNAICPLANTOCQHRATFLAKLAGYKGEENDKDYLEFLM 187
Db      261 THFLALSPOTEGILHAIWMSGSVLCPTQPPRNWYRLAQKIGYTGDNKDKATFEFLR 320
OY      188 KAKPODLIKLEKVLTLER 207
Db      321 SMSGEIYKATATVLSNDEK 340

```

Search completed: April 4, 2003, 09:13:06  
 Job time : 17.9846 secs



GenCore version 5.1.4.p5.4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 4, 2003, 09:10:33 ; Search time 6.92664 Seconds  
(without alignments)  
2872.940 Million cell updates/sec

Title: US-09-776-910-43

Perfect score: 1095  
Sequence: 1 QVDFITGKVGSGEDCLYLSV.....KAKPDLIKLEKVLLEER 207

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: PIR\_73:\*  
2: PIR1:\*  
3: PIR2:\*  
4: PIR3:\*  
5: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	483	44.1	540	2 A35986	esterase B1 - sout
2	475	43.4	540	2 S53370	carboxylesterase (
3	464	42.4	503	2 S53372	carboxylesterase (
4	463	42.3	540	2 S53371	carboxylesterase (
5	395	36.1	564	2 A34325	juvenile-hormone e
6	373	34.1	583	2 S10712	acetylcholinestera
7	370	33.8	614	2 A39256	acetylcholinestera
8	365	33.5	596	1 ACRYE	acetylcholinestera
9	366	33.4	614	2 JH0811	acetylcholinestera
10	365	33.4	564	2 S36787	carboxylesterase (
11	364	33.3	599	1 A38868	acetylcholinestera
12	362	33.1	614	2 JH0314	acetylcholinestera
13	358	32.7	584	2 S48724	acetylcholinestera
14	357	32.6	552	2 S36786	carboxylesterase (
15	356	32.6	603	2 S70849	carboxylesterase (
16	353	32.3	602	1 ACHU	cholinesterase (EC
17	349	31.9	544	2 B34089	carboxylesterase (EC
18	348	31.8	767	2 S47639	acetylcholinestera
19	347	31.7	547	2 S55233	juvenile hormone e
20	346	31.6	545	2 S58972	carboxylesterase (
21	345	31.6	545	2 S58980	carboxylesterase (
22	345	31.6	581	2 C39768	cholinesterase (EC
23	344	31.5	545	2 S58978	carboxylesterase (
24	344	31.5	545	2 S58970	carboxylesterase (
25	344	31.5	545	2 S58975	carboxylesterase (
26	344	31.5	545	2 S58982	carboxylesterase (
27	344	31.5	545	2 S58983	carboxylesterase (
28	344	31.5	545	2 S58977	carboxylesterase (
29	344	31.5	545	2 S58973	carboxylesterase (

30	344.5	31.5	612	2 A34967	sterol esterase (E
31	343.5	31.4	545	2 S58976	carboxylesterase (
32	343	31.3	548	2 T32907	hypothetical prote
33	343	31.3	599	2 A57701	sterol esterase (E
34	342.5	31.3	545	2 S58979	carboxylesterase (
35	341.5	31.2	545	2 S58969	carboxylesterase (
36	341.5	31.2	545	2 S58981	carboxylesterase (
37	340.5	31.1	545	2 S58974	carboxylesterase (
38	340.5	31.1	545	2 S58968	carboxylesterase (
39	337	30.8	544	2 A34089	carboxylesterase (
40	337	30.8	544	2 C41426	carboxylesterase (
41	337	30.8	544	2 A41426	carboxylesterase (
42	337	30.8	544	2 B40122	carboxylesterase (
43	337	30.8	548	2 A28022	carboxylesterase (
44	336	30.7	544	2 A40122	carboxylesterase (
45	335.5	30.6	545	2 S58971	carboxylesterase (

#### ALIGNMENTS

##### RESULT 1

A35986  
esterase B1 - southern house mosquito

C:Species: Culex pipiens quinquefasciatus (southern house mosquito)

C>Date: 16-Nov-1990 #sequence\_revision 13-Jan-1993 #text\_change 21-Jul-2000

C/Accession: A35986

R/Kouches, C.; Pauplin, Y.; Agarwal, M.; Lemieux, L.; Herzog, M.; Abdon, M.; Beyssat

Proc. Natl. Acad. Sci. U.S.A. 87, 2574-2578, 1990

A>Title: Characterization of amplification core and esterase B1 gene responsible for

A:Reference number: A35986; MWID:90207238; PMID:2320576

A:Accession: A35986

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-540 <MOU>

A/Cross-references: GB:M32328; NID:9156687; PIDN:AA28289.1; PID:9156688

A>Note: the authors translated the codon CGT for residue 213 as Ala, and CGT for resi

C:Superfamily: cholinesterase; cholinesterase homology

Query Match 44.1%; Score 483; DB 2; Length 540;

Best Local Similarity 44.9%; Pred. No. 6.4e-38;

Matches 88; Conservative 45; Mismatches 63; Indels 0; Gaps 0;

QY 8 KVCSEEDCLVLYVNNINPEKRPVLYIHGGFTIIGENHRMDYGPDIKKVLLINI 67

Db 77 KIYCEESLKIINWFAKINPSTPLPVLVLYGGFTGTEGLGDPFLVQKDIYVSP 136

QY 68 QYRIGALGFLVNSDINVPNGNLKQDVALLKRNKNCNNGNDNITVFESGGAAS 127

Db 137 NYRIGALGFLVCOSEDDGVPNGNLKQDNLIRWVLEINIAAFGDPKRYTLAHSAGAA 196

QY 128 THYVMLLEQRTGFEHRIIGLSGNALICPLANTCOHRAFTLAKYKGEENDVLEFLM 187

Db 197 VQYHLISDASKDLFQRRIVVSGTYSWSLTKRNMVYERLAKAIGMDGGESGALRFLR 256

QY 188 KAKPDLIKLEKVL 203

Db 257 RAKPDIVAHQEKLT 272

##### RESULT 2

S53370  
carboxylesterase (EC 3.1.1.1) B2 - southern house mosquito

C:Species: Culex pipiens quinquefasciatus (southern house mosquito)

C>Date: 15-Jul-1995 #sequence\_revision 08-Sep-1995 #text\_change 21-Jul-2000

C/Accession: S53370; S44211

R/Vaughan, A.; Rodriguez, M.; Hemingway, J.

Biochem. J. 305, 651-658, 1995

A>Title: The independent gene amplification of electrophoretically indistinguishable

A:Reference number: S53370; MWID:95134253; PMID:7530448

A:Accession: S53370

A:Molecule type: mRNA

A:Residues: 1-540 <VAU>



OY 170 LAGYKEDND 179  
Db 268 LQILGNORD 277

# RESULT 6

10712

acetylcholinesterase (EC 3.1.1.7) - bovine

C:Species: Bos primigenius taurus (cattle)

C>Date: 21-Nov-1993 #sequence\_revision 23-Mar-1995 #text\_change 12-May-1995

C:Accession: S10712; A39734; B39734; B25650

R:Doctor, B.P.; Chapman, T.C.; Christner, C.E.; Deal, C.D.; de la Hoz, D.M.; Gentry, M.K.

FEBS Lett. 266, 123-127, 1990

A:Title: Complete amino acid sequence of fetal bovine serum acetylcholinesterase and its

A:Reference number: S10712; MUID:90306335; PMID:2365060

A:Accession: S10712

A:Molecule type: protein

A:Residues: 1-583 <DOC>

A:Experimental source: fetal serum

R:Roberts, W.L.; Doctor, B.P.; Foster, J.D.; Rosenberry, T.L.

J. Biol. Chem. 266, 7481-7487, 1991

A:Title: Bovine brain acetylcholinesterase primary sequence involved in intersubunit dis

A:Reference number: A39734; MUID:91210255; PMID:2019579

A:Accession: A39734

A:Molecule type: protein

A:Residues: 1-38 <RO>

A:Experimental source: fetal serum

R:Bon, S.; Chang, J.Y.; Strosberg, A.D.

FEBS Lett. 209, 206-212, 1986

A:Title: Identical N-terminal peptide sequences of asymmetric forms and of low-salt-sol

A:Reference number: A91370; MUID:87080761; PMID:3792544

A:Accession: B25650

A:Molecule type: protein

A:Residues: 'XS', 3-12 <BON>

A:Experimental source: caudate nucleus

C:Superfamily: cholinesterase; cholinesterase homology

C:Keywords: carboxylic ester hydrolase; glycoprotein

F:32-538/Domain: cholinesterase homology <CH>

F:61,265,350,464,541/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:203/Active site: Ser #status predicted

Query Match 34.1%; Score 373; DB 2; Length 583;

Best Local Similarity 42.3%; Pred. No. 2, 1e-27;

Matches 85; Conservative 36; Mismatches 72; Indels 8; Gaps 4;

C:Accession: A39256; S03959  
R:Soreq, H.; Ben-Aziz, R.; Prody, C.A.; Seidman, S.; Gnatt, A.; Neville, L.; Lieberman-H  
Proc. Natl. Acad. Sci. U.S.A. 87, 9688-9692, 1990  
A:Title: Molecular cloning and construction of the coding region for human acetylcholin  
A:Reference number: A39256; MUID:91088577; PMID:2263619  
A:Accession: A39256  
A:Molecule type: DNA  
A:Residues: 1-614 <SOR>  
A:Cross-references: GB:M55040; NID:q177974; PIDN:AA68151.1; PID:q177975  
A:Note: this sequence represents composite of clones including clone ABGACHE from adu  
nce should represent an authentic brain splice form  
R:Chajlant, V.; Derr, D.; Charles, B.; Schnell, E.; August, T.  
FEBS Lett. 247, 279-282, 1989  
A:Title: Purification and partial amino acid sequence analysis of human erythrocyte a  
A:Reference number: S03959; MUID:89232136; PMID:2714437  
A:Accession: S03959  
A:Molecule type: protein  
A:Residues: 256-266, 'Y', 268-273; 306-308, 'X', 310-313, 'X', 315-316, 'D', 318-323, 'D', 325-3  
Y', 532-551 <CH>  
A:Experimental source: erythrocytes  
A:Note: this form was a disulfide-linked homodimer  
C:Genetics: YF  
A:Gene: GDB:ACHE; YF  
A:Cross-references: GDB:118746; OMIM:100740  
A:Map position: 7q22-7q22  
C:Superfamily: cholinesterase; cholinesterase homology  
C:Keywords: alternative splicing; carboxylic ester hydrolase; glycoprotein; phosphati  
F:63-559/Domain: cholinesterase homology <CH>

Query Match 33.8%; Score 370; DB 2; Length 614;  
Best Local Similarity 42.3%; Pred. No. 4, 2e-27;  
Matches 85; Conservative 34; Mismatches 74; Indels 8; Gaps 4;

OY 12 SEDCLYVYNNLNPEKRPVLYIHGGFTIGENHRDMGDPYFIKKD-VVLTIOYR 70  
Db 124 SEDCLYVYNNLPYPRPSPVLYIYGGFTIGENHRDMGDPYFIKKD-VVLTIOYR 183  
OY 71 LGALGFLTNSDNLVNGNGLKDVWALRWIKKNCANFGNPNITVFGESGAASSTHY 130  
Db 184 VGAFGLALPG-SREAPGNVGLDRLALQWGVENVAAGGDPSTVTLTGESGAASVGM 242  
OY 131 MMLTEQTRGLFHRGILMSGNAICPLANT--QCQHRATFLAKIAGY--GEDNDKYLE 184  
Db 243 HLSPSPKGLFHRVAVLQSGAPNGPMTVGMGEARRATLALHVGCPGCGNDTEIVA 302  
OY 185 FLMAKAPDILKEKYVLTLE 205  
Db 303 CLRPRADVLVHNEHVLPOE 323

# RESULT 8

ACRE

acetylcholinesterase (EC 3.1.1.7) precursor, 11S form [validated] - Pacific electric

N:Alternate names: acetylcholinesterase, asymmetric form

C:Species: Torpedo californica (Pacific electric ray)

C>Date: 17-Mar-1987 #sequence\_revision 08-Nov-1996 #text\_change 15-Sep-2000

C:Accession: A00773; A60820; A31962; B31962; A23902; B41117; S15677

R:Schumacher, M.; Camp, S.; Mauler, Y.; Newton, M.; Machee-quigley, K.; Taylor, S.S.

Nature 319, 407-409, 1986

A:Title: Primary structure of Torpedo californica acetylcholinesterase deduced from 1

A:Reference number: A00773; MUID:86118676; PMID:3753747

A:Accession: A00773

A:Molecule type: mRNA

A:Residues: 'NS', 11-596 <SCH>

A:Cross-references: GB:X03439; NID:964389

A:Experimental source: electric organ

A:Note: Parts of this sequence, including the amino and carboxyl ends of the mature p  
R:Schumacher, M.; Camp, S.; Mauler, Y.; Newton, M.; Machee-quigley, K.; Taylor, S.S.  
Fed. Proc. 45, 2976-2981, 1986  
A:Title: Primary structure of acetylcholinesterase: implications for regulation and f  
A:Reference number: A60820; MUID:87054662; PMID:3536598  
A:Accession: A60820  
A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA  
 A:Residues: 22-596 <SC2>  
 R:Schumacher, M.; Maulet, Y.; Camp, S.; Taylor, P.  
 J. Biol. Chem. 263, 18979-18987, 1988  
 A:Title: Multiple messenger RNA species give rise to the structural diversity in acetylcholinesterase  
 A:Reference number: A92701; MUID:89066695; PMID:3198606  
 A:Accession: A31962  
 A:Molecule type: mRNA  
 A:Residues: 1-23 <SC3>  
 A:Cross-references: EMBL:X03439; NID:964389  
 A:Experimental source: clones AChE-11 and AChE-18  
 A:Note: revision to sequence A00773  
 A:Accession: B31962  
 A:Molecule type: DNA  
 A:Residues: 499-565 <SC4>  
 A:Cross-references: GB:X03439; NID:964389  
 A:Experimental source: clone AChE-1  
 R:Macphée-Quigley, K.; Taylor, P.; Taylor, S.  
 J. Biol. Chem. 260, 12185-12189, 1985  
 A:Title: Primary structures of the catalytic subunits from two molecular forms of acetylcholinesterase  
 A:Reference number: A23902; MUID:86008285; PMID:3900071  
 A:Accession: A23902  
 A:Molecule type: protein  
 A:Residues: 22, B, 24-45; 214-237 <MAC>  
 A:Note: active site Ser identification  
 R:Kreienkamp, H.J.; Weise, C.; Raba, R.; Aaviksaar, A.; Hucho, F.  
 Proc. Natl. Acad. Sci. U.S.A. 88, 6117-6121, 1991  
 A:Title: Anionic subsites of the catalytic center of acetylcholinesterase from Torpedo  
 A:Reference number: M1117; MUID:91296772; PMID:2068091  
 A:Accession: B4117  
 A:Molecule type: protein  
 A:Residues: 100-108 <KRE>  
 A:Note: substrate binding site  
 R:Maulet, Y.; Camp, S.; Gibney, G.; Rachinsky, T.L.; Ekstrom, T.J.; Taylor, P.  
 Neuron 4, 289-301, 1990  
 A:Title: Single gene encodes glycopospholipid-anchored and asymmetric acetylcholinesterase  
 A:Reference number: PS0113; MUID:90166618; PMID:2306366  
 A:Accession: S15677  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 557-596 <MAN>  
 A:Cross-references: EMBL:X56516  
 R:Macphée-Quigley, K.; Vedvick, T.S.; Taylor, P.; Taylor, S.S.  
 J. Biol. Chem. 261, 13565-13570, 1986  
 A:Title: Profile of the disulfide bonds in acetylcholinesterase.  
 A:Reference number: A43099; MUID:87008586; PMID:3759980  
 A:Contents: annotation: disulfide bonds  
 R:Sussman, J.L.; Harel, M.; Silman, I.  
 submitted to the Brookhaven Protein Data Bank, October 1991  
 A:Reference number: A50061; PDB:1ACE  
 A:Contents: annotation: X-ray crystallography, 2.8 angstroms, residues 26-481, 511-555 of R:Sussman, J.L.; Harel, M.; Frolow, F.; Oefner, C.; Goldman, A.; Tokar, L.; Silman, I.  
 Science 253, 872-879, 1991  
 A:Title: Atomic structure of acetylcholinesterase from Torpedo californica: a prototypic AChE  
 A:Reference number: A43098; MUID:91439328; PMID:1678899  
 A:Contents: annotation: X-ray crystallography, 2.8 angstroms, residues 26-481, 511-555 of C:Comment: Synapses usually contain this 11S (asymmetric) form of cholinesterase with a cholinesterase occurs on the outer surfaces of cell membranes, including those of erythrocytes  
 C:Complex: 11S form is disulfide linked homodimer; 18S form is homotetramer, a dimer of C:Function:  
 A:Description: hydrolyzes acetylcholine to choline and acetate  
 A:Pathway: neurotransmitter degradation  
 C:Superfamily: cholinesterase; cholinesterase homology  
 C:Keywords: alternative splicing; carboxylic ester hydrolase; glycoprotein; membrane protein  
 F:1-21/Domain: signal sequence #status predicted <STC>  
 F:22-596/Product: acetylcholinesterase, 11S form #status experimental <MAT>  
 F:51-551/Domain: cholinesterase homology <CHE>  
 F:80, 478, 554/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F:88-115, 275-286, 423-542/Disulfide bonds: #status experimental  
 F:105/Binding site: substrate (Trp) #status experimental  
 F:221/Active site: Ser #status experimental  
 F:348, 461/Active site: Glu, His #status predicted  
 F:437/Binding site: carbohydrate (Asn) (covalent) #status experimental

F:593/Disulfide bonds: interchain #status experimental  
 Query Match 33.5%; Score 366.5; DB 1; Length 596;  
 Best Local Similarity 40.4%; Pred. No. 8, 8e-27;  
 Matches 80; Conservative 43; Mismatches 68; Indels 7; Gaps 5;  
 QY 12 SEDCLYSLVYTNLNPETRPVLYVTHGGFFLIGENHRDMYGPDPYK-KDVLVLIINOYR 70  
 DB 112 SEDCLYSLVYTNLNPETRPVLYVTHGGFFLIGENHRDMYGPDPYK-KDVLVLIINOYR 170  
 QY 71 LGALGFLSLNSEDLPVGNAGLKDYMALRWIKNNCANFGNPDNTTVGESAGAASTHY 130  
 DB 171 VGFAGFLALHGSQ-EAPGVNGLDQRMALQWVDNLOPFQGPQVTVTFGESAGASVGM 229  
 QY 131 MMLTEQTRGLFHRGILMSGNAICPLANT--TQCHRAFTLAKAGYKGEQNDKDVLEFLM 187  
 DB 230 HILSPGSRDLFRRAILQSSGSPNCMAVSVAEGRRAVELGRNLNC-NLNSDELHCLR 288  
 QY 188 KAKPDILKLEEKVLTLE 205  
 DB 289 EKKPDELIDVENMVLPEFD 306  
 RESULT 9  
 JH0811  
 acetylcholinesterase (EC 3.1.1.7) catalytic chain precursor - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 18-Jun-1999  
 A:Accession: JH0811  
 R:Legay, C.; Bon, S.; Vernier, P.; Cousen, F.; Massoulié, J.  
 J. Neurochem. 60, 337-346, 1993  
 A:Title: Cloning and expression of a rat acetylcholinesterase subunit: generation of A:Reference number: JH0811; MUID:93107932; PMID:8417155  
 A:Accession: JH0811  
 A:Molecule type: mRNA  
 A:Residues: 1-614 <LEG>  
 A:Cross-references: GB:S50879; NID:9262092; PIDN:AAB24586.1; PID:9262093  
 A:Experimental source: striatum  
 C:Comment: This protein is responsible for hydrolysis of acetylcholine at cholinergic C:Superfamily: cholinesterase; cholinesterase homology  
 C:Keywords: carboxylic ester hydrolase; glycoprotein; membrane protein; muscle; nerve  
 F:1-31/Domain: signal sequence #status predicted <STC>  
 F:32-614/Product: acetylcholinesterase catalytic chain #status predicted <MAT>  
 F:63-569/Domain: cholinesterase homology <CHE>  
 F:100-127, 288-303, 440-560/Disulfide bonds: #status predicted  
 F:234, 365, 478/Active site: Ser, Glu, His #status predicted  
 F:296, 381, 495/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 Query Match 33.4%; Score 366; DB 2; Length 614;  
 Best Local Similarity 41.3%; Pred. No. 1e-26;  
 Matches 83; Conservative 35; Mismatches 75; Indels 8; Gaps 4;  
 QY 12 SEDCLYSLVYTNLNPETRPVLYVTHGGFFLIGENHRDMYGPDPYK-KDVLVLIINOYR 70  
 DB 124 SEDCLYSLVYTNLNPETRPVLYVTHGGFFLIGENHRDMYGPDPYK-KDVLVLIINOYR 183  
 QY 71 LGALGFLSLNSEDLPVGNAGLKDYMALRWIKNNCANFGNPDNTTVGESAGAASTHY 130  
 DB 184 VGFAGFLALHGSQ-EAPGVNGLDQRMALQWVDNLOPFQGPQVTVTFGESAGASVGM 242  
 QY 131 MMLTEQTRGLFHRGILMSGNAICPLANT--TQCHRAFTLAKAGYK--GEQNDKDVLE 184  
 DB 243 HILSPGSRDLFRRAILQSSGSPNCMAVSVAEGRRAVELGRNLNC-NLNSDELHCLR 302  
 QY 185 FLMKAKPDILKLEEKVLTLE 205  
 DB 303 CLKTPAQDLVDHEHVLPOE 323  
 RESULT 10  
 S36787  
 carboxylesterase (EC 3.1.1.1) F64 precursor - green peach aphid  
 C:Species: Myzus persicae (green peach aphid)

C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
 C:Accession: S36787  
 R:Field: L.M.; Williamson, M.S.; Moores, G.D.; Devonshire, A.L.  
 Biochem. J. 294, 569-574, 1993  
 A:Title: Cloning and analysis of the esterase genes conferring insecticide resistance in  
 A:Reference number: S36786; MUID:93384534; PMID:8373371  
 A:Accession: S36787  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-564 <FTE>  
 A:Cross-references: EMBL:X74555; NID:9397512; PIDN:CAA52649.1; PID:9397513  
 C:Superfamily: cholinesterase; cholinesterase homology  
 C:Keywords: carboxylic ester hydrolase  
 F:52-552/Domain: cholinesterase homology <CHE>

Query Match 33.4%; Score 365.5; DB 1; Length 564;  
 Best Local Similarity 40.8%; Pred. No. 1e-26;  
 Matches 82; Conservative 42; Mismatches 64; Indels 13; Gaps 8;

OY 2 VDEITG-KVCGSECLVSYVTNNLNPEK----RPVLVYIHGGGFIIGENHRDMYGPDY 56  
 Db 92 IEFSGSKITIQEDCLFNTVTPKLPQNSAGDLMNVYVHGGGYFGES--ILYGFHY 149  
 OY 57 FI-KKDVLIINQYRGLGFLSLNSEDLPVGNAGLKDQVMALEKNNCANFGNPDN 115  
 Db 150 LLDNDPYYVSNIRLSTGLFAS--TGQGVLPNNGLKDQVMALEKNNCANFGNPDN 207  
 OY 116 ITVEGSAAGASTHYMLTEQTRGLFHRGILMSGNAICPLANTQ-COHRATFLAKIAGYK 174  
 Db 208 VITGMSAGASVHNHLLISPMKSGFNRATIQSGSACFCHMSTAEVAKTKTYIANLLGCP 267  
 OY 175 GEDNDKDLVEFLMKAKKPDLL 195  
 Db 268 -TNSVETVECL-RSRPAKAI 286

RESULT 11  
 A38868  
 acetylcholinesterase (EC 3.1.1.7) precursor - marbled electric ray  
 C:Species: Torpedo marmorata (marbled electric ray)  
 C>Date: 23-Apr-1993 #sequence\_revision 15-Nov-1996 #text\_change 11-Jun-1999  
 C:Accession: A38868; A29682; S15696; A25650  
 R:Massoulié, J.; Bon, S.  
 Submitted to the EMBL Data Library, June 1992  
 A:Reference number: A38868  
 A:Accession: A38868  
 A:Molecule type: mRNA  
 A:Residues: 1-599 <MAS>  
 A:Cross-references: EMBL:X05497; NID:964414; PIDN:CAA29047.1; PID:964415  
 R:Storay, J.L.; Krejci, E.; Massoulié, J.  
 EMBO J. 6, 1865-1873, 1987  
 A:Title: cDNA sequences of Torpedo marmorata acetylcholinesterase: primary structure of  
 A:Reference number: A29682; MUID:88004392; PMID:2820709  
 A:Accession: A29682  
 A:Molecule type: mRNA  
 A:Residues: 1-40, 'G', 'A', '228-272', 'G', '274-284', 'E', '286-420', 'N', '422-599' <SIR>  
 A:Cross-references: EMBL:X05497  
 R:Storay, J.L.; Duval, N.; Anselmet, A.; Bon, S.; Krejci, E.; Legay, C.; Osterlund, M.;  
 EMBO J. 7, 2983-2993, 1988  
 A:Title: Complex alternative splicing of acetylcholinesterase transcripts in Torpedo eide  
 A:Reference number: S01293; MUID:89030590; PMID:3181125  
 A:Accession: S15696  
 A:Molecule type: mRNA  
 A:Residues: 526-599 <SIR>  
 A:Cross-references: EMBL:X13172; NID:964416; PIDN:CAA31570.1; PID:964417  
 A:Experimental source: clone pACHE2  
 R:Bon, S.; Chang, Y.Y.; Stroberg, A.D.  
 FEBS Lett. 209, 206-212, 1986  
 A:Title: Identical N-terminal peptide sequences of asymmetric forms and of low-salt-sol  
 inesterase.  
 A:Reference number: A91370; MUID:87080761; PMID:3792544  
 A:Accession: A25650  
 A:Molecule type: protein

A:Residues: 25-40, 'G', '42-47' <BON>  
 C:Genetics:  
 A:Gene: Ache  
 C:Function:  
 A:Description: hydrolyzes acetylcholine to choline and acetate  
 A:Pathway: neurotransmitter degradation  
 C:Superfamily: cholinesterase; cholinesterase homology  
 C:Keywords: alternative splicing; carboxylic ester hydrolase; glycoprotein; neurotran  
 F:1-24/Domain: signal sequence #status predicted <SIG>  
 F:25-599/Product: acetylcholinesterase #status predicted <MAT>  
 F:74-554/Domain: cholinesterase homology <CHE>  
 F:83,440,481,557/Binding site: carbohydrate (asn) (covalent) #status predicted  
 F:91,118,278-289,426-545/Disulfide bonds: #status predicted  
 F:224,351,464/Active site: Ser, Glu, His #status predicted  
 F:596/Disulfide bonds: interchain #status predicted

Query Match 33.3%; Score 364.5; DB 1; Length 599;  
 Best Local Similarity 40.4%; Pred. No. 1.4e-26;  
 Matches 80; Conservative 44; Mismatches 67; Indels 7; Gaps 5;

OY 12 SEDCLVSYVTNNLNPEKRPVLYIHGGGFIIGENHRDMYGPDY-IKKDVLIINQYR 70  
 Db 115 SEDCLVNTWVSPRPS-ATVMLWYGGGFGSSTLDVYNGKTYATEEVVLSLSTR 173  
 OY 71 LGALGFLSLNSEDLPVGNAGLKDQVMALEKNNCANFGNPDNITVEGSAASTHY 130  
 Db 174 VGAFGLALNGSQ-EAPGNGLLDQRRALQWVNDIQFQGGDKTYTLTGESAGRASVGM 232  
 OY 131 MMLTEQTRGLFHRGILMSGNAICPLAN--TQCQHRATFLAKIAGYKGEDNDKDLVEFLM 187  
 Db 233 HILSPGSRDLFRRAILLQSGSPNCPMASVVAEGRRAVELFRRLNLC-NLNSDEDLIOCLR 291  
 OY 188 KAKRPDLIKLEEKVYTLTE 205  
 Db 292 EKKRQELIDVEMVLPED 309

RESULT 12  
 JH0314  
 acetylcholinesterase (EC 3.1.1.7) precursor - mouse  
 C:Species: Mus musculus (house mouse)  
 C>Date: 12-Feb-1993 #sequence\_revision 12-Feb-1993 #text\_change 18-Jun-1999  
 C:Accession: JH0314  
 R:Rechinsky, T.L.; Camp, S.; Li, Y.; Ekstrom, T.J.; Newton, M.; Taylor, P.  
 Neuron 5, 317-327, 1990  
 A:Title: Molecular cloning of mouse acetylcholinesterase: tissue distribution of alte  
 A:Reference number: JH0314; MUID:90380429; PMID:2400605  
 A:Accession: JH0314  
 A:Molecule type: mRNA  
 A:Residues: 1-614 <RAC>  
 A:Cross-references: EMBL:X56518; NID:949844; PIDN:CAA39867.1; PID:949845  
 A:Experimental source: Brain  
 C:Superfamily: cholinesterase; cholinesterase homology  
 C:Keywords: carboxylic ester hydrolase; glycoprotein; membrane protein; muscle; nerve  
 F:1-31/Domain: signal sequence #status predicted <SIG>  
 F:33-614/Product: acetylcholinesterase #status predicted <MAT>  
 F:63-569/Domain: cholinesterase homology <CHE>  
 F:100-127,288-303,440-560/Disulfide bonds: #status predicted  
 F:224/Active site: Ser #status predicted  
 F:296,381,495/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 33.1%; Score 362; DB 2; Length 614;  
 Best Local Similarity 41.3%; Pred. No. 2.4e-26;  
 Matches 83; Conservative 34; Mismatches 76; Indels 8; Gaps 4;

OY 12 SEDCLVSYVTNNLNPEKRPVLYIHGGGFIIGENHRDMYGPDYTK-KDVLIINQYR 70  
 Db 124 SEDCLVNTWVSPRPSPTPIWYIYGGGFGSASLVDYDGRFLAQQVGAVALSMNR 183  
 OY 71 LGALGFLSLNSEDLPVGNAGLKDQVMALEKNNCANFGNPDNITVEGSAASTHY 130  
 Db 184 VGFGLALPQ-SREAPGNGLLDQRRALQWVNDIQFQGGDKTYTLTGESAGRASVGM 242









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OM protein - protein search, using sw model

Run on: April 4, 2003, 09:09:07 ; Search time 3.86293 Seconds  
(without alignments)  
2222.555 Million cell updates/sec

Title: US-09-776-910-43

Perfect score: 1095  
Sequence: 1 QVDFITGKVGSGEDCLYLSV.....KAKPQDLIKLEKVLTEER 207

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database: SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match Length	ID	Description
1	483	44.1	540	EST1_CULPI	P16854 culex pipie
2	390.5	35.7	564	EST1_HELVI	P12992 heliothis v
3	383	35.0	613	ACES_BOVIN	P23795 bos taurus
4	381	34.8	357	CHL1_BRLA	Q95000 branchiosto
5	380	34.7	611	ACES_FELCA	Q62763 felis silve
6	370	33.8	614	ACES_HUMAN	P23203 homo sapien
7	369	33.7	584	ACES_RABIT	Q29499 oryctolagus
8	369	33.7	634	ACES_RABIT	Q94863 brachydanio
9	367	33.5	633	ACES_ELEEL	Q42275 electrophor
10	366.5	33.5	586	ACES_TORCA	P40588 torpedo cal
11	366	33.4	614	ACES_RAT	P31366 rattus norv
12	365.5	33.4	564	EST1_MYRPE	P35502 myzus persi
13	365.5	33.4	581	ACES_BUNFA	Q92035 bungarus fa
14	364.5	33.3	590	ACES_TORMA	P07692 torpedo mar
15	362	33.0	614	ACES_MOUSE	P21836 mus musculu
16	361.5	33.0	574	CHLE_HORSE	P81908 equus cabal
17	357.5	32.6	552	EST1_MOUSE	P35501 myzus persi
18	356.5	32.6	603	CHLE_MOUSE	Q03311 mus musculu
19	353.5	32.3	602	CHLE_HUMAN	P06276 homo sapien
20	349	31.9	544	EST1_DROME	P18167 drosophila
21	348.5	31.8	767	ACES_CHICK	P36196 gallus galli
22	345.5	31.6	581	CHLE_RABIT	P21927 oryctolagus
23	344.5	31.5	545	EST1_DROME	P25726 drosophila
24	344.5	31.5	612	BAL_RAT	P07882 rattus norv
25	343.5	31.4	547	EST1_DROPS	P25727 drosophila
26	343	31.3	599	BAL_MOUSE	Q64285 mus musculu
27	341.5	31.2	545	EST1_DROPS	P25725 drosophila
28	339	31.0	542	EST6_DROMA	P47982 drosophila
29	337	30.8	544	EST6_DROME	P08171 drosophila
30	331.5	30.3	742	BAL_HUMAN	P19835 homo sapien
31	331	30.2	542	EST6_DROSI	Q08662 drosophila
32	327	29.9	629	ACES_LEPDE	Q27677 leptinotars
33	324	29.6	566	EST1_PIG	Q29550 sus scrofa

34	322.5	29.5	565	1	ES10_RAT	P16303 rattus norv
35	321.5	29.4	597	1	BAL_BOVIN	P30122 bos taurus
36	320.5	29.3	338	1	ACES_MYXGL	Q92081 myxine glut
37	319	29.1	489	1	PNBA_BACST	P37967 bacillus su
38	318.5	29.1	532	1	EST2_RABIT	P14943 oryctolagus
39	318.5	29.1	561	1	EST1_MESAU	Q64419 mesocricetu
40	318.5	29.1	567	1	EST1_HUMAN	P23141 homo sapien
41	317.5	29.0	561	1	EST4_RAT	Q64573 rattus norv
42	314	28.7	620	1	ACES_CAEBR	Q27459 caenorhabdi
43	313.5	28.6	337	1	CHL2_BRLA	Q95001 branchiosto
44	313.5	28.6	349	1	EST1_RAT	P10939 rattus norv
45	313	28.6	554	1	ESTM_MOUSE	Q63880 mus musculu

## ALIGNMENTS

RESULT 1	ID	EST1_CULPI	STANDARD	PRT	540 AA.
AC	P16854:				
DT	01-AUG-1990 (Rel. 15, Created)				
DT	01-AUG-1990 (Rel. 15, Last sequence update)				
DT	01-FEB-1994 (Rel. 28, Last annotation update)				
DE	Esterase B1 precursor (EC 3.1.1.1).				
GN	Bl.				
OS	Culex pipiens (House mosquito).				
OC	Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;				
OC	Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;				
OC	Culicoidae; Culex.				
OX	NCBI_TaxID=7175;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=TEM-R;				
RX	MEDLINE=90207238; PubMed=2320576;				
RA	Mouches C., Pauplin Y., Agarwal M., Lemieux L., Herzog M.,				
RA	Abadon M., Baysat-Arnaouty V., Hylien O., de Saint Vincent B.R.,				
RA	Georgiou G.P., Pasteur N.;				
RT	Characterization of amplification core and esterase B1 gene				
RT	responsible for insecticide resistance in Culex.;				
RL	Proc. Natl. Acad. Sci. U.S.A. 87:2574-2578(1990).				
CC	- FUNCTION: OVERPRODUCTION OF NONSPECIFIC ESTERASES IS A COMMON				
CC	MECHANISM OF RESISTANCE TO ORGANOPHOSPHATE INSECTICIDES.				
CC	- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a				
CC	carboxylic anion.				
CC	- MISCELLANEOUS: THERE ARE TWO SUCH ESTERASES: A AND B. ALLELES OF				
CC	BOTH A AND B ARE KNOWN.				
CC	- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
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CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>				
CC	or send an email to <a href="mailto:license@sib-sib.ch">license@sib-sib.ch</a> ).				
CC	-----				
DR	EMBL: M32328; AAA28289.1; -				
DR	PIR: A35986; A35986.				
DR	HSSP: P21836; IMAA.				
DR	InterPro: IPR002018; Carboxylesterase.				
DR	InterPro: IPR000379; Ser_esterase_site.				
DR	Pfam: PF00135; Coesterase_1.				
DR	PROSITE: PS00941; CARBOXYLESTERASE_B_1; 1.				
DR	PROSITE: PS00941; CARBOXYLESTERASE_B_2; FALSE_NEG.				
KW	Hydrolase; Serine esterase; Glycoprotein; Multigene family; Signal.				
FT	SIGNAL	1	540		
FT	CHAIN	?	?		
FT	ACT_SITE	191	191		
FT	ACT_SITE	442	442		
FT	DISULFID	68	81		
FT	CARBOHYD	452	452		
SQ	SEQUENCE	540 AA;	60806 MW;	F73B25B3A7157C95 CRC64;	

Query Match 44.1%; Score 483; DB 1; Length 540;  
 Best Local Similarity 44.9%; Pred. No. 1.6e-37;  
 Matches 88; Conservative 45; Mismatches 63; Indels 0; Gaps 0;

QY 8 KYCGSEDCILYSYNNLNDEPKRVLVYIHGGFTIGENHNDMGDDYFIKKDVLVINT 67  
 1  
 77 KIVCGEDSFKINFAKINPSTPLPYMLYIGGGFTIGETSGTELYGPDPLVQKDIYLVSR 136  
 1  
 QY 68 QYRIGALGFLSUNSEDLNPGNGLKDOYMALWIKNNANPEGNDNTVFEESGAAS 127  
 1  
 DB 137 NTRIGALGFLCCQSEODGVGNAGLKDQNLALRWLENTIAAFGGDKRVLVLACHSAGAS 196  
 1  
 QY 128 THYMLTEQTRGLFHRGILMSGNAICPLANTOCQRAFTLAKYKKGEDNDKVFLEFLM 187  
 1  
 DB 197 VGYHLSDASKDLFORRYIMSSGTSYSSWLTTRNNVETLAKAIGMDGGEGSALRFLR 256  
 1  
 QY 188 KAKPDILKLEKVL 203  
 1  
 DB 257 RAKPEDIVAHQEKLT 272  
 1

RESULT 2  
 ESTD\_HELVY STANDARD; PRT; 564 AA.  
 AC P12992;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE Juvenile hormone esterase precursor (EC 3.1.1.59) (JH esterase).  
 OS Heliothis virescens (Noctuid moth) (Owlet moth).  
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
 OC Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata;  
 OC Ditrysia; Noctuoidea; Noctuidae; Heliothinae; Heliothis.  
 NCBI\_TaxID=7102;  
 RX MEDLINE=89308671; PubMed=2745451;  
 RA Hanzlik T.N., Yehia A.I.A.-A., Harshman L.G., Hammock B.D.;  
 RT "Isolation and sequencing of cDNA clones coding for juvenile hormone  
 esterase from *Heliothis virescens*. Evidence for a catalytic mechanism  
 for the serine carboxylsterases different from that of the serine  
 proteases.";  
 RT J. Biol. Chem. 264:12419-12425(1989).  
 RN [2]  
 RP REVISIONS.  
 RA Hanzlik T.N.;  
 RL Submitted (DEC-1997) to the EMBL/Genbank/DBS databases.  
 CC -I- FUNCTION: JH ESTERASE PLAYS A CRUCIAL ROLE IN THE DECREASE OF  
 JH ACTIVITY IN LEPIDOPTERAN INSECTS, BY HYDROLYZING THE METHYL  
 ESTER OF JH. IT IS ALSO INVOLVED IN THE TRANSPORT OF JH.  
 CC -I- CATALYTIC ACTIVITY: Methyl (2E,6E)-(10R,11S)-10,11-epoxy-3,7,11-  
 trimethyltrideca-2,6-dienolate + H(2)O = (2E,6E)-(10R,11S)-10,11-  
 epoxy-3,7,11-trimethyltrideca-2,6-dienolate + methanol.  
 CC -I- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYL ESTERASE/LIPASE FAMILY.  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC EMBL: J04955; AAB88629.1; -  
 DR PIR: A34325; A34325.  
 DR HSR: P37967; I0E3.  
 DR InterPro: IPR002018; Carboxylesterase.  
 DR InterPro: IPR000379; Ser-estrs\_site.  
 DR Pfam: PF00135; Coesterase\_1.  
 DR PROSITE: PS00122; CARBOXYL ESTERASE\_B\_1; 1.  
 DR PROSITE: PS00941; CARBOXYL ESTERASE\_B\_2; FALSE\_NEG.  
 KW Hydrolase; Serine esterase; Glycoprotein; Signal.

FT SIGNAL 1 19  
 FT CHAIN 20 564  
 FT ACT\_SITE 220 220  
 FT ACT\_SITE 351 351  
 FT ACT\_SITE 465 465  
 FT DISULFID 89 109  
 FT CARBOHYD 81 81  
 FT CARBOHYD 180 180  
 FT CARBOHYD 402 402  
 FT CARBOHYD 515 515  
 FT VARIANT 29 29  
 FT VARIANT 52 52  
 SQ SEQUENCE 564 AA; 62614 MW; D140E5DD91914E8D CRC64;

Query Match 35.7%; Score 390.5; DB 1; Length 564;  
 Best Local Similarity 38.4%; Pred. No. 7.3e-29;  
 Matches 84; Conservative 42; Mismatches 76; Indels 17; Gaps 7;

QY 1 QVDFITGKYCG-----SEDCILYSVY--NNLNDEPKR-----RPLVYIHGGFTIGENHR 49  
 1  
 DB 91 QTVVLGRLMAASEMSEACIYANIHVPMQSL-PRVAGTTPRLRLIVFIHGGGAFPGSGHE 149  
 1  
 QY 50 DMGPDYFIKKDVLVINTQYRIGALGFLSUNSEDLNPGNGLKDOYMALWIKNNCANF 109  
 1  
 DB 150 DLHGPYLVTKNIVITFNVFGLFSMNT--TKIPGNAGHLDQVTLIRVQRAKNE 207  
 1  
 QY 110 GGNPDNITVFGESAGASAHYMLTEQTRGLFHRGILMSGNAICPLANTOCQRAFTLAK 169  
 1  
 DB 208 GGPSPDITTAGSAGASAAHLTLTKATBELFKRALIMSGTSYFTTSPLEAAYISKO 267  
 1  
 QY 170 LAGYKG-EDNKDVLLEFLMKAKPDILKLEKVLTEER 207  
 1  
 DB 268 LQILGINTPEIRHQLIDLPAB--KLINEANAVALIEQ 304  
 1

RESULT 3  
 ACES\_BOVIN STANDARD; PRT; 613 AA.  
 AC P23795; 097579;  
 DT 01-NOV-1991 (Rel. 20, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Acetylcholinesterase precursor (EC 3.1.1.7) (ACHE).  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.  
 RC TISSUE-Kidney;  
 RX MEDLINE=98359754; PubMed=9693127;  
 RA Mendelson I., Korman C., Ariel N., Shaffer A., Velan B.;  
 RT "Bovine acetylcholinesterase: cloning, expression and  
 characterization.";  
 RT Biochem. J. 334:251-259(1998).  
 RN [2]  
 RP SEQUENCE OF 31-613 (ISOFORM H).  
 RC TISSUE-Retal serum;  
 RX MEDLINE=90306335; PubMed=2365060;  
 RA Doctor B.P., Chapman T.C., Christner C.E., Deal C.D., de la Hoz D.M.,  
 RA Gentry M.K., Ogert R.A., Rush R.S., Smyth K.K., Wolfe A.D.;  
 RT "Complete amino acid sequence of fetal bovine serum  
 acetylcholinesterase and its comparison in various regions with other  
 cholinesterases.";  
 RT FEBS Lett. 266:123-127(1990).  
 RL -I- FUNCTION: RAPIDLY HYDROLYZES CHOLINE RELEASED INTO THE SYNAPSE.  
 CC -I- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.  
 CC -I- SUBUNIT: ISOFORM H GENERATES GPI-ANCHORED DIMERS; DISULFIDE  
 LINKED. ISOFORM T GENERATES MULTIPLE STRUCTURES, RANGING FROM  
 MONOMERS AND DIMERS TO COLLAGEN-TAILED AND HYDROPHOBIC-TAILED  
 FORMS, IN WHICH CATALYTIC TETRAMERS ARE ASSOCIATED WITH ANCHORING

CC PROTEINS THAT ATTACH THEM TO THE BASAL LAMINA OR TO CELL  
 CC MEMBRANES. IN THE COLLAGEN-TAILED FORMS, ISOFORM T SUBUNITS ARE  
 CC ASSOCIATED WITH A SPECIFIC COLLAGEN, COL1, WHICH TRIGGERS THE  
 CC FORMATION OF ISOFORM T TRIMERS, FROM MONOMERS AND DIMERS  
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS, H AND T (SHOWN HERE); ARE  
 CC PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: AF061815; AAC64270.1; -  
 DR EMBL: AF061813; AAC64270.1; JOINED.  
 DR EMBL: AF061814; AAC64270.1; JOINED.  
 DR PIR: S10712; S10712.  
 DR HSSP: P22303; ZCUL.  
 DR GlycosylatedB: P23795; -  
 DR InterPro: IPR002018; Carboxylesterase.  
 DR InterPro: IPR000997; Cholinesterase.  
 DR InterPro: IPR000379; Ser-estrs\_site.  
 DR Pfam: PF00135; Coesterase; 1.  
 DR PRINTS: PR00878; CHOLINESTRASE.  
 DR PROSITE: PS00122; CARBOXYLESTERASE\_B.1; 1.  
 DR PROSITE: PS00941; CARBOXYLESTERASE\_B.2; 1.  
 KM Hydrolyase; Serine esterase; Synapse; Membrane; Nerve; Muscle; Signal;  
 KM Neurotransmitter degradation; Glycoprotein; Alternative splicing.  
 FT SIGNAL 1 30  
 FT CHAIN 31 613  
 FT ACT\_SITE 233 233  
 FT ACT\_SITE 364 364  
 FT ACT\_SITE 477 477  
 FT ACT\_SITE 99 126  
 FT DISULFID 287 302  
 FT DISULFID 439 559  
 FT DISULFID 610 610  
 FT CARBOHYD 91 91  
 FT CARBOHYD 295 295  
 FT CARBOHYD 380 380  
 FT CARBOHYD 494 494  
 FT VARSPLIC 574 613  
 FT CONFLICT 46 46  
 FT CONFLICT 169 169  
 FT CONFLICT 212 212  
 FT CONFLICT 323 323  
 FT CONFLICT 352 352  
 FT CONFLICT 424 424  
 FT CONFLICT 524 524  
 FT CONFLICT 549 554  
 FT CONFLICT 571 571  
 SQ SEQUENCE 613 AA; 67663 MW; 698D4F0DF8624B12 CRC64;  
 Query Match 35.0%; Score 383; DB 1; Length 613;  
 Best Local Similarity 42.8%; Pred. No. 4,1e-28;  
 Matches 86; Conservative 35; Mismatches 72; Indels 8; Gaps 4;  
 QY 12 SEDCLYLSYTNMNPETKRPVLYVYHGGFTIGENHRDMYGPDYFKD-VLLINIOYR 70  
 DB 123 SEDCLYLNWVOPSPAP-RGATVLYVWYGGFGFSGLSDYDGRYLARMEDEVVYVSNMR 182  
 QY 71 LGALGFLSLNSEDNLNPNAGLKDQVMAIRKNNKNCANFGNPNITVFGESAGASTHY 130  
 DB 183 VGAFGLTSGE--AAPNAGLIDQHLALQWVQONISFGSDPKYVIFESAGASVNM 241  
 QY 131 MMLTEQRTGLFHRGILMSGNAICPLANT---OCQRAFTLAKLAGYGEQNDKDV-L 186  
 DB 242 HILSPSRGLFHRVAVLQSGAPNGPMAVYGVGARARRATLLAVLVCPPGAGAGNDTEIVA 301

QY 185 FLMAKRPQDLIKLEEVLTLE 205  
 DB 302 CLRARPAQDLVDHEWVLPQE 322  
 RESULT 4  
 CH1L\_BRLA STANDARD; PRT; 357 AA.  
 AC 095000;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Cholinesterase 1 (EC 3.1.1.8) (Fragment).  
 GN CHE1  
 OS Branchiostoma lanceolatum (Common lancelet) (Amphioxus).  
 OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;  
 OC Branchiostoma.  
 OX NCBI\_TaxID=7740;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97216845; PubMed=9062997;  
 RA Sutherland D., McClellan J.S., Milner D., Soong W., Axon N.,  
 RA Sanders M., Hester A., Kao Y.H., Poczarnek T., Rout S.,  
 RA Pezzementi L.;  
 RT "Two cholinesterase activities and genes are present in amphioxus.";  
 RL J. Exp. Zool. 277:213-229(1997).  
 CC -1- CATALYTIC ACTIVITY: An acetylcholine + H(2)O = choline + a  
 CC carboxylic acid anion.  
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: U74378; AAB18262.1; -  
 DR HSSP: P21836; IMAA.  
 DR InterPro: IPR002018; Carboxylesterase.  
 DR InterPro: IPR000379; Ser-estrs\_site.  
 DR Pfam: PF00135; Coesterase; 1.  
 DR PROSITE: PS00122; CARBOXYLESTERASE\_B.1; 1.  
 DR PROSITE: PS00941; CARBOXYLESTERASE\_B.2; 1.  
 KM Hydrolyase; Serine esterase; Glycoprotein; Multigene family.  
 FT NON\_TER 1 1  
 FT ACT\_SITE 112 112  
 FT ACT\_SITE 244 244  
 FT ACT\_SITE 357 357  
 FT DISULFID 166 179  
 FT NON\_TER 357 357  
 SQ SEQUENCE 357 AA; 39462 MW; A2CBDE841704DCDF CRC64;  
 Query Match 34.8%; Score 381; DB 1; Length 357;  
 Best Local Similarity 43.5%; Pred. No. 3.3e-28;  
 Matches 87; Conservative 38; Mismatches 67; Indels 8; Gaps 5;  
 QY 12 SEDCLYLSYTNMNPETKRPVLYVYHGGFTIGENHRDMYGPDYFKD-KDVVLIINIOYR 70  
 DB 4 SEDCLYLNWVOPSPAP-RGATVLYVWYGGFGFSGLSDYDGRYLARMEDEVVYVSNMR 62  
 QY 71 LGALGFLSLNSEDNLNPNAGLKDQVMAIRKNNKNCANFGNPNITVFGESAGASTHY 130  
 DB 63 LGALGFLTSGE--AAPNAGLIDQHLALQWVQONISFGSDPKYVIFESAGASVNM 120  
 QY 131 MMLTEQRTGLFHRGILMSGNAICPLANT---OCQRAFTLAKLAGYGEQNDKDV-L 186  
 DB 121 HILSPSRGLFHRVAVLQSGAPNGPMAVYGVGARARRATLLAVLVCPPGAGAGNDTEIVA 180  
 QY 187 MKAKRPQDLIKLEEVLTLE 206

Db 181 REVSAGTLDHEWNVLDSD 200

## RESULT 5

ACES\_FELCA STANDARD; PRT; 611 AA.  
 AC 062763; 062762;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Acetylcholinesterase precursor (EC 3.1.1.7) (AChE).  
 GN AChE.  
 OS *Felis silvestris catus* (Cat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
 OC NCBI\_TaxID=9685;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
 RX MEDLINE-20334351; PubMed-10874122;  
 RA Bartels C.F., Xie W., Miller-Lindholm A.K., Schopfer L.M.,  
 RA Lockridge O.;  
 RT Determination of the DNA sequences of acetylcholinesterase and  
 RT butyrylcholinesterase from cat and demonstration of the existence of  
 RT both in cat plasma.";  
 RT Biochem. Pharmacol. 60:479-487(2000).  
 CC -1- FUNCTION: RAPIDLY HYDROLYSES CHOLINE RELEASED INTO THE SYNAPSE (BY  
 CC SIMILARITY).  
 CC -1- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.  
 CC -1- SUBUNIT: ISOFORM H GENERATES GPI-ANCHORED DIMERS, DISULFIDE  
 CC LINKED. ISOFORM T GENERATES MULTIPLE STRUCTURES, RANGING FROM  
 CC MONOMERS AND DIMERS TO COLLAGEN-TAILED AND HYDROPHOBIC-TAILED  
 CC FORMS, IN WHICH CATALYTIC TETRAMERS ARE ASSOCIATED WITH ANCHORING  
 CC PROTEINS THAT ATTACH THEM TO THE BASAL LAMINA OR TO CELL  
 CC MEMBRANES. IN THE COLLAGEN-TAILED FORMS, ISOFORM T SUBUNITS ARE  
 CC ASSOCIATED WITH A SPECIFIC COLLAGEN, COL1, WHICH TRIGGERS THE  
 CC FORMATION OF ISOFORM T TETRAMERS, FROM MONOMERS AND DIMERS (BY  
 CC SIMILARITY).  
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: H AND T (SHOWN HERE); ARE  
 CC PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.  
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 CC -----  
 CC DR EMBL; AF053485; AAC08995.1; -;  
 CC DR EMBL; AF053485; AAC08996.1; -;  
 CC DR HSSP; P22303; 2CLF.  
 CC DR InterPro: IPR002018; Carboxylesterase.  
 CC DR InterPro: IPR000997; Cholinesterase.  
 CC DR InterPro: IPR000379; Ser-estrin-site.  
 CC DR Pfam: PF00135; Coesterase; 1.  
 CC DR PRINTS: PR00878; CHOLINESTERASE.  
 CC DR PROSITE: PS00122; CARBOXYLESTERASE\_B\_1; 1.  
 CC DR PROSITE: PS00941; CARBOXYLESTERASE\_B\_2; 1.  
 CC DR Hydroxylase: Serine esterase; Synapse; Membrane; Nerve; Muscle; Signal;  
 CC Neurotransmitter degradation; Glycoprotein; Alternative splicing.  
 CC KW Neurotransmitter degradation; Glycoprotein; Alternative splicing.  
 CC ST SIGNL 1  
 CC FT CHAIN 1  
 CC FT ACT\_SITE 32 611  
 CC FT ACT\_SITE 231 231  
 CC FT ACT\_SITE 362 362  
 CC FT ACT\_SITE 475 475  
 CC FT DISULFID 97 124  
 CC FT DISULFID 285 300  
 CC FT DISULFID 357 357  
 CC FT DISULFID 437 437  
 CC FT DISULFID 608 608  
 CC FT CARBOHYD 293 293  
 CC FT CARBOHYD 378 378  
 CC FT CARBOHYD 492 492  
 CC FT CARBOHYD 492 492

FT VARSPIC 572 611 DTIDEAROMKAEFFHMSYVWMMKNDFHYSKODRCSDL  
 FT FT -> ASKAPSTCGPAHGAAPRPRGLSLPLLLFLLSR  
 FT FT LIR (IN ISOFORM H).  
 SQ SEQUENCE 611 AA; 67298 MW; DPA5C0885422527 CRC64;

Query Match 34.7%; Score 380; DB 1; Length 611;  
 Best Local Similarity 42.8%; Pred. No. 7.7e-28;  
 Matches 86; Conservative 35; Mismatches 72; Indels 8; Gaps 4;

QY 12 SEDCLLYSYTNLNPETRPVLYIHGGGFTIGENHRDMYGRDFIKND-VLLINIOYR 70  
 Db 121 SEDCLLYNWTTPYRPASPPVLYWYGGFYSGASSIPLDQREFLAQEGTVLSMNR 180  
 QY 71 LGALGFLSUNSEDLNPAGNGLKDYALRMKINMCANGNDNITVYGESAGAATHY 130  
 Db 181 VGAFGLALPG-SREAPGNVGLDQRLALQWODNVATFGGPMSTYTERGESAGAAYGM 239  
 QY 131 MLEDTQRLGFLHNGILMSGNAICPLANT---QCHRAFLAKIAGK---GEDNDKDYIE 184  
 Db 240 HLSPSPRGFLHRAVLQSGAPNGPMATVGVGEARRRATLLARLVGCPGAGAGNDTEIA 299  
 QY 185 FLKAKAPQDLIKLEKVTILE 205  
 Db 300 CLRTPAQDLVDHEWNVLPDE 320

## RESULT 6

ACES\_HUMAN STANDARD; PRT; 614 AA.  
 AC P22303; O9BXP7; Q16169;  
 DT 01-AUG-1991 (Rel. 19, Created)  
 DT 01-AUG-1991 (Rel. 19, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Acetylcholinesterase precursor (EC 3.1.1.7) (AChE).  
 GN *Homo sapiens* (human).  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-91088577; PubMed-2263619;  
 RA Scoreq H., Ben-Aziz R., Prody C.A., Seidman S., Gnat A., Neville L.,  
 RA Lileman-Hurwitz J., Lev-Lehman E., Ginzberg D., Lipidot-Lifson Y.,  
 RA Zakut H.;  
 RT "Molecular cloning and construction of the coding region for human  
 RT acetylcholinesterase reveals a G + C-rich attenuating structure.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 87:9688-9692(1990).  
 RL [2]  
 RL SEQUENCE OF 521-614 FROM N.A.  
 RX MEDLINE-21138439; PubMed-11239002;  
 RA Wilson M.D., Riemer C., Martindale D.W., Schnupf P., Boright A.P.,  
 RA Cheung T.L., Hardy D.M., Schwartz S., Scherer S.W., Tsai L.-C.,  
 RA Miller W., Koop B.F.;  
 RT "Comparative analysis of the gene-dense AChE/TFR2 region on human  
 RT chromosome 7q22 with the orthologous region on mouse chromosome 5.";  
 RL Nucleic Acids Res. 29:1352-1365(2001).  
 RN [3]  
 RN PARTIAL SEQUENCE FROM N.A. (ISOFORM 2).  
 RP MEDLINE-94131004; PubMed-8299725;  
 RX Kappel R., Ben Aziz-Alaya R., Sternfeld M., Ehrlich G., Ginzberg D.,  
 RX Tarroni P., Clement F., Zakut H., Scoreq H.;  
 RA "Expression of three alternative acetylcholinesterase messenger RNAs  
 RA in human tumor cell lines of different tissue origins.";  
 RL Exp. Cell Res. 210:268-277(1994).  
 RL [4]  
 RL PARTIAL SEQUENCE.  
 RC TISSUE=Erythrocyte;  
 RX MEDLINE-89232136; PubMed-2714437;  
 RA Chajajani V., Derr D., Earles B., Schmeil E., August T.;  
 RT "Purification and partial amino acid sequence analysis of human  
 RT erythrocyte acetylcholinesterase.";  
 RL FEBS Lett. 247:279-282(1989).

[illegible]

```

CC CHOLINESTERASE. WITH A COLLAGEN-LIKE PART DISULFIDE-BONDED TO THE
CC CATALYTIC PART. A DIFFERENT, GLOBULAR TYPE OF CHOLINESTERASE
CC OCCURS ON THE OUTER SURFACES OF CELL MEMBRANES, INCLUDING THOSE OF
CC ERYTHROCYTES.
CC -1- MISCELLANEOUS: THIS IS THE CATALYTIC SUBUNIT OF AN ASYMMETRIC OR
CC SOLUBLE FORM OF AChE.
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch)
CC -----
DR EMBL: U06303; AAA53235.1; -
DR HSSP: P22303; 2CLT
DR InterPro: IPR002018; CarboxylesteraseB.
DR InterPro: IPR000379; Ser_estrs_site.
DR Pfam: PF00135; Coesterase_1.
DR PROSITE: PS00122; CARBOXYLESTERASE_B.1; 1.
DR PROSITE: PS00941; CARBOXYLESTERASE_B.2; 1.
KW Hydrolase; Serine esterase; Synapse; Membrane; Nerve; Muscle; Signal;
KM Neurotransmitter degradation; Glycoprotein.
FT NON_TER 1 1
FT SIGNAL <1 1
FT CHAIN 2 584 POTENTIAL.
FT ACT_SITE 204 204 ACETYLCHOLINESTERASE.
FT ACT_SITE 335 335 BY SIMILARITY.
FT ACT_SITE 448 448 BY SIMILARITY.
FT DISULFID 70 97 BY SIMILARITY.
FT DISULFID 258 273 BY SIMILARITY.
FT DISULFID 410 530 BY SIMILARITY.
FT DISULFID 581 581 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 361 266 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 351 351 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 465 465 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 584 AA; 64630 MW; 2AE157F30636499E CRC64;

Query Match 33.7%; Score 369; DB 1; Length 584;
Best Local Similarity 42.6%; Pred. No. 7.8e-27;
Matches 86; Conservative 34; Mismatches 72; Indels 10; Gaps 5;

QY 12 SEDCLLYSVTYNNLNPEKRPVLYVTHGGGFLIGNHRDMYGPDIYKLD-VYLIINQYR 70
DB 94 SEDCLLYNWTFYPRPTSPFTPLWITVYGGGYSGASISLDYGGFVLVOABSTYLVANNYR 153
QY 71 LGALGFLLNSDLVWPNGAGLKQVVALRWIKNNKCANFGGNPDNITVFGSAGASTHY 130
DB 154 VQAFSEFTCLPG-SREAPNGVGLLDQRLALQVQENVAFAFGDPASVTLFEGSAGASVGL 212
QY 131 MMLTQGTGFLPHRGLTMSGNALICPLANT---QCHRAFTLAKLA---GKGEDNDKDYI 183
DB 213 HLLSPRSGLTHRAVLQSGAPNGPWAYVGVGEARRATLTARLAVCPGPGAG-GNDTEY 271
QY 184 EFLMAKAPQDILIKLEKYLTLE 205
DB 272 ACLRTRPADQLVDHEMRVLPQE 293

RESULT 8
ACES_BRARE
ID ACES_BRARE STANDARD; PRT; 634 AA.
AC Q9DDE3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Acetylcholinesterase precursor (EC 3.1.1.7) (ACHE).
GN ACHE.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;

```

CC Cyprinidae; Danio.  
CC NCBI\_TaxID=7955;  
CC [1]  
CC  
CC SEQUENCE FROM N.A.  
CC MEDLINE=20576389; PubMed=11016933;  
CC Bertrand C., Chatonnet A., Takke C., Yan Y., Postlethwait J.,  
CC Toulant J.-P., Cousin X.;  
CC "zebrfish acetylcholinesterase is encoded by a single gene localized  
CC on linkage group 7, gene structure and polymorphism; molecular forms  
CC and expression pattern during development.";  
CC J. Biol. Chem. 276:464-474(2001).  
CC  
CC -1- FUNCTION: RAPIDLY HYDROLYZES CHOLINE RELEASED INTO THE SYNAPSE.  
CC  
CC -1- CATALYTIC ACTIVITY: Acetylcholine + H<sub>2</sub>O = choline + acetate.  
CC  
CC -1- SUBUNIT: DIMERS AND COLLAGEN-TAILED FORMS, IN WHICH CATALYTIC  
CC TETRAMERS ARE ASSOCIATED WITH ANCHORING PROTEINS THAT ATTACH THEM  
CC TO THE BASAL LAMINA OR TO CELL MEMBRANES. IN THE COLLAGEN-TAILED  
CC FORMS, SUBUNITS ARE ASSOCIATED WITH A SPECIFIC COLLAGEN, COLO,  
CC WHICH TRIGGERS THE FORMATION OF ISOPFORM T TETRAMERS FROM DIMERS.  
CC  
CC -1- MISCELLANEOUS: NO OTHER ISOPFORMS EXIST. THIS PROTEIN CORRESPONDS  
CC TO THE T ISOPFORM IN OTHER SPECIES.  
CC  
CC -1- SIMILARITY: BELONGS TO THE CARBOXYLESTERASE TYPE-B FAMILY.  
CC  
CC -----  
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[illegible]





RL J. Biol. Chem. 261:13565-13570(1986).  
 RN [6]  
 RP STRUCTURE OF THE GPI-ANCHOR.  
 RX MEDLINE-94079692; PubMed=8257440;  
 RA Mehler A., Varon L., Silman I., Homans S.W., Ferguson M.A.:  
 "Structure of the glycosyl-phosphatidylinositol membrane anchor of  
 acetylcholinesterase from the electric organ of the electric-fish,  
*Torpedo californica*.";  
 RT Biochem. J. 296:473-479(1993).  
 RL [7]  
 RP GPI-ANCHOR.  
 RX MEDLINE-96176649; PubMed=8597567;  
 RA Bucht G., Hjalmarsson K.:  
 "Residues in *Torpedo californica* acetylcholinesterase necessary for  
 processing to a glycosyl phosphatidylinositol-anchored form.";  
 RT Biochim. Biophys. Acta 1292:223-232(1996).  
 RL [8]  
 RP MUTAGENESIS.  
 RX MEDLINE-91017542; PubMed=2217185;  
 RA Gibney G., Camp S., Dionne M., McPhee-Quigley K., Taylor P.:  
 "Mutagenesis of essential functional residues in  
 acetylcholinesterase.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 87:7546-7550(1990).  
 RL [9]  
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).  
 RX MEDLINE-91343328; PubMed=1678899;  
 RA Sussman J.L., Harel M., Frolow F., Oefner C., Goldman A., Tokar L.,  
 Silman I.:  
 "Atomic structure of acetylcholinesterase from *Torpedo californica*: a  
 prototypic acetylcholine-binding protein.";  
 RT Science 253:872-879(1991).  
 RL [10]  
 RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS) OF COMPLEX WITH FASCICULIN.  
 RX MEDLINE-96363673; PubMed=8747462;  
 RA Harel M., Kleywegt G.J., Ravelli R.B., Silman I., Sussman J.L.:  
 "Crystal structure of an acetylcholinesterase-fasciculin complex:  
 interaction of a three-fingered toxin from snake venom with its  
 target.";  
 RT structure 3:1355-1366(1995).  
 RL [11]  
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).  
 RX MEDLINE-97143314; PubMed=8989325;  
 RA Ravess M.L., Harel M., Pang Y.P., Silman I., Kozikowski A.P.,  
 Sussman J.L.:  
 "Structure of acetylcholinesterase complexed with the nootropic  
 alkaloid, (-)-huperzine A.";  
 RT Nat. Struct. Biol. 4:57-63(1997).  
 RL [12]  
 RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).  
 RX MEDLINE-99249780; PubMed=10231521;  
 RA Barcolucci C., Perola E., Cellai L., Brufani M., Lamba D.:  
 "Back door" opening implied by the crystal structure of a  
 carbamoylated acetylcholinesterase.";  
 RT Biochemistry 38:5714-5719(1999).  
 RL [13]  
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).  
 RX MEDLINE-99282167; PubMed=1033814;  
 RA Millard C.B., Kryger G., Orendtlich A., Greenblatt H.M., Harel M.,  
 Ravess M.L., Segall Y., Barak D., Shaffer A., Silman I.,  
 Sussman J.L.:  
 "Crystal structures of aged phosphorylated acetylcholinesterase:  
 nerve agent reaction products at the atomic level.";  
 RT Biochemistry 38:7032-7039(1999).  
 RL [14]  
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).  
 RX MEDLINE-20074924; PubMed=10606746;  
 RA Greenblatt H.M., Kryger G., Lewis T., Silman I., Sussman J.L.:  
 "Structure of acetylcholinesterase complexed with (-)-galanthamine at  
 2.3-A resolution.";  
 RT FEBS Lett. 463:321-326(1999).  
 RL [15]  
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).  
 RX MEDLINE-99197295; PubMed=10368299;

RA Kryger G., Silman I., Sussman J.L.:  
 "Structure of acetylcholinesterase complexed with E2020 (Arliept(R)):  
 RT implications for the design of new anti-alzheimer drugs.";  
 RL structure 7:297-307(1999).  
 CC -1- FUNCTION: RAPIDLY HYDROLYZES CHOLINE RELEASED INTO THE SYNAPSE.  
 CC MAY BE INVOLVED IN CELL-CELL INTERACTIONS.  
 CC -1- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.  
 CC -1- SUBUNIT: THE H FORM IS AN HOMODIMER; THE ASYMMETRIC FORM IS A  
 CC DISULFIDE-BONDED OLIGOMER COMPOSED OF A COLLAGENIC SUBUNIT (Q) AND  
 CC A VARIABLE NUMBER OF T CATALYTIC SUBUNITS.  
 CC -1- SUBCELLULAR LOCATION: THE H FORM IS ATTACHED TO THE MEMBRANE BY A  
 CC GPI-ANCHOR.  
 CC -1- ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS: H/GLOBULAR (SHOWN HERE)  
 CC AND T; ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- TISSUE SPECIFICITY: AChE IS FOUND IN THE SYNAPSES AND TO A LOWER  
 CC EXTENT IN EXTRAJUNCTIONAL AREAS OF MUSCLE AND NERVE, AND ON  
 CC ERYTHROCYTE MEMBRANES.  
 CC -1- PTM: AN INTERCHAIN DISULFIDE BOND IS PRESENT IN WHAT BECOMES  
 CC POSITION 593 OF THE T ISOFORM.  
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLSTERASE/LIPASE FAMILY.  
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 CC -----  
 DR EMBL: X03439; CAA27169.1; -  
 DR EMBL: X56516; -; NOT\_ANNOTATED\_CDS.  
 DR EMBL: X56517; -; NOT\_ANNOTATED\_CDS.  
 DR PIR: A00773; ACRYE.  
 DR PIR: A34026; A34026.  
 DR PIR: A31962; A31962.  
 DR PDB: 2ACE; 08-NOV-96.  
 DR PDB: 3ACE; 16-DEC-98.  
 DR PDB: 4ACE; 16-DEC-98.  
 DR PDB: 1ACJ; 31-AUG-94.  
 DR PDB: 2ACK; 11-FEB-98.  
 DR PDB: 1AMN; 03-APR-96.  
 DR PDB: 1FSS; 03-SEP-97.  
 DR PDB: 1VOT; 16-JUN-97.  
 DR PDB: 1AX9; 11-FEB-98.  
 DR PDB: 1EVE; 22-MAR-99.  
 DR PDB: 1CFJ; 01-APR-99.  
 DR PDB: 1OCE; 18-MAY-99.  
 DR PDB: 2DFP; 28-JUN-99.  
 DR PDB: 1SOM; 25-JUN-99.  
 DR PDB: 1DX6; 02-JAN-00.  
 DR InterPro: IPR002018; Carboxylesterase.  
 DR InterPro: IPR000997; Cholinesterase.  
 DR InterPro: IPR000379; Ser-estrs\_site.  
 DR Pfam: PF00135; Coesterase\_1.  
 DR PRINTS: PR00878; CHOLNESTRASE.  
 DR PROSITE: PS00122; CARBOXYLSTERASE\_B\_1; 1.  
 DR PROSITE: PS00941; CARBOXYLSTERASE\_B\_2; 1.  
 KW Hydrolyase: Serine esterase; Synapse; Membrane; Nerve; Muscle; Signal;  
 KW Neurotransmitter degradation; Glycoprotein; GPI-anchor; 3D-structure;  
 KW Alternative splicing.  
 KW SIGNAL 1 21  
 FT CHAIN 22 564  
 FT PROPEP 565 586  
 FT ACT\_SITE 221 221  
 FT ACT\_SITE 348 348  
 FT ACT\_SITE 461 461  
 FT DISULFID 88 115  
 FT DISULFID 275 286  
 FT DISULFID 423 542  
 FT DISULFID 558 558  
 FT CARBOHYD 80 80  
 FT CARBOHYD 437 437  
 FT  
 ACETYLCHOLINESTERASE.  
 REMOVED IN MATURE FORM.  
 INTERCHAIN.  
 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 N-LINKED (GLCNAC. . .) (POTENTIAL).





	RESULT 14		
AC	ACES_TORMA	STANDARD:	PRT: 590 AA.
DT	p07692;		
DT	01-APR-1988 (Rel. 07, Created)		
DT	01-JUN-1994 (Rel. 29, Last sequence update)		
DT	16-OCT-2001 (Rel. 40, Last annotation update)		
DE	Acetylcholinesterase precursor (EC 3.1.1.7) (ChE).		
OS	Torpedo marmorata (Marbled electric ray).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;		
OC	Elasmobranchii; Squalae; Hypnosqualea; Pristiogalea; Batoidae;		
OC	Torpediniformes; Torpedinoidei; Torpedinidae; Torpedo.		
OX	NCBI_TaxID=7788;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RP	TISSUE-Electric organ;		
RX	MEDLINE=88004392; PubMed=2820709;		
RA	Sikorav J.-L., Krejci E., Massoulié J.;		
RT	"DNA sequences of Torpedo marmorata acetylcholinesterase: primary		
RT	structure of the precursor of a catalytic subunit, existence of		
RL	multiple 5'-untranslated regions.";		
EMBO	J. 6:1865-1873(1987).		
RN	[2]		
RP	ALTERNATIVE SPLICING.		
RP	TISSUE-Electric organ;		
RC	MEDLINE=89030590; PubMed=3181125;		
RX	Sikorav J.-L., Duval N., Anselmet A., Bon S., Krejci E., Legay C.,		
RA	Osterlund M., Reimund B., Massoulié J.;		
RT	"Complex alternative splicing of acetylcholinesterase transcripts in		
RT	Torpedo electric organ; primary structure of the precursor of the		
RL	glycolipid-anchored dimeric form.";		
EMBO	J. 7:2983-2993(1988).		
RN	[3]		
RP	SUBUNITS INTERACTIONS.		
RP	TISSUE-Electric organ;		
RC	MEDLINE=92371432; PubMed=1380451;		
RX	Duval N., Krejci E., Grassi J., Consens F., Massoulié J., Bon S.;		
RA	"Molecular architecture of acetylcholinesterase collagen-tailed		
RT	form: construction of a glycolipid-tailed tetramer.";		
RL	EMBO J. 11:3255-3261(1992).		
RN	[4]		
RP	SUBUNITS INTERACTIONS, AND REVISION TO 421.		
RP	MEDLINE=92348506; PubMed=1639848;		
RX	Duval N., Massoulié J., Bon S.;		
RA	"H and T subunits of acetylcholinesterase from Torpedo, expressed in		
RT	COS cells, generate all types of globular forms.";		
CC	J. Cell Biol. 118:641-653(1992).		
-I-	FUNCTION: RAPIDLY HYDROLYZES CHOLINE RELEASED INTO THE SYNAPSE.		
CC	MAY BE INVOLVED IN CELL-CELL INTERACTIONS.		
-I-	CATALYTIC ACTIVITY: acetylcholine + H(2)O = choline + acetate.		
CC	-I- SUBUNIT: THE H FORM IS AN HOMODIMER; THE ASYMMETRIC FORM IS A		
CC	DISULFIDE-BONDED OLIGOMER COMPOSED OF A COLLAGENIC SUBUNIT (Q) AND		
CC	A VARIABLE NUMBER OF T CATALYTIC SUBUNITS.		

[illegible]



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OM protein - protein search, using sw model

Run on: April 4, 2003, 09:09:58 ; Search time 20.6467 Seconds  
(without alignments)  
2065.788 Million cell updates/sec

Title: US-09-776-910-43

Perfect score: 1095

Sequence: 1 QVDFITGKVCSEDCLYLV.....KAKPDLIKLEKVLLEER 207

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 segs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_21.\*

1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mmc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1089	99.5	570	5	Q25252 lucilia cup
2	843	77.0	570	5	Q9U4T9 O9U4T9 haematobia
3	836	76.3	570	5	Q9X270 musca domes
4	812.5	74.2	556	5	Q24201 drosophila
5	812.5	74.2	572	5	Q9V1B5 drosophila
6	802.5	73.3	345	5	Q9V1B3 drosophila
7	653.5	59.7	567	5	Q9V1B3 drosophila
8	652.5	59.6	558	5	Q24202 drosophila
9	640	58.4	286	5	Q9N1S2 drosophila
10	612	55.9	297	5	Q9N1S1 drosophila
11	610	55.7	554	5	Q9V1B0 drosophila
12	605	55.3	565	5	Q9N1S9 drosophila
13	596	54.4	572	5	Q24203 drosophila
14	591	54.0	572	5	Q9V1B1 drosophila
15	590	53.9	570	5	Q9V1B5 drosophila
16	590	53.9	549	5	Q24204 drosophila

17	589	53.8	401	5	Q9N160 drosophila
18	588	53.7	564	5	Q9N161 drosophila
19	578	52.8	553	5	Q24194 drosophila
20	578	52.8	565	5	Q9V1C3 drosophila
21	573	52.3	554	5	Q9V1C2 drosophila
22	569	52.0	554	5	Q9V1N0 drosophila
23	569	52.0	554	5	Q24195 drosophila
24	561	51.2	542	5	Q9S030 drosophila
25	561	51.2	542	5	Q24198 drosophila
26	561	51.2	542	5	Q9V1C9 drosophila
27	546.5	49.9	566	5	Q9W243 drosophila
28	544	49.7	446	5	Q9N1S5 drosophila
29	528	48.2	540	5	Q8W089 drosophila
30	526	48.0	540	5	Q8W088 drosophila
31	524	47.9	467	5	P91597 culix pipie
32	523	47.8	467	5	P91596 culix pipie
33	523	47.8	540	5	Q23733 culix quing
34	523	47.8	540	5	P92025 culix quing
35	518	47.3	467	5	P91598 culix pipie
36	499.5	45.6	541	5	Q24197 drosophila
37	499.5	45.6	541	5	Q9V1C0 drosophila
38	498	45.5	568	5	Q9V1B6 drosophila
39	497	45.4	540	5	Q9G095 culix trita
40	495	45.2	540	5	P91920 culix tarsa
41	494.5	45.2	360	5	Q9U9R1 drosophila
42	493	45.0	463	5	Q961J7 drosophila
43	480	43.8	532	5	Q961J6 anisopetrom
44	479	43.7	568	5	Q24200 drosophila
45	478	43.7	532	5	Q61727 anisopetrom

## ALIGNMENTS

RESULT 1  
ID Q25252 PRELIMINARY; PRT; 570 AA.  
AC Q25252; Q25247;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
DE Alpha esterase (LCAE7) (Carboxylesterase).  
GN Lucilia cuprina (Greenbottle fly) (Australian sheep blowfly).  
OS Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Oestroidea; Calliphoridae; Lucilia.  
OX NCBI\_TaxID=7375;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Newcomb R.D., East P.D., Russell R.J., Oakeshott J.G.;  
RC STRAIN=LS2;  
RL Insect Mol. Biol. 5:0-0(0).  
RN [2]  
RP SEQUENCE OF 70-181 FROM N.A.  
RA Newcomb R.D., East P.D., Russell R.J., Oakeshott J.G.;  
RC STRAIN=LS2;  
RL Insect Mol. Biol. 0:0-0(0).  
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.  
DR EMBL: U56636; AAB6728.1; -;  
DR EMBL: U49421; AAA92012.1; -;  
DR HSSP: P37967; IOE3.  
DR InterPro: IPR002018; Carboxylesterase.  
DR Pfam: PFR00379; Ser-estrs\_site.  
DR PROSITE: PS00122; CARBOXYLESTERASE\_B\_1; 1.  
KW Hydrolase.  
SQ SEQUENCE 570 AA: 65416 MW: 399D72B3A0F338FD CRC64;

Query Match 99.5%; Score 1089; DB 5; Length 570;  
Best Local Similarity 99.5%; Pred. No. 1.2e-96;  
Matches 206; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 QVDFITGKVGSEDCLYSVYTNLNPETKRPVLYIHGGGFIIGENHRDMYGPDYFIKK 60
DB 97 QVDFITGKVGSEDCLYSVYTNLNPETKRPVLYIHGGGFIIGENHRDMYGPDYFIKK 156
QY 61 DVLINIOYRLGALGFLSNSEDLNVPNGAGLKDQVMAIRKNNCANFGNDPNTITVFG 120
DB 157 DVLINIOYRLGALGFLSNSEDLNVPNGAGLKDQVMAIRKNNCANFGNDPNTITVFG 216
QY 121 ESAGAASTHYMMLTEQRTGLFHRGILMSGNAICPLANTQCOHRAFTLAKLAGYKGEDNDK 180
DB 217 ESAGAASTHYMMLTEQRTGLFHRGILMSGNAICPLANTQCOHRAFTLAKLAGYKGEDNDK 276
QY 181 DYLEFLMKAKPODLIKLEKVTLEER 207
DB 277 DYLEFLMKAKPODLIKLEKVTLEER 303

RESULT 2
QY 094U9 PRELIMINARY; PRT; 570 AA.
AC 094U9.
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Alpha E7 esterase.
GN AEF7.
OS Haematobia irritans irritans.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Muscoidea; Muscidae; Haematobia.
OX NCBI_TaxID=75445;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CAMP COOLEY 4/97;
RX MEDLINE=20445807; PubMed=10989298;
RA Guerrero F.D.;
RT "Cloning of a horn fly cDNA, H1alphaE7, encoding an esterase whose
transcript concentration is elevated in diazotol-resistant flies.";
RL Insect Biochem. Mol. Biol. 30:1107-1115(2000).
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DB EMBL: AF139082; AAF14517.1;
DR HSSP: P37967; 10E3.
DR InterPro: IPR002018; CarbesteraseB.
DR Pfam: PF00135; Coesterase; 1.
DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
KW Hydrolase.
SQ SEQUENCE 570 AA; 65613 MW; 18DA0A9A94AB970D CRC64;

Query Match 77.0%; Score 843; DB 5; Length 570;
Best Local Similarity 76.2%; Pred. No. 7,1e-73;
Matches 157; Conservative 20; Mismatches 29; Indels 0; Gaps 0;

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AC 09XZ70;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Carboxylesterase MdaE7 (Ec 3.1.1.1).
GN MDAE7.
OS Musca domestica (House fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Muscoidea; Muscidae; Musca.
OX NCBI_TaxID=7370;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RUTGERS DIAZINON-R;
RX MEDLINE=99381228; PubMed=10451921;
RA Claudianos C., Russell R.J., Oakeshot J.G.;
RT "The same amino acid substitution in orthologous esterases confers
organophosphate resistance on the house fly and a blowfly.";
RL Insect Biochem. Mol. Biol. 29:675-686(1999).
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DB EMBL: AF133341; AAD29685.1;
DR HSSP: P37967; 10E3.
DR InterPro: IPR002018; CarbesteraseB.
DR Pfam: PF00135; Coesterase; 1.
DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
KW Hydrolase.
SQ SEQUENCE 570 AA; 65421 MW; 08AFEBEF284003BB CRC64;

Query Match 76.3%; Score 836; DB 5; Length 570;
Best Local Similarity 74.8%; Pred. No. 3,4e-72;
Matches 154; Conservative 26; Mismatches 26; Indels 0; Gaps 0;

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QY 1 QVDFITGKVGSEDCLYSVYTNLNPETKRPVLYIHGGGFIIGENHRDMYGPDYFIKK 60
DB 97 QVDFITGKVGSEDCLYSVYTNLNPETKRPVLYIHGGGFIIGENHRDMYGPDYFIKK 156
QY 61 DVLINIOYRLGALGFLSNSEDLNVPNGAGLKDQVMAIRKNNCANFGNDPNTITVFG 120
DB 157 DVLINIOYRLGALGFLSNSEDLNVPNGAGLKDQVMAIRKNNCANFGNDPNTITVFG 216
QY 121 ESAGAASTHYMMLTEQRTGLFHRGILMSGNAICPLANTQCOHRAFTLAKLAGYKGEDNDK 180
DB 217 ESAGAASTHYMMLTEQRTGLFHRGILMSGNAICPLANTQCOHRAFTLAKLAGYKGEDNDK 276
QY 181 DYLEFLMKAKPODLIKLEKVTLEER 206
DB 277 DYLEFLMKAKPODLIKLEKVTLEER 302

RESULT 4
QY 024201 PRELIMINARY; PRT; 556 AA.
AC 024201.
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Alpha esterase (Fragment).
GN ALPHA-EST7 OR AE7 OR CG1112.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC Rodin C., Medvedevsky K.M., Russell R.J., Oakeshot J.G.;
RL J. Mol. Evol. 0:0-0(0).
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DB EMBL: U51050; AAB01149.1;
DR HSSP: P21836; 1MAA.
DR PDBase: FBgn0015575; alpha-Est7.
DR InterPro: IPR002018; CarbesteraseB.

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RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinelt K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zhong X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of *Drosophila melanogaster*."  
RT Science 287:2185-2195(2000).  
[2]  
RN SEQUENCE FROM N.A.  
RP STRAIN-BERKELEY.  
RC Stapleton M., Broksstein P., Hong L., Aghayani A., Carlson J.,  
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,  
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,  
RA Nuno J.F., Pacלב J., Paragas V., Park S., Phouanavong S., Wan K.,  
RA Yu C., Lewis S.E., Rubin G.M., Genliker S.;  
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.  
CC EMBL: AE003671; AAF34010.1; -;  
CC EMBL: AY051473; AAK92897.1; -;  
CC HSSP: P21836; IMAA.  
DR FlyBase: FBgn0015575; alpha-Est7.  
DR InterPro: IPR002018; Carboxylesterase.  
DR InterPro: IPR000379; Ser-esters\_site.  
DR Pfam: PF00135; Coesterase; 1.  
DR PROSITE: PS00122; CARBOXYLESTERASE\_B\_1; 1.  
KW Hydrolase.  
SQ SEQUENCE 572 AA; 65435 MW; 693D9360DA18AE27 CRC64;  
  
Query Match 74.2%; Score 812.5; DB 5; Length 572;  
Best Local Similarity 73.1%; Pred. No. 6.3e-70;  
Matches 152; Conservative 26; Mismatches 29; Indels 1; Gaps 1.  
  
QY 1 QVDFITGKVGSGSDCLYLSVTYNNINPETKRPVLVYINGGFIIGENHRMDYGPDYFIKK 60  
Db |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||::: 156  
QY 97 QVQFVEFDKVGESDCLYLVNTYNNKPKDKARFVWYIHGGFIIIGEANREMYGPDYFKME 156  
Db |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||::: 120  
QY 61 DVLVLTINQVYLGALGFLINSFDLWVPGAGLKDQVMALEKIKNNCANFGENDNTIVYG 120  
Db |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||::: 157  
QY 121 ESAGAASTHYMTLEDTBRLGFLFRGILMSGNAICPLA-NTQCNHAFPLAKIAGYKGGEND 179  
Db |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||::: 216  
QY 217 ESAGGASTHYMTLDTDTGCLFRHGLIGSSALCPMAYNGDITNHPYIAKLVGKGGEND 276  
Db |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||::: 217  
QY 180 KDYLEFLMKAKPDLIKLEKVLTEER 207  
Db |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||::: 277  
Db KDYLEFLQNKAKDLITVEENVLTLEER 304  
  
RESULT 6  
Q9N153 PRELIMINARY; PRT. 345 AA.  
AC Q9N153;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE Alpha-esterase 7 (Fragment).  
GN AE7A OR AE7.  
OS Drosophila buzzatii (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachyera; Muscomorpha;  
OC Ephyridae; Drosophilidae; Drosophila.  
OX NCBI\_Taxid=7264;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC Robin C., Claudianos C., Russell R.J., Oakeshott J.G.;  
RT "The alpha-esterase cluster of *Drosophila buzzatii*."  
RT Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.  
 DR EMBL: AF216215; AAF26729.1; -  
 DR HSSP: P21836; IMAA.  
 DR FlyBase: FBgn0029447; DbuzAe7a.  
 DR InterPro: IPR002018; Carbesteraseb.  
 DR InterPro: IPR000379; Ser\_estrs\_site.  
 DR Pfam: PF00135; Coesterase\_1.  
 DR PROSITE: PS00122; CARBOXYLESTERASE\_B\_1; 1.  
 KM Hydrolyase.  
 FT NON\_TER  
 FT NON\_TER  
 SQ SEQUENCE 345 AA; 38472 MW; C08564A34E4EC87A CRC64;  
 Query Match 73.3%; Score 802.5; DB 5; Length 345;  
 Best Local Similarity 74.9%; Pred. No. 3e-69;  
 Matches 155; Conservative 23; Mismatches 28; Indels 1; Gaps 1;  
 QY 1 QVDFITGKVCSEDCILSYVTNNLNPETKRPVLVYHGGGFTIGENHRDMGPDYFIKK 60  
 DB 28 QVHFVDFRVEGSEDCILSYVTNNLNPETKRPVLVYHGGGFTIGENHRDMGPDYFIKE 87  
 QY 61 DVLVINTQYRLGALGFLSLNSFDLWPNAGLKDQVMALEMTKNNCANFGNPDITVEG 120  
 DB 88 DVLVLTQYRLGALGFLSLKTPGLWPNAGLKDQVMALEMTKNNCASFGDPTVEG 147  
 QY 121 ESAGASTHYWMLTEOTRGFLHGIIMSGNAICPLA-NTQCOHRAFTLAKIAGYGEDND 179  
 DB 148 ESAGASTHYWMLTDOTGFLHGIILQSGSAIGPMAFGDITSRFRILAKIAGYGEDND 207  
 QY 180 KDVEFLMKAKPDILKLEKVLTLER 206  
 DB 208 KDVLQFLQVVARADILRVEQVLTPEE 234  
 RESULT 7  
 QYVIB3 PRELIMINARY; PRT; 567 AA.  
 AC 09VIB3:  
 DT 01-MAY-2000 (TREMblrel. 13, Created)  
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)  
 DE Alpha-EST8 protein.  
 GN ALPHA-EST8 OR CG1121.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BERKELEY;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amaniatis P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.H.C., Blazer R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abril J.F., Abmayant A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Bendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,  
 RA Burks K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,  
 RA Foster L., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeagwam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz L., Kulp D., Lai Z.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Maitel B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pauley J.M.,  
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puti V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen T.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Sytkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster.";  
 RL Science 287:2185-2195(2000).  
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.  
 DR EMBL: AE003671; AAF34012.1; -  
 DR HSSP: P37967; 10E3.  
 DR FlyBase: FBgn0015576; alpha-Est8.  
 DR InterPro: IPR002018; Carbesteraseb.  
 DR InterPro: IPR000379; Ser\_estrs\_site.  
 DR Pfam: PF00135; Coesterase\_1.  
 DR PROSITE: PS00122; CARBOXYLESTERASE\_B\_1; 1.  
 DR PROSITE: PS00941; CARBOXYLESTERASE\_B\_2; 1.  
 KM Hydrolyase.  
 FT NON\_TER  
 SQ SEQUENCE 567 AA; 64831 MW; 07D6AC72786F14A CRC64;  
 Query Match 59.7%; Score 653.5; DB 5; Length 567;  
 Best Local Similarity 59.8%; Pred. No. 1.4e-54;  
 Matches 123; Conservative 34; Mismatches 50; Indels 1; Gaps 1;  
 QY 1 QVDFITGKVCSEDCILSYVTNNLNPETKRPVLVYHGGGFTIGENHRDMGPDYFIKK 60  
 DB 90 QVNTVLKQVQSEDCILSYVTNNLNPETKRPVLVYHGGGFTIGENHRDMGPDYFIKE 149  
 QY 61 DVLVINTQYRLGALGFLSLNSFDLWPNAGLKDQVMALEMTKNNCANFGNPDITVEG 120  
 DB 150 HVLVLTISYRLGALGFLSLADELDVGNAGLKDQVMALEMTKNNCASFGDPTVEG 209  
 QY 121 ESAGASTHYWMLTEOTRGFLHGIIMSGNAICPLANTQCOHRAFTLAKIAGYGEDND 179  
 DB 210 ESAGASTHYWMLTDQKGLHGIIMSGNALPMAOTPHIWPYRLAOTGYTDAND 269  
 QY 180 KDVEFLMKAKPDILKLEKVLTLER 207  
 DB 270 RDIFAHLKCKKASSMLKVAEDITMEER 297  
 RESULT 8  
 Q24202 PRELIMINARY; PRT; 558 AA.  
 ID 024202:  
 AC 024202:  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)  
 DE Alpha esterase (Fragment).  
 GN ALPHA-EST8 OR CG1121.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC Robin C., Medveczky K.M., Russell R.J., Oakeshott J.G.;  
 RL J. Mol. Evol. 0:0-0(0).  
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.  
 DR EMBL: U51052; BAB01151.1; -  
 DR HSSP: P37967; 10E3.  
 DR FlyBase: FBgn0015576; alpha-Est8.  
 DR InterPro: IPR002018; Carbesteraseb.

DR InterPro; IPR000379; Ser-estrs\_-site.  
 DR Pfam; PF00135; Coesterase; 1.  
 DR PROSITE; PS00122; CARBOXYLESTERASE\_B\_1; 1.  
 DR PROSITE; PS00941; CARBOXYLESTERASE\_B\_2; 1.  
 KW Hydrolase.  
 FT NON\_TER 1  
 SQ SEQUENCE 558 AA; 63916 MW; BF6F62C8FF212720 CRC64;

Query Match 59.6%; Score 652.5; DB 5; Length 558;  
 Best Local Similarity 58.7%; Pred. No. 1.8e-54;  
 Matches 122; Conservative 35; Mismatches 50; Indels 1; Gaps 1;

QY 1 QVDFITGKVCSEDCILYSVYTNINLPETKRPVLYIHGGFFIIGENHRDMYGPDPYFKK 60  
 DB 81 QVNIYVKVOGSEDCILYVYTRRELPHRPLVLYVIGGGFGQMGESRDLYSPDYIME 140  
 QY 61 DVVLINIQRYLALGFLSLNSEDLVPGNAGIKQDVMLRWIKNNCANFGNPNITVFG 120  
 DB 141 HVLVIVISRYLALGFLSLADELDVPGNAGIKQDVMLRWYKRNCOFFGDDPDNITVFG 200  
 QY 121 ESAGASTHYMMLTEOTRGLEFRHGLMSGNAICPLANTOCO-HRAFTLAKLAGYGEEND 179  
 DB 201 ESAGASTHYMMLTDQAGLEFRHGLMSGNALAPWAGPTPHIINPYRLAQAATGTGDAND 260  
 QY 180 KDVEFLMKAKPQDLIKLEEKVLTLEER 207  
 DB 261 RDIFAHLKKCKASSMLKVAEDITITMEER 288

RESULT 9  
 Q9NT52 PRELIMINARY; PRT; 286 AA.

DT 01-OCT-2000 (TREMblrel. 15, Created)  
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)  
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)  
 DE Alpha-esterase 8 (Fragment).  
 GN AE8A OR AE8.  
 OS Drosophila buzzatii (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7264;  
 RN 11)  
 RP SEQUENCE FROM N.A.  
 RA Robin C., Claudianos C., Russell R.J., Oakeshott J.G.;  
 RT "The alpha-esterase cluster of Drosophila buzzatii."  
 RL Submitted (DEC-1999) to the EMBL/Genbank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.  
 DR EMBL; AF216216; AAF26730.1; -.  
 DR HSSP; P21836; IMAA.  
 DR FlyBase; FBgn0029446; Dpuz\AE8a.  
 DR InterPro; IPR002018; Carbesterase.  
 DR InterPro; IPR000379; Ser-estrs\_-site.  
 DR Pfam; PF00135; Coesterase; 1.  
 DR PROSITE; PS00122; CARBOXYLESTERASE\_B\_1; 1.  
 DR PROSITE; PS00941; CARBOXYLESTERASE\_B\_2; UNKNOWN\_1.  
 KW Hydrolase.  
 FT NON\_TER 1  
 FT NON\_TER 286  
 SQ SEQUENCE 286 AA; 32409 MW; ADCCAFD124D2A953 CRC64;

Query Match 58.4%; Score 640; DB 5; Length 286;  
 Best Local Similarity 56.5%; Pred. No. 1.2e-53;  
 Matches 117; Conservative 38; Mismatches 52; Indels 0; Gaps 0;

QY 1 QVDFITGKVCSEDCILYSVYTNINLPETKRPVLYIHGGFFIIGENHRDMYGPDPYFKK 60  
 DB 28 QVNIYVKVOGSEDCILYVYTRRELPHRPLVLYVIGGGFGQMGESRDLYSPDYIME 87  
 QY 61 DVVLINIQRYLALGFLSLNSEDLVPGNAGIKQDVMLRWIKNNCANFGNPNITVFG 120  
 DB 88 HVLVIVISRYLALGFLSLADELDVPGNAGIKQDVMLRWYKRNCOFFGDDPDNITVFG 147

QY 121 ESAGASTHYMMLTEOTRGLEFRHGLMSGNAICPLANTOCO-HRAFTLAKLAGYGEENDK 180  
 DB 148 ESAGASTHYMMLTEOTRGLEFRHGLMSGNALAPWAGPTPHIINPYRLAQAATGTGDAND 260  
 QY 181 KDVEFLMKAKPQDLIKLEEKVLTLEER 207  
 DB 208 EIFKHLQCKASSMLKVAEDITITMEER 234

RESULT 10

Q9NT51 PRELIMINARY; PRT; 297 AA.

DT 01-OCT-2000 (TREMblrel. 15, Created)  
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)  
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)  
 DE Alpha-esterase 9 (Fragment).  
 GN AE9A OR AE9.  
 OS Drosophila buzzatii (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7264;  
 RN 11)  
 RP SEQUENCE FROM N.A.  
 RA Robin C., Claudianos C., Russell R.J., Oakeshott J.G.;  
 RT "The alpha-esterase cluster of Drosophila buzzatii."  
 RL Submitted (DEC-1999) to the EMBL/Genbank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.  
 DR EMBL; AF216217; AAF26731.1; -.  
 DR HSSP; P37967; 10E3.  
 DR FlyBase; FBgn0029445; Dpuz\AE9a.  
 DR InterPro; IPR002018; Carbesterase.  
 DR InterPro; IPR000379; Ser-estrs\_-site.  
 DR Pfam; PF00135; Coesterase; 1.  
 DR PROSITE; PS00122; CARBOXYLESTERASE\_B\_1; 1.  
 KW Hydrolase.  
 FT NON\_TER 297  
 FT NON\_TER 297  
 SQ SEQUENCE 297 AA; 33635 MW; 89CF7761871B362D CRC64;

Query Match 55.9%; Score 612; DB 5; Length 297;  
 Best Local Similarity 55.6%; Pred. No. 6.2e-51;  
 Matches 115; Conservative 35; Mismatches 57; Indels 0; Gaps 0;

QY 1 QVDFITGKVCSEDCILYSVYTNINLPETKRPVLYIHGGFFIIGENHRDMYGPDPYFKK 60  
 DB 81 QHFEVEMTDGSEDCILYVYTRRELPHRPLVLYVIGGGFGQMGESRDLYSPDYIME 140  
 QY 61 DVVLINIQRYLALGFLSLNSEDLVPGNAGIKQDVMLRWIKNNCANFGNPNITVFG 120  
 DB 141 DVVLINISRYLALGFLSLADELDVPGNAGIKQDVMLRWYKRNCOFFGDDPDNITVFG 200  
 QY 121 ESAGASTHYMMLTEOTRGLEFRHGLMSGNAICPLANTOCO-HRAFTLAKLAGYGEENDK 180  
 DB 201 DSAGASVHYMMLTEOTRGLEFRHGLMSGNALAPWAGPTPHIINPYRLAQAATGTGDAND 260  
 QY 181 DVLEFLMKAKPQDLIKLEEKVLTLEER 207  
 DB 261 EWFELMKAKPQDLIKLEEKVLTLEER 287

RESULT 11

Q9VTB0 PRELIMINARY; PRT; 554 AA.

DT 01-MAY-2000 (TREMblrel. 13, Created)  
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)  
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)  
 DE Alpha-EST9 protein.  
 GN ALPHA-EST9 OR CG1128.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxId=7227;  
 RN  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BERKELEY;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,  
 RA Branton R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch L., Basley E.M.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley S.,  
 RA Beeson K.Y., Benos P.V., Bernan B.P., Brokstein P., Brotler P.,  
 RA Borokova D., Botchan M.R., Bouck J., Broksstein P., Brotler P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu L.B., Davies P.,  
 RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies I.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Dudin K.J., Evangelista C.C., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Foster C., Gabrielian A.E., Garg N.S., Guan P., Harris M.,  
 RA Fostek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.H., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Kennison J.A., Ketchum K.A.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lal Z.,  
 RA Li X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Pollard J.R., Puri V., Reese M.G.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J.R., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Sidenkiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svitskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveril J.S., Zhan M., Zhang G., Zhao X., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT The genome sequence of *Drosophila melanogaster*.;  
 RL Science 287:2185-2195(2000)  
 CC EMBL: AEO03671; AAF54014.1; -;  
 DR HSSP: P37967; 1OE3.  
 DR FLYBASE: FBgn0015577; alpha-Est9.  
 DR InterPro: IPR002018; Carboxylesterase.  
 DR InterPro: IPR000997; Cholinesterase.  
 DR InterPro: IPR000379; Ser-estrs\_site.  
 DR Pfam: PF00135; Coesterase.1.  
 DR PRINTS: PR00878; CHOLNESTRASE.  
 DR PROSITE: PS00122; CARBOXYLESTERASE\_B\_1; 1.  
 KW Hydrolyase.  
 SO SEQUENCE 554 AA; 63670 MW; 0A72368389DFC2B CRC64;

Query Match 55.7%; Score 610; DB 5; Length 554;  
 Best Local Similarity 56.0%; Pred. No. 2.2e-50;  
 Matches 116; Conservative 34; Mismatches 57; Indels 0; Gaps 0;

QY 1 QVDFITGVGSEDECLYVYTNINLPETKRPVLYIHGGFFITGENHDMYGPDIYTK 60  
 DB 81 QKHFVEMTDSDECLYVYTNINLPETKRPVLYIHGGFFITGENHDMYGPDIYTK 140  
 QY 61 DVLINIOYRIGALGFLSLNSEDNLVPGNAGIKDQVALLRMKNNKCANFGGPNPTIVFG 120  
 DB 141 DVVVISINRILGFLGLDIPDELDPVGNAGIKDQVALLRMKNNKCANFGGPNPTIVFG 200  
 QY 121 ESAGASTHYMMLTEOTRGLFHRGILMSGNAICPLANTQCCHRAFTLAKLAGYGEDNDK 180  
 DB 201 DSAGSASVHYMMTEOTRGLFHRGILMSGNAICPLANTQCCHRAFTLAKLAGYGEDNDK 260

QY 181 DVLFLMKAKPODLIKLEKVLTEER 207  
 DB 261 DWEEFLKAKGSEILKANGELCIDEK 287

## RESULT 12

ID Q9N159 PRELIMINARY; PRT: 565 AA.

AC Q9N159; 01-OCT-2000 (TREMBLrel. 15, Created)

DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE Alpha-esterase 2.

GN AE2A OR AE2.

OS Drosophila buzzatii (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI\_TaxId=7264;

RN [1]

RP SEQUENCE FROM N.A.

RA Robin C., Claudianos C., Russell R.J., Oakeshott J.G.;

RT "The alpha-esterase cluster of *Drosophila buzzatii*."

RL Submitted (DEC-1999) to the EMBL/Genbank/DBD databases.

CC EMBL: AF216210; AAF26723.1; -;

DR HSSP: P37967; 1OE3.

DR FLYBASE: FBgn0029452; Dbnz/AE2A.

DR InterPro: IPR002018; Carboxylesterase.

DR InterPro: IPR000997; Cholinesterase.

DR Pfam: PF00135; Coesterase.1.

DR PRINTS: PR00878; CHOLNESTRASE.

KW Hydrolyase.

SO SEQUENCE 565 AA; 64618 MW; 0BC92E956B23006E CRC64;

Query Match 55.3%; Score 605; DB 5; Length 565;  
 Best Local Similarity 55.8%; Pred. No. 7e-50;  
 Matches 115; Conservative 39; Mismatches 52; Indels 0; Gaps 0;

QY 1 QVDFITGVGSEDECLYVYTNINLPETKRPVLYIHGGFFITGENHDMYGPDIYTK 60  
 DB 97 QNNMVMGLIESEDECLYVYTNINLPETKRPVLYIHGGFFITGENHDMYGPDIYTK 156  
 QY 61 DVLINIOYRIGALGFLSLNSEDNLVPGNAGIKDQVALLRMKNNKCANFGGPNPTIVFG 120  
 DB 157 NVVLVTINRIGALGFLSLNSEDNLVPGNAGIKDQVALLRMKNNKCANFGGPNPTIVFG 216  
 QY 121 ESAGASTHYMMLTEOTRGLFHRGILMSGNAICPLANTQCCHRAFTLAKLAGYGEDNDK 180  
 DB 217 ESAGASTHYMMLTEOTRGLFHRGILMSGNAICPLANTQCCHRAFTLAKLAGYGEDNDK 276  
 QY 181 DVLFLMKAKPODLIKLEKVLTEER 206  
 DB 277 DILRYLTKASARQIASHDEIVTLDE 302

## RESULT 13

ID Q24203 PRELIMINARY; PRT: 572 AA.

AC Q24203; 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE Alpha-esterase.

GN ALPHA-EST9 OR AE9 OR CG1128.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI\_TaxId=7227;

RN [1]

RP SEQUENCE FROM N.A.  
 RA Robin C., Medveczky K.M., Russell R.J., Oakeshott J.G.:  
 RL J. Mol. Evol. 0:0-0(0).  
 CC -1 SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.  
 DR EMBL: 051053; AB01152.1; -.  
 DR HSSP: P37967; 10E3.  
 DR FlyBase: FBgn0015577; alpha-Est9.  
 DR InterPro: IPR002018; Carboxylesterase.  
 DR InterPro: IPR000379; Ser\_estrs\_site.  
 DR Pfam: PF00135; Coesterase; 1.  
 DR PROSITE: PS00122; CARBOXYLESTERASE\_B\_1; 1.  
 KM Hydrolase.  
 SQ SEQUENCE 572 AA; 65660 MW; 37F1440F68AD2BD8 CRC64;  
 Query Match 54.4%; Score 596; DB 5; Length 572;  
 Best Local Similarity 52.0%; Pred. No. 5,2e-49;  
 Matches 117; Conservative 34; Mismatches 56; Indels 18; Gaps 1;  
 QY 1 QVDFITGKVCSEDCCLYSVTNNLNPEKRPVLYIHGGFTIGENHRMGDPYFIKK 60  
 DB 81 QKTFEEMTDGSEDCCLYLVNVTKNLPYTPKPMFVWVIYGGFGFGEASRECYSPDYLLRE 140  
 QY 61 DVLINIOYRLGAL-----GFLSNSEDLVNPGNGLKQVMAIRNI 102  
 DB 141 DVVVISINRRLGRLGNDTWMKKHIFNISLPGFLCLDPELDVPGNAGLKQVIALRWY 200  
 QY 103 KNCNCFGNDNTVFGESAGASTHYMLTEQTRGLFHRIILMSGNAICPLANTQCOH 162  
 DB 201 KANCSRFSGDSANITIFGDSAGSASVHYMMITEQTRGLFHKAICMSGNTLSPMAVTPQRN 260  
 QY 163 RAFLTLAKLAGKGDNDKVDLEFLMKAKPODLIKLEKVTLEER 207  
 DB 261 WPRYLAVOAGYAGENNTRDWEFLKNAKGEIILKANGELCIDCEK 305  
 RESULT 14  
 QYVIBI PRELIMINARY: PRT: 572 AA.  
 AC Q9VIBI.  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
 DE Alpha-Est9 protein.  
 GN ALPHA-EST9 OR CG1128.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BERKELEY;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton R.C., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champs M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Barker E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Brill J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.T., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,  
 RA Borova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,  
 RA Butris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Chertis J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunn P.,  
 RA Dudin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,  
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lascko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Mekulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nussken D.R., Paclet J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA She B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weisslock G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers R.W., Rubin G.M., Venter J.C.;  
 RA "the genome sequence of Drosophila melanogaster";  
 RL Science 287:2185-2195(2000).  
 CC -1 SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.  
 DR EMBL: AE003671; AA054015.1; -.  
 DR HSSP: P37967; 10E3.  
 DR FlyBase: FBgn0015577; alpha-Est9.  
 DR InterPro: IPR002018; Carboxylesterase.  
 DR InterPro: IPR000997; Cholinesterase.  
 DR InterPro: IPR000379; Ser\_estrs\_site.  
 DR Pfam: PF00135; Coesterase; 1.  
 DR PRINTS: PR00878; CHOLINESTRASE.  
 DR PROSITE: PS00122; CARBOXYLESTERASE\_B\_1; 2.  
 KM Hydrolase.  
 SQ SEQUENCE 572 AA; 65767 MW; 9138FB95713DF350 CRC64;  
 Query Match 54.0%; Score 591; DB 5; Length 572;  
 Best Local Similarity 51.6%; Pred. No. 1.6e-48;  
 Matches 116; Conservative 34; Mismatches 57; Indels 18; Gaps 1;  
 QY 1 QVDFITGKVCSEDCCLYSVTNNLNPEKRPVLYIHGGFTIGENHRMGDPYFIKK 60  
 DB 81 QKTFEEMTDGSEDCCLYLVNVTKNLPYTPKPMFVWVIYGGFGFGEASRECYSPDYLLRE 140  
 QY 61 DVLINIOYRLGAL-----GFLSNSEDLVNPGNAGLKQVMAIRNI 102  
 DB 141 DVVVISINRRLGRLGNDTWMKKHIFNISLPGFLCLDPELDVPGNAGLKQVIALRWY 200  
 QY 103 KNCNCFGNDNTVFGESAGASTHYMLTEQTRGLFHRIILMSGNAICPLANTQCOH 162  
 DB 201 KANCSRFSGDSANITIFGDSAGSASVHYMMITEQTRGLFHKAICMSGNTLSPMAVTPQRN 260  
 QY 163 RAFLTLAKLAGKGDNDKVDLEFLMKAKPODLIKLEKVTLEER 207  
 DB 261 WPRYLAVOAGYAGENNTRDWEFLKNAKGEIILKANGELCIDCEK 305  
 RESULT 15  
 QYVIBI PRELIMINARY: PRT: 530 AA.  
 AC Q9VIBI.  
 DT 01-MAR-2001 (TREMBlrel. 16, Created)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
 DE Alpha-Est10 protein.  
 GN ALPHA-EST10 OR CG1131.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BERKELEY;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,



GenCore version 5.1.4-p5.4578  
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OM protein - protein search, using sw model

Run on: April 4, 2003, 09:10:57 ; Search time 5.7278 Seconds  
(without alignments)  
1063.331 Million cell updates/sec

Title: US-09-776-910-43

Perfect score: 1095

Sequence: 1 QVDFITGKVGSEDCILYLVY.....KAKFQDLIKLEKVLTEER 207

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 10%

Listing first 45 summaries

Database : Issued\_Patents\_AA.\*  
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2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep.\*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep.\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep.\*  
5: /cgn2\_6/ptodata/1/1aa/PCUS.COMB.pep.\*  
6: /cgn2\_6/ptodata/1/1aa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1095	100.0	207	4	US-09-068-960-43
2	1095	100.0	570	4	US-09-068-960-2
3	1095	100.0	570	4	US-09-068-960-4
4	1095	100.0	570	4	US-09-068-960-6
5	1095	100.0	570	4	US-09-068-960-10
6	1089	99.5	570	4	US-08-668-524-3
7	1089	99.5	570	4	US-09-068-960-8
8	1072	97.9	570	2	US-08-668-524-4
9	826	75.4	207	4	US-09-068-960-13
10	819	74.8	570	4	US-09-068-960-15
11	812.5	74.2	572	2	US-08-668-524-8
12	496.5	45.3	528	3	US-08-747-221B-37
13	496.5	45.3	528	4	US-09-005-051-37
14	432	39.5	530	3	US-08-747-221B-53
15	432	39.5	530	4	US-09-005-051-53
16	432	39.5	550	3	US-08-747-221B-19
17	432	39.5	550	4	US-09-005-051-19
18	429	39.2	505	4	US-08-747-221B-14
19	429	39.2	505	3	US-09-005-051-14
20	429	39.2	550	3	US-08-747-221B-58
21	429	39.2	550	4	US-09-005-051-58
22	391.5	35.8	570	4	US-08-747-221B-54
23	391.5	35.8	570	4	US-09-005-051-54
24	391.5	35.8	570	4	US-08-747-221B-25
25	391.5	35.8	570	4	US-09-005-051-25
26	390.5	35.7	570	4	US-08-747-221B-55
27	390.5	35.7	570	4	US-09-005-051-55

28	390.5	35.7	595	3	US-08-747-221B-31	Sequence 31, Appl
29	390.5	35.7	595	4	US-09-005-051-31	Sequence 31, Appl
30	370	33.8	600	2	US-08-370-156-4	Sequence 4, Appl
31	370	33.8	600	3	US-08-814-095-4	Sequence 4, Appl
32	370	33.8	600	4	US-08-975-084-1	Sequence 1, Appl
33	370	33.8	614	1	US-07-732-962A-2	Sequence 2, Appl
34	370	33.8	614	2	US-08-370-156-2	Sequence 2, Appl
35	370	33.8	614	3	US-08-446-100-19	Sequence 19, Appl
36	370	33.8	614	3	US-08-446-100-22	Sequence 21, Appl
37	370	33.8	614	3	US-08-446-100-23	Sequence 22, Appl
38	370	33.8	614	3	US-08-814-095-2	Sequence 23, Appl
39	370	33.8	614	5	PCT-US92-06106-2	Sequence 2, Appl
40	370	33.8	617	2	US-08-370-156-6	Sequence 2, Appl
41	370	33.8	617	3	US-08-814-095-6	Sequence 6, Appl
42	370	33.8	617	3	US-08-814-095-6	Sequence 6, Appl
43	368	33.6	614	3	US-08-446-100-25	Sequence 25, Appl
44	366.5	33.5	575	1	US-08-348-920-1	Sequence 1, Appl
45	363.5	33.2	575	1	US-08-348-920-2	Sequence 2, Appl

## ALIGNMENTS

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RESULT 1
US-09-068-960-43
Sequence 43, Application us/09068960A
Patent No. 6235515
GENERAL INFORMATION:
APPLICANT: Commonwealth Scientific and Industrial Rsrch. Org.
TITLE OF INVENTION: MALATHION CARBOXYL ESTERASE
FILE REFERENCE: Attorney Docket No. 6235515 50179-051
CURRENT APPLICATION NUMBER: us/09/068,960A
EARLIER FILING DATE: 1998-05-20
EARLIER APPLICATION NUMBER: PCT/AU96/00746
EARLIER FILING DATE: 1996-11-22
EARLIER APPLICATION NUMBER: AU 6751
EARLIER FILING DATE: 1995-11-23
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 43
LENGTH: 207
TYPE: PRT
ORGANISM: Lucilia cuprina
US-09-068-960-43

Query Match      100.0%; Score 1095; DB 4; Length 207;
Best Local Similarity 100.0%; Pred. No. 2.3e+124;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVDFITGKVGSEDCILYLVYTNLNPEYKRPVLYVYHGGFTIGENHRDMPDYFIKK 60
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Db 1 QVDFITGKVGSEDCILYLVYTNLNPEYKRPVLYVYHGGFTIGENHRDMPDYFIKK 60
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QY 61 DVLVINTQYRIGALGFLTNSSEDLNVPNGAGLADQVVALRWIKNCANFGNDNTVFG 120
    |||
Db 61 DVLVINTQYRIGALGFLTNSSEDLNVPNGAGLADQVVALRWIKNCANFGNDNTVFG 120
    |||

QY 121 ESAGAASTHMMLEQYRGLFHRRGILMSGNAICPLANTOCORHAFYTLAKYKGGDNK 180
    |||
Db 121 ESAGAASTHMMLEQYRGLFHRRGILMSGNAICPLANTOCORHAFYTLAKYKGGDNK 180
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QY 181 DVEFLMKARPODLIKLEKVLTEER 207
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Db 181 DVEFLMKARPODLIKLEKVLTEER 207
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RESULT 2
US-09-068-960-2
Sequence 2, Application us/09068960A
Patent No. 6235515
GENERAL INFORMATION:
APPLICANT: Commonwealth Scientific and Industrial Rsrch. Org.
TITLE OF INVENTION: MALATHION CARBOXYL ESTERASE
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FILE REFERENCE: Attorney Docket No. 6235515 50179-051
CURRENT FILING DATE: 1998-05-20
EARLIER APPLICATION NUMBER: PCT/AU96/00746
EARLIER FILING DATE: 1996-11-22
EARLIER APPLICATION NUMBER: AU 6751
EARLIER FILING DATE: 1995-11-23
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 2
LENGTH: 570
TYPE: PRT
ORGANISM: Lucilia cuprina
US-09-068-960-2

Query Match          100.0%; Score 1095; DB 4; Length 570;
Best Local Similarity 100.0%; Pred. No. 1e-123;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVDFITGKVGSEDCILYSLVYTNLNLPETKRPVLVYIHGGFTIGENHRDMYGPDYFIKK 60
DB 97 QVDFITGKVGSEDCILYSLVYTNLNLPETKRPVLVYIHGGFTIGENHRDMYGPDYFIKK 156
QY 61 DVLINIOYRLGALGFLSINSEDLNVPNGAGLKDQVMAIRKNNCANFGNPDNITVFG 120
DB 157 DVLINIOYRLGALGFLSINSEDLNVPNGAGLKDQVMAIRKNNCANFGNPDNITVFG 216
QY 121 ESAGAASTHYMMLTEOTRGLFHRGILMSGNAICPLANTOCOHRAFTLAKLAGYKGEDNDK 180
DB 217 ESAGAASTHYMMLTEOTRGLFHRGILMSGNAICPLANTOCOHRAFTLAKLAGYKGEDNDK 276
QY 181 DYLEFLMKAKPODLIKLEKVLTLLEER 207
DB 277 DYLEFLMKAKPODLIKLEKVLTLLEER 303

RESULT 3
US-09-068-960-4
Sequence 4, Application US/09068960A
Patent No. 6235515
GENERAL INFORMATION:
APPLICANT: Commonwealth Scientific and Industrial Rsrch. Org.
TITLE OF INVENTION: MALATHION CARBOXYL ESTERASE
FILE REFERENCE: Attorney Docket No. 6235515 50179-051
CURRENT APPLICATION NUMBER: US/09/068,960A
CURRENT FILING DATE: 1998-05-20
EARLIER APPLICATION NUMBER: PCT/AU96/00746
EARLIER FILING DATE: 1996-11-22
EARLIER APPLICATION NUMBER: AU 6751
EARLIER FILING DATE: 1995-11-23
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 4
LENGTH: 570
TYPE: PRT
ORGANISM: Lucilia cuprina
US-09-068-960-4

Query Match          100.0%; Score 1095; DB 4; Length 570;
Best Local Similarity 100.0%; Pred. No. 1e-123;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVDFITGKVGSEDCILYSLVYTNLNLPETKRPVLVYIHGGFTIGENHRDMYGPDYFIKK 60
DB 97 QVDFITGKVGSEDCILYSLVYTNLNLPETKRPVLVYIHGGFTIGENHRDMYGPDYFIKK 156
QY 61 DVLINIOYRLGALGFLSINSEDLNVPNGAGLKDQVMAIRKNNCANFGNPDNITVFG 120
DB 157 DVLINIOYRLGALGFLSINSEDLNVPNGAGLKDQVMAIRKNNCANFGNPDNITVFG 216
QY 121 ESAGAASTHYMMLTEOTRGLFHRGILMSGNAICPLANTOCOHRAFTLAKLAGYKGEDNDK 180
DB 217 ESAGAASTHYMMLTEOTRGLFHRGILMSGNAICPLANTOCOHRAFTLAKLAGYKGEDNDK 276
QY 181 DYLEFLMKAKPODLIKLEKVLTLLEER 207
DB 277 DYLEFLMKAKPODLIKLEKVLTLLEER 303
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QY 181 DYLEFLMKAKPODLIKLEKVLTLLEER 207
DB 277 DYLEFLMKAKPODLIKLEKVLTLLEER 303

RESULT 4
US-09-068-960-6
Sequence 6, Application US/09068960A
Patent No. 6235515
GENERAL INFORMATION:
APPLICANT: Commonwealth Scientific and Industrial Rsrch. Org.
TITLE OF INVENTION: MALATHION CARBOXYL ESTERASE
FILE REFERENCE: Attorney Docket No. 6235515 50179-051
CURRENT APPLICATION NUMBER: US/09/068,960A
CURRENT FILING DATE: 1998-05-20
EARLIER APPLICATION NUMBER: PCT/AU96/00746
EARLIER FILING DATE: 1996-11-22
EARLIER APPLICATION NUMBER: AU 6751
EARLIER FILING DATE: 1995-11-23
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 6
LENGTH: 570
TYPE: PRT
ORGANISM: Lucilia cuprina
US-09-068-960-6

Query Match          100.0%; Score 1095; DB 4; Length 570;
Best Local Similarity 100.0%; Pred. No. 1e-123;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVDFITGKVGSEDCILYSLVYTNLNLPETKRPVLVYIHGGFTIGENHRDMYGPDYFIKK 60
DB 97 QVDFITGKVGSEDCILYSLVYTNLNLPETKRPVLVYIHGGFTIGENHRDMYGPDYFIKK 156
QY 61 DVLINIOYRLGALGFLSINSEDLNVPNGAGLKDQVMAIRKNNCANFGNPDNITVFG 120
DB 157 DVLINIOYRLGALGFLSINSEDLNVPNGAGLKDQVMAIRKNNCANFGNPDNITVFG 216
QY 121 ESAGAASTHYMMLTEOTRGLFHRGILMSGNAICPLANTOCOHRAFTLAKLAGYKGEDNDK 180
DB 217 ESAGAASTHYMMLTEOTRGLFHRGILMSGNAICPLANTOCOHRAFTLAKLAGYKGEDNDK 276
QY 181 DYLEFLMKAKPODLIKLEKVLTLLEER 207
DB 277 DYLEFLMKAKPODLIKLEKVLTLLEER 303

RESULT 5
US-09-068-960-10
Sequence 10, Application US/09068960A
Patent No. 6235515
GENERAL INFORMATION:
APPLICANT: Commonwealth Scientific and Industrial Rsrch. Org.
TITLE OF INVENTION: MALATHION CARBOXYL ESTERASE
FILE REFERENCE: Attorney Docket No. 6235515 50179-051
CURRENT APPLICATION NUMBER: US/09/068,960A
CURRENT FILING DATE: 1998-05-20
EARLIER APPLICATION NUMBER: PCT/AU96/00746
EARLIER FILING DATE: 1996-11-22
EARLIER APPLICATION NUMBER: AU 6751
EARLIER FILING DATE: 1995-11-23
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 10
LENGTH: 570
TYPE: PRT
ORGANISM: Lucilia cuprina
US-09-068-960-10

Query Match          100.0%; Score 1095; DB 4; Length 570;
Best Local Similarity 100.0%; Pred. No. 1e-123;
```





ADDRESSEE: Lowe Price Lebanc & Becker  
STREET: 99 Canal Center Plaza, Suite 300  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: USA  
ZIP: 22314  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/669,524  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Price, Robert L.  
REGISTRATION NUMBER: 22,685  
REFERENCE/DOCKET NUMBER: 1451-021  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-684-1111  
TELEFAX: 703-684-1124  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 570 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-669-524-4

Query Match 97.9% Score 1072; DB 2; Length 570;  
Best Local Similarity 98.1%; Pred. No. 6,3e-121;  
Matches 203; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 QVDFITGKVGSEDCILYSVYTNINLPETKRPVLYIHGGGFIIGENHRDMYGPDYFIKK 60  
DB 97 QVDFITGKVGSEDCILYSVYTNINLPETKRPVLYIHGGGFIIGENHRDMYGPDYFIKK 156  
QY 61 DVLINIOYRLGALGFLSINSEDLNVPNGAGLKDQVMAIRKNNCANFGNPDNITVFG 120  
DB 157 DVLINIOYRLGALGFLSINSEDLNVPNGAGLKDQVMAIRKNNCANFGNPDNITVFG 216  
QY 121 ESAGASTHYMMLEQTRGLFHRGILMSGNAICPLANTOCQHRATFLAKLAGYKGEDNDK 180  
DB 217 ESAGASTHYMMLEQTRGLFHRGILMSGNAICPMANTQCQHRATFLAKLAGYKGEDNDK 276  
QY 181 DYLEFLMKAKPQDLIKLEKVTLEER 207  
DB 277 DYLEFLMKAKPQDLIKLEKVTLEER 303

RESULT 9  
US-09-068-960-15  
Sequence 15, Application US/09068960A  
Patent No. 6235515  
GENERAL INFORMATION:  
APPLICANT: Commonwealth Scientific and Industrial Resrch. Org.  
TITLE OF INVENTION: MALATHION CARBOXYLESTERASE  
FILE REFERENCE: Attorney Docket No. 6235515 50179-051  
CURRENT FILING DATE: 1998-05-20  
EARLIER APPLICATION NUMBER: PCT/AU96/00746  
EARLIER FILING DATE: 1996-11-22  
EARLIER APPLICATION NUMBER: AU 6751  
EARLIER FILING DATE: 1995-11-23  
NUMBER OF SEQ ID NOS: 43  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 15  
LENGTH: 207  
TYPE: PRT  
ORGANISM: Musca domestica  
US-09-068-960-15

Query Match 75.4%; Score 826; DB 4; Length 207;  
Best Local Similarity 74.6%; Pred. No. 8.2e-92;  
Matches 153; Conservative 25; Mismatches 27; Indels 0; Gaps 0;

QY 1 QVDFITGKVGSEDCILYSVYTNINLPETKRPVLYIHGGGFIIGENHRDMYGPDYFIKK 60  
DB 1 QVDFITGKVGSEDCILYSVYTNINLPETKRPVLYIHGGGFIIGENHRDMYGPDYFIKK 60  
QY 61 DVLINIOYRLGALGFLSINSEDLNVPNGAGLKDQVMAIRKNNCANFGNPDNITVFG 120  
DB 61 DVLINIOYRLGALGFLSINSEDLNVPNGAGLKDQVMAIRKNNCANFGNPDNITVFG 120  
QY 121 ESAGASTHYMMLEQTRGLFHRGILMSGNAICPLANTOCQHRATFLAKLAGYKGEDNDK 180  
DB 121 ESAGASTHYMMLEQTRGLFHRGILMSGNAICPMANTQCQHRATFLAKLAGYKGEDNDK 180  
QY 181 DYLEFLMKAKPQDLIKLEKVTLEER 205  
DB 181 DYLEFLMKAKPQDLIKLEKVTLEER 205

RESULT 10  
US-09-068-960-13  
Sequence 13, Application US/09068960A  
Patent No. 6235515  
GENERAL INFORMATION:  
APPLICANT: Commonwealth Scientific and Industrial Resrch. Org.  
TITLE OF INVENTION: MALATHION CARBOXYLESTERASE  
FILE REFERENCE: Attorney Docket No. 6235515 50179-051  
CURRENT FILING DATE: 1998-05-20  
EARLIER APPLICATION NUMBER: PCT/AU96/00746  
EARLIER FILING DATE: 1996-11-22  
EARLIER APPLICATION NUMBER: AU 6751  
EARLIER FILING DATE: 1995-11-23  
NUMBER OF SEQ ID NOS: 43  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 13  
LENGTH: 570  
TYPE: PRT  
ORGANISM: Musca domestica  
US-09-068-960-13

Query Match 74.8%; Score 819; DB 4; Length 570;  
Best Local Similarity 73.7%; Pred. No. 2.7e-90;  
Matches 151; Conservative 27; Mismatches 27; Indels 0; Gaps 0;

QY 1 QVDFITGKVGSEDCILYSVYTNINLPETKRPVLYIHGGGFIIGENHRDMYGPDYFIKK 60  
DB 97 QVDFITGKVGSEDCILYSVYTNINLPETKRPVLYIHGGGFIIGENHRDMYGPDYFIKK 156  
QY 61 DVLINIOYRLGALGFLSINSEDLNVPNGAGLKDQVMAIRKNNCANFGNPDNITVFG 120  
DB 157 DVLINIOYRLGALGFLSINSEDLNVPNGAGLKDQVMAIRKNNCANFGNPDNITVFG 216  
QY 121 ESAGASTHYMMLEQTRGLFHRGILMSGNAICPLANTOCQHRATFLAKLAGYKGEDNDK 180  
DB 217 ESAGASTHYMMLEQTRGLFHRGILMSGNAICPMANTQCQHRATFLAKLAGYKGEDNDK 276  
QY 181 DYLEFLMKAKPQDLIKLEKVTLEER 205  
DB 277 DYLEFLMKAKPQDLIKLEKVTLEER 301

RESULT 11  
US-08-669-524-8  
Sequence 8, Application US/08669524  
Patent No. 5843758  
GENERAL INFORMATION:  
APPLICANT: RUSSELL, Robyn J.  
APPLICANT: NEWCOMB, Richard D.  
APPLICANT: ROBIN, Geoffrey C.

RESULT 12  
 US-08-747-221B-37  
 ; Sequence 37, Application US/08/47221B  
 ; Patent No. 6063610  
 ;  
 ; GENERAL INFORMATION:  
 ;  
 ; APPLICANT: Silver, Gary W.  
 ;  
 ; APPLICANT: Wisniewski, Nancy  
 ;  
 ; TITLE OF INVENTION: No. 6063610e1 Carboxylesterase Nucleic Acid  
 ;  
 ; TITLE OF INVENTION: Molecules, Proteins and Uses Thereof  
 ;  
 ; NUMBER OF SEQUENCES: 66  
 ;  
 ; CORRESPONDENCE ADDRESS:  
 ;  
 ; ADDRESSEE: Carol Talkington Verser, Ph.D.  
 ;  
 ; ADDRESSEE: Heska Corporation

RESULT 13  
 US-09-005-051-37  
 : Sequence 37, Application US/09005051  
 : Patent No. 6291222  
 :  
 GENERAL INFORMATION:  
 :  
 APPLICANT: Silver, Gary W.  
 :  
 APPLICANT: Wisniewski, Nancy  
 :  
 TITLE OF INVENTION: No. 6291222el Carboxylesterase Nucleic  
 :  
 TITLE OF INVENTION: Molecules, Proteins and Uses Thereof  
 :  
 NUMBER OF SEQUENCES: 66  
 :  
 CORRESPONDENCE ADDRESS:  
 :  
 ADDRESSEE: Carol Talkington Verser, Ph.D.  
 :  
 ADDRESSEE: Heska Corporation  
 :  
 STREET: 1825 Sharp Point Drive  
 :  
 CITY: Fort Collins  
 :  
 STATE: Colorado  
 :  
 COUNTRY: USA  
 :  
 ZIP: 80525  
 :  
 COMPUTER READABLE FORM:  
 :  
 MEDIUM TYPE: Floppy disk  
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 COMPUTER: IBM PC compatible  
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 OPERATING SYSTEM: Windows 95  
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 SOFTWARE: Wordperfect for Windows, Version 7.0

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/005,051  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/747,221  
FILING DATE: No. 6291222ember 12, 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Verser, Carol Talkington  
REGISTRATION NUMBER: 37,459  
REFERENCE/DOCKET NUMBER: FC-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 970/493-7272  
TELEFAX: 970/484-9505  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 528 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-005-051-37

Query Match 45.3%; Score 496.5; DB 4; Length 528;  
Best Local Similarity 49.5%; Pred. No. 2,6e-51;  
Matches 97; Conservative 36; Mismatches 58; Indels 5; Gaps 3;

QY 2 VDFITKVGSGEDCLLYSYTNNINPTKRPVLYIHGGGFTIGENHRMYPGYFIKKD 61  
DB 69 VHEIKKIKVGAEDCLYLVNVPKTSKLLPFWVWVHGGGFTIGENHRMYPGYFIKKD 128  
QY 62 VLVINIOYRIGALGFLSLNSEDNLVPGNAGLDQVVALRWIKNNCANFGSPDNTVFG 121  
DB 129 IYVTFNRYRLGFLFNLIEE--APGNVGLMDQVVALKWKNNIASFGDPPNNTVIGE 186  
QY 122 SAGASTHYMMLTEQTRGIFHRGILMSGNAICPL--LNTQCQRAFTLAKIAGYGEDND 179  
DB 187 SAGGASVHYMLSDLSKGFHKAISQSGAFNFWALQHDNNKEMERLCKLGHV--VDNE 245  
QY 180 KDVEFLMKAKRPDILK 195  
DB 246 TEALKILROAPIDDLI 261

RESULT 14  
US-08-747-221B-53  
Sequence 53, Application US/08747221B  
Patent No. 6063610  
GENERAL INFORMATION:  
APPLICANT: Silver, Gary W.  
APPLICANT: Wisniewski, Nancy  
TITLE OF INVENTION: No. 6063610e1 Carboxylesterase Nucleic Acid  
TITLE OF INVENTION: Molecules, Proteins and Uses Thereof  
NUMBER OF SEQUENCES: 66  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Carol Talkington Verser, Ph.D.  
ADDRESSEE: Heska Corporation  
STREET: 1825 Sharp Point Drive  
CITY: Fort Collins  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80525  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: Wordperfect for Windows, Version 7.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/747,221B  
FILING DATE: No. 6063610ember 12, 1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Verser, Carol Talkington  
REGISTRATION NUMBER: 37,459

REFERENCE/DOCKET NUMBER: FC-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 970/493-7272  
TELEFAX: 970/484-9505  
INFORMATION FOR SEQ ID NO: 53:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 530 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-747-221B-53

Query Match 39.5%; Score 432; DB 3; Length 530;  
Best Local Similarity 43.9%; Pred. No. 1,7e-43;  
Matches 86; Conservative 32; Mismatches 74; Indels 4; Gaps 3;

QY 2 VDFITKVGSGEDCLLYSYTNNINPTKRPVLYIHGGGFTIGENHRMYPGYFIKKD 61  
DB 68 LNFELKRIEGDEDLVNVYAPKTSKLLPFWVWVHGGGFTIGENHRMYPGYFIKKD 127  
QY 62 VLVINIOYRIGALGFLSLNSEDNLVPGNAGLDQVVALRWIKNNCANFGSPDNTVFG 121  
DB 128 IYVTFNRYRLGFLFNLIEE--GAPGNVGLMDQVVALKWKNNIASFGDPPNNTVIGE 185  
QY 122 SAGASTHYMMLTEQTRGIFHRGILMSGNAICPL--LNTQCQRAFTLAKIAGYGEDND 180  
DB 186 SAGGASVHYMLSDLSKGFHKAISQSGAFNFWALQHDNNKEMERLCKLGHV--VDNE 244  
QY 181 KDVEFLMKAKRPDILK 196  
DB 245 DALEFLQAPVDSLK 260

RESULT 15  
US-09-005-051-53  
Sequence 53, Application US/09005051  
Patent No. 6291222  
GENERAL INFORMATION:  
APPLICANT: Silver, Gary W.  
APPLICANT: Wisniewski, Nancy  
TITLE OF INVENTION: No. 6291222e1 Carboxylesterase Nucleic Acid  
TITLE OF INVENTION: Molecules, Proteins and Uses Thereof  
NUMBER OF SEQUENCES: 66  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Carol Talkington Verser, Ph.D.  
ADDRESSEE: Heska Corporation  
STREET: 1825 Sharp Point Drive  
CITY: Fort Collins  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80525  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: Wordperfect for Windows, Version 7.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/005,051  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/747,221  
FILING DATE: No. 6291222ember 12, 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Verser, Carol Talkington  
REGISTRATION NUMBER: 37,459  
REFERENCE/DOCKET NUMBER: FC-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 970/493-7272  
TELEFAX: 970/484-9505  
INFORMATION FOR SEQ ID NO: 53:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 530 amino acids

TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-005-051-53

Query Match 39.5%; Score 432; DB 4; Length 530;  
Best Local Similarity 43.9%; Pred. No. 1.7e-43;  
Matches 86; Conservative 32; Mismatches 74; Indels 4; Gaps 3;

QY 2 VDEFTGKVGSGEDCLVSYTNNLNPEYRRLVYIHGGFTIGENHNDMGPDYFIKQD 61  
Db 68 LNFETLKIEGDEDCLVNVAAPKTTSDKRLPVFVWVGSGFVTSQNLFEQSPDYLVND 127  
QY 62 VVLTINQYRLGALGFSLNSDNLNPGNAGLKDQVALRMKNNCANFGNDNTVFGE 121  
Db 128 VIEFVENYRLGPLGFLELE--GAPGNVGLDQVALKTKENTIEKFGDPENTITIGV 185  
QY 122 SAGASTHYMTTEQTRGIFHRGIIIMSGNAICPLA-NTCCQHRATFLAKLAGYKGEDNDK 180  
Db 186 SAGGASVHYLLSHSTTGLYKRAIAQSGSALNPMWAFORHPVKRSIQLAETILGHP-TNNTQ 244  
QY 181 DYLEFLMKAKPODLTK 196  
Db 245 DALEFLQKAPVDSLK 260

Search completed: April 4, 2003, 09:18:12  
Job time: 7.7278 secs

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GenCore version 5.1.4-p5.4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 4, 2003, 09:16:33 ; Search time 8.92471 Seconds  
(without alignments)  
1417.991 Million cell updates/sec

Title: US-09-776-910-43

Perfect score: 1095  
Sequence: 1 QVDFITGKVGSEDCDLYLSV.....KAKPOLIKLEKVLLEER 207

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 248812 segs, 61136040 residues

Total number of hits satisfying chosen parameters: 248812

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published\_Applications\_AA:\*

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2: /cgn2\_6/ptodata/2/pubpaa/PCF\_NEW\_PUB.pep:\*

3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*

4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*

5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*

6: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*

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8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*

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14: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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2	401.5	36.7	612	9	US-09-875-353-4
3	391	35.7	585	10	US-09-934-323-4
4	361.5	33.0	574	10	US-09-748-739A-21
5	359.5	32.8	574	10	US-09-748-739A-23
6	356.5	32.6	574	10	US-09-748-739A-22
7	353.5	32.3	574	10	US-09-748-739A-4
8	353.5	32.3	574	10	US-09-748-739A-6
9	353.5	32.3	574	10	US-09-748-739A-8
10	353.5	32.3	574	10	US-09-748-739A-17
11	353.5	32.3	574	10	US-09-748-739A-18
12	353.5	32.3	574	10	US-09-748-739A-19
13	353.5	32.3	574	10	US-09-748-739A-20
14	353.5	32.3	602	10	US-09-748-739A-2
15	331.5	30.3	568	9	US-09-418-176-4
16	331.5	30.3	722	9	US-09-418-176-3
17	331.5	30.3	747	9	US-09-418-176-2
18	323.5	29.5	535	9	US-09-738-626-4754
19	322.5	29.5	549	9	US-10-102-806-689

20	322.5	29.5	565	10	US-09-895-860-5	Sequence 5, App1
21	321.5	29.4	545	9	US-09-978-295A-254	Sequence 254, App
22	321.5	29.4	545	9	US-09-978-697-254	Sequence 254, App
23	321.5	29.4	545	9	US-09-978-192A-254	Sequence 254, App
24	321.5	29.4	545	9	US-09-999-832A-254	Sequence 254, App
25	321.5	29.4	545	9	US-09-978-189-254	Sequence 254, App
26	321.5	29.4	545	9	US-10-174-590-58	Sequence 58, App1
27	321.5	29.4	545	9	US-10-174-758-58	Sequence 58, App1
28	321.5	29.4	545	9	US-10-175-727-58	Sequence 58, App1
29	321.5	29.4	545	9	US-10-173-706-58	Sequence 58, App1
30	321.5	29.4	545	9	US-10-175-738-58	Sequence 58, App1
31	321.5	29.4	545	9	US-10-175-752-58	Sequence 58, App1
32	321.5	29.4	545	9	US-10-176-482-58	Sequence 58, App1
33	321.5	29.4	545	9	US-10-176-757-58	Sequence 58, App1
34	321.5	29.4	545	9	US-10-176-913-58	Sequence 58, App1
35	321.5	29.4	545	9	US-10-180-552-58	Sequence 58, App1
36	321.5	29.4	545	9	US-10-180-557-58	Sequence 58, App1
37	321.5	29.4	545	9	US-10-173-700-58	Sequence 58, App1
38	321.5	29.4	545	9	US-10-174-572-58	Sequence 58, App1
39	321.5	29.4	545	9	US-10-174-582-58	Sequence 58, App1
40	321.5	29.4	545	9	US-10-174-588-58	Sequence 58, App1
41	321.5	29.4	545	9	US-10-175-739-58	Sequence 58, App1
42	321.5	29.4	545	9	US-10-175-740-58	Sequence 58, App1
43	321.5	29.4	545	9	US-10-175-743-58	Sequence 58, App1
44	321.5	29.4	545	9	US-10-176-488-58	Sequence 58, App1
45	321.5	29.4	545	9	US-10-176-488-58	Sequence 58, App1

## ALIGNMENTS

RESULT 1

US-10-023-515-4

Sequence 4, Application US/10023515

Publication No. US20020182636A1

GENERAL INFORMATION:

APPLICANT: Curtiss, Rory A. J.

TITLE OF INVENTION: 53010, A NOVEL HUMAN CARBOXYL ESTERASE

TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF

FILE REFERENCE: 10448-122001

CURRENT FILING DATE: 2001-12-18

PRIOR APPLICATION NUMBER: 60/256,369

PRIOR FILING DATE: 2000-12-18

PRIOR APPLICATION NUMBER: 60/279,508

PRIOR FILING DATE: 2001-03-28

NUMBER OF SEQ ID NOS: 6

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 4

LENGTH: 574

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Consensus sequence

US-10-023-515-4

Query Match 36.7% Score 401.5; DB 9; Length 574;

Best Local Similarity 41.3% Pred. No. 5.9e-35;

Matches 86; Conservative 43; Mismatches 64; Indels 15; Gaps 6;

QY 12 SEDCLVLYVT-NMLINETKRPVLVYIHGGFTIGENHR---DMYGPDIYRK-DVLLIN 66

Db 91 SEDCLVLYVTIKTKRKNSKLPMVWYHGGGFMFGSCHSLPLSDGSESLARCGNIVVS 150

QY 67 IYRGLALGFLSLNSEDLVNPGNAGLKQYVALRWIKNNCANFGNPDNITYGESAGAA 126

Db 151 INKRLGLGLSLGDDDLPSGNGVGLDRLALRWODNIAAFGDPNSVTIGESAGAA 210

QY 127 STYHMMTE-----QIRGFHFGILMSGNAICPLA---NTQCHAFPLAKAGKGD 177

Db 211 SVSILLISNGDNPSPSKGLFHRAISOSGSLSPMAIQSESNRGRAKELARLLGC-NET 269





[illegible]



APPLICATION NUMBER: PCT/SE96/00318  
FILING DATE: 12-MAR-1996  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: SE 9501939-4  
 FILING DATE: 24-MAY-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Thelma A. Chen Cleland  
 REGISTRATION NUMBER: 40,948  
 REFERENCE/DOCKET NUMBER: 1103326-0206  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 819-8200  
 TELEFAX: (212) 354-8113  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 568 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 HYPOTHETICAL: NO  
 ORIGINAL SOURCE:  
 ORGANISM: Homo sapiens  
 TISSUE TYPE: Mammary gland  
 FEATURE:  
 NAME/KEY: Peptide  
 LOCATION: 1..568  
 OTHER INFORMATION: /label= Variant\_C  
 PUBLICATION INFORMATION:  
 AUTHORS: Hansson, Lennart  
 AUTHORS: Blackberg, Lars  
 AUTHORS: Edlund, Michael  
 AUTHORS: Lundberg, Lennart  
 AUTHORS: Stromqvist, Mats  
 AUTHORS: Hernehl, Olle  
 TITLE: Recombinant Human Milk Bile Salt-stimulated  
 TITLE: Lipase  
 JOURNAL: J. Biol. Chem.  
 VOLUME: 268  
 ISSUE: 35  
 PAGES: 26692-26698  
 DATE: Dec. 15-1993  
 US-09-418-176-4

Query Match 30.3%; Score 331.5; DB 9; Length 568;  
 Best Local Similarity 37.4%; Pred. No. 2.1e-27;  
 Matches 76; Conservative 31; Mismatches 53; Indels 43; Gaps 7;

QY 11 GSEDCIYLSVYTNLNLPETRR--PVLVIYIHGGFIIGENHRDMY-----GPDYFIKKD 61  
 DB 76 GDEDCILINIWVPGKQVSRDLPMIWIYGAFLMSGHGAFUNNYLYDGEIATPGN 135  
 QY 62 VVLINIQYRLGALGFLSLNSEDINVPGNAGLKDQVVALRWIKNKCANFGSNPDNITVEGE 121  
 DB 136 VIVVTENYRVGPGFLS--TGDANLPNGNYGLRDQHMALWVKRRIAAFGDPPNITLFGGE 193  
 QY 122 SAGAASTHYWMLTEOTRGFLHRCILMSGNAI-----CPLAN--- 157  
 DB 194 SAGGASVSLQTLSPYKGLIRRAISQSGVALSPWVIOKNPLFWAKKVAEKVGCPCVGDAAAR 253  
 QY 158 -TQC---QHRAPFLA---KLAG 172  
 DB 254 MAQCLKVTDPRALTLAKVPLAG 276

Search completed: April 4, 2003, 09:34:08  
 Job time: 10.9247 secs

RESULT 7  
US-09-068-960-10  
Sequence 10, Application US/09068960A  
Patent No. 6235515  
GENERAL INFORMATION:  
APPLICANT: Commonwealth Scientific and Industrial Rsrch. Org.  
TITLE OF INVENTION: MALATHION CARBOXYLESTERASE  
FILE REFERENCE: Attorney Docket No. 6235515 50179-051  
CURRENT APPLICATION NUMBER: US/09/068,960A  
CURRENT FILING DATE: 1998-05-20  
EARLIER APPLICATION NUMBER: PCT/AU96/00746

[illegible]

RESULT 8  
 : Sequence 3 Application US/08669524  
 : Patent No. 5843758  
 : GENERAL INFORMATION:  
 : APPLICANT: RUSSELL, Robyn J.  
 : APPLICANT: NEWCOMB, Richard D.  
 : APPLICANT: ROBIN, Geoffrey C.  
 : APPLICANT: BOYCE, Thomas M.  
 : APPLICANT: CAMPBELL, Peter M.  
 : APPLICANT: PARKER, Anthony G.  
 : APPLICANT: OAKSHOTT, John G.  
 : APPLICANT: SMYTH, Kerrie A.  
 : TITLE OF INVENTION: ENZYME BASED BIOREMEDIATION  
 : NUMBER OF SEQUENCES: 22  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: Lowe Price Leblanc & Becker  
 : STREET: 99 Canal Center Plaza, Suite 300  
 : CITY: Alexandria  
 : STATE: Virginia  
 : COUNTRY: USA  
 : ZIP: 22314  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: PatentIn Release #1.0, Version #1.30  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/669,524  
 : FILING DATE:  
 : CLASSIFICATION: 435  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: Price, Robert L.  
 : REGISTRATION NUMBER: 22,685  
 : REFERENCE/DOCKET NUMBER: 1451-021  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: 703-684-1124  
 : TELEFAX: 703-684-1124  
 : INFORMATION FOR SEQ. ID NO.: 3:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 570 amino acids

TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-669-524-3

Query Match 75.5%; Score 825; DB 2; Length 570;  
Best Local Similarity 74.6%; Pred. No. 3.7e-92;  
Matches 153; Conservative 25; Mismatches 27; Indels 0; Gaps 0;

QY 1 QDFTSGKPTGSEDCLYLVNTNDINPDKRPVWFHGGGFTFGEANRNNYGPDPYEMK 60  
DB 97 QVDFITGKVCSEDCLYLVNTNNINPETKRPVLYIHGGGFTFGEANRNNYGPDPYEMK 156  
QY 61 PVLVTVQYRLGVLGFLSLKSENINVPGNAGLKDQVMAIRWFKSNIAIFGGDVNDITVFG 120  
DB 157 DVVLINIOYRLGALGFLSLNSEDVLPNGAGLKDQVMAIRWFKSNKNCANFGNPNITVFG 216  
QY 121 ESAGGASTHYMMITTEOTRGLFHRGIMSGNSCASSASTECOSRALTMAKRVYKGEENK 180  
DB 217 ESAGGASTHYMMITTEOTRGLFHRGIMSGNAICPMANTOCORRAFTLAKLAGYKGEDNDK 276  
QY 181 DLEFLMAKPNYDLIKEPOVLTPE 205  
DB 277 DVLEFLMAKPNYDLIKEPOVLTPE 301

RESULT 9  
US-09-068-960-8  
Sequence 8, Application US/09068960A  
Patent No. 6235513  
GENERAL INFORMATION:  
APPLICANT: Commonwealth Scientific and Industrial Rsrch. Org.  
TITLE OF INVENTION: MALATHION CARBOXYL ESTERASE  
FILE REFERENCE: Attorney Docket No. 6235515 50179-051  
CURRENT APPLICATION NUMBER: US/09/068,960A  
CURRENT FILING DATE: 1998-05-20  
EARLIER APPLICATION NUMBER: PCT/AU96/00746  
EARLIER FILING DATE: 1996-11-22  
EARLIER APPLICATION NUMBER: AU 6751  
EARLIER FILING DATE: 1995-11-23  
NUMBER OF SEQ ID NOS: 43  
SOFTWARE: Patentln Ver. 2.0  
SEQ ID NO 8  
LENGTH: 570  
TYPE: PRT  
ORGANISM: Lucilia cuprina  
US-09-068-960-8

Query Match 75.5%; Score 825; DB 4; Length 570;  
Best Local Similarity 74.6%; Pred. No. 3.7e-92;  
Matches 153; Conservative 25; Mismatches 27; Indels 0; Gaps 0;

QY 1 QDFTSGKPTGSEDCLYLVNTNDINPDKRPVWFHGGGFTFGEANRNNYGPDPYEMK 60  
DB 97 QVDFITGKVCSEDCLYLVNTNNINPETKRPVLYIHGGGFTFGEANRNNYGPDPYEMK 156  
QY 61 PVLVTVQYRLGVLGFLSLKSENINVPGNAGLKDQVMAIRWFKSNIAIFGGDVNDITVFG 120  
DB 157 DVVLINIOYRLGALGFLSLNSEDVLPNGAGLKDQVMAIRWFKSNKNCANFGNPNITVFG 216  
QY 121 ESAGGASTHYMMITTEOTRGLFHRGIMSGNSCASSASTECOSRALTMAKRVYKGEENK 180  
DB 217 ESAGGASTHYMMITTEOTRGLFHRGIMSGNAICPMANTOCORRAFTLAKLAGYKGEDNDK 276  
QY 181 DLEFLMAKPNYDLIKEPOVLTPE 205  
DB 277 DVLEFLMAKPNYDLIKEPOVLTPE 301

RESULT 10  
US-08-669-524-4  
Sequence 4, Application US/08669524

Patent No. 5843758  
GENERAL INFORMATION:  
APPLICANT: RUSSELL, Robyn J.  
APPLICANT: NEWCOMB, Richard D.  
APPLICANT: ROBIN, Geoffrey C.  
APPLICANT: BOYCE, Thomas M.  
APPLICANT: CAMPBELL, Peter M.  
APPLICANT: PARKER, Anthony G.  
APPLICANT: OAKESHOTY, John G.  
APPLICANT: SMYTH, Kertie A.  
TITLE OF INVENTION: ENZYME BASED BIOREMEDIATION  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lowe Price Leblanc & Becker  
STREET: 99 Canal Center Plaza, Suite 300  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: USA  
ZIP: 22314

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentln Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/669,524  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Price, Robert L.  
REGISTRATION NUMBER: 22,685  
REFERENCE/DOCKET NUMBER: 1451-021  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-684-1111  
TELEFAX: 703-684-1124  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 570 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-669-524-4

Query Match 74.2%; Score 811; DB 2; Length 570;  
Best Local Similarity 73.7%; Pred. No. 1.9e-90;  
Matches 151; Conservative 25; Mismatches 29; Indels 0; Gaps 0;

QY 1 QDFTSGKPTGSEDCLYLVNTNDINPDKRPVWFHGGGFTFGEANRNNYGPDPYEMK 60  
DB 97 QVDFITGKVCSEDCLYLVNTNNINPETKRPVLYIHGGGFTFGEANRNNYGPDPYEMK 156  
QY 61 PVLVTVQYRLGVLGFLSLKSENINVPGNAGLKDQVMAIRWFKSNIAIFGGDVNDITVFG 120  
DB 157 DVVLINIOYRLGALGFLSLNSEDVLPNGAGLKDQVMAIRWFKSNKNCANFGNPNITVFG 216  
QY 121 ESAGGASTHYMMITTEOTRGLFHRGIMSGNSCASSASTECOSRALTMAKRVYKGEENK 180  
DB 217 ESAGGASTHYMMITTEOTRGLFHRGIMSGNAICPMANTOCORRAFTLAKLAGYKGEDNDK 276  
QY 181 DLEFLMAKPNYDLIKEPOVLTPE 205  
DB 277 DVLEFLMAKPNYDLIKEPOVLTPE 301

RESULT 11  
US-08-669-524-8  
Sequence 8, Application US/08669524  
Patent No. 5843758  
GENERAL INFORMATION:  
APPLICANT: RUSSELL, Robyn J.  
APPLICANT: NEWCOMB, Richard D.  
APPLICANT: ROBIN, Geoffrey C.

```

APPLICANT: BOYCE, Thomas M.
APPLICANT: CAMPBELL, Peter M.
APPLICANT: PARKER, Anthony G.
APPLICANT: OAKSHOTT, John G.
APPLICANT: SMITH, Kerrie A.
TITLE OF INVENTION: ENZYME BASED BIOREMEDIATION
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESS: Lowe Price Leblanc & Becker
STREET: 99 Canal Center Plaza, Suite 300
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22314

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/669,524
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Price, Robert L.
REGISTRATION NUMBER: 22,685
REFERENCE/DOCKET NUMBER: 1451-021
TELEPHONE: 703-684-1111
TELEFAX: 703-684-1124
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 572 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-669-524-8

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Query Match 67.3%; Score 736; DB 2; Length 572;
Best Local Similarity 67.5%; Pred. No. 2,9e-81;
Matches 141; Conservative 25; Mismatches 41; Indels 2; Gaps 2;

QY 1 QTFISGKPTSEDCLYLVNTYNDLNDPKRRPVWVFIHGGFTFGANRWYGPDYFMKPVY 60
DB 97 QVQFPEKDESEDCLYLVNTYNNKPKARPVWVWVHGGFTFGANRWYGPDYFMKE 156
QY 61 PVLVTVQYRGLVGLFSLKSENLVPGNAGLKDQVVALRMFKNSNIAIFGSDVNTIVFG 120
DB 157 DVVLVTVQYRGLVGLFSLKSENLVPGNAGLKDQVVALRMFKNSNIAIFGSDVNTIVFG 216
QY 121 ESAGASHTYMMTEQTRGLFHRGIMSGNSMCSA--STECQSRALTMARVYKGEENE 179
DB 217 ESAGASHTYMMTEQTRGLFHRGILDSGSAICPMAYNGDITNHPYRIAKLVYKGEEND 276
QY 180 KDLFLMKANPYDLIRKEEPOVL-PERM 207
DB 277 KDVLFLQNVAKADLIRVEENVLLLEERM 305

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RESULT 12
US-08-747-221B-37
Sequence 37, Application US/08747221B
Patent No. 6063610
GENERAL INFORMATION:
APPLICANT: Silver, Gary W.
APPLICANT: Wisniewski, Nancy
TITLE OF INVENTION: No. 6063610e1 Carboxylesterase Nucleic Acid
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESS: Heska Corporation

```

```

STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/747,221B
FILING DATE: No. 6063610ember 12, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: FC-1
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 528 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-747-221B-37

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Query Match 42.4%; Score 463.5; DB 3; Length 528;
Best Local Similarity 47.3%; Pred. No. 5.9e-48;
Matches 98; Conservative 34; Mismatches 64; Indels 11; Gaps 4;

QY 4 FISGKPTSEDCLYLVNTYNDLNDPKRRPVWVFIHGGFTFGANRWYGPDYFMKPVY 63
DB 71 FIKRIKVGAECDCLYLVNYPKTSKSLPVWVWVHGGFTFGANRWYGPDYFMKPVY 130
QY 64 LVTVQYRGLVGLFSLKSENLVPGNAGLKDQVVALRMFKNSNIAIFGSDVNTIVGES 123
DB 131 LVTVQYRGLVGLFSLKSENLVPGNAGLKDQVVALRMFKNSNIAIFGSDVNTIVGES 188
QY 124 GASTHYMMTEQTRGLFHRGIMSGNSMCSASTECQSR--ALTMARVYKGEENE 181
DB 189 GASTHYMMTEQTRGLFHRGILDSGSAICPMAYNGDITNHPYRIAKLVYKGEEND 247
QY 182 ILFLMKANPYDLIRKEEPOVL-PERM 202
DB 248 ALKILRQAPIDLDLIRKEEPOVL-PERM 274

```

```

RESULT 13
US-09-005-051-37
Sequence 37, Application US/09005051
Patent No. 6291222
GENERAL INFORMATION:
APPLICANT: Silver, Gary W.
APPLICANT: Wisniewski, Nancy
TITLE OF INVENTION: No. 6291222e1 Carboxylesterase Nucleic Acid
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESS: Heska Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0

```

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/005,051  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/747,221  
 FILING DATE: No. 6291222ember 12, 1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Verser, Carol Talkington  
 REGISTRATION NUMBER: 37,459  
 REFERENCE/DOCKET NUMBER: FC-1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 970/493-7272  
 TELEFAX: 970/484-9505  
 INFORMATION FOR SEQ ID NO: 37:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 528 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-005-051-37

Query Match 42.4%; Score 463.5; DB 4; Length 528;  
 Best Local Similarity 47.3%; Pred. No. 5,9e-48;  
 Matches 98; Conservative 34; Mismatches 64; Indels 11; Gaps 4;  
 QY 4 FISKPTGSEDCLYLVNTDLPDKRPVWFIHGGGFTFGEANRWYGPDYFMKRPV 63  
 DB 71 FIKKIVGAEDCLVLYVYVKTSEKSLPVMWVHGGGFTGSGNSMGPPELMDGYV 130  
 QY 64 LVTVQVRLGVGLFSLKSENLNPGNAGLKDQVALRFRKSNIAIFGADVNTIVGES 123  
 DB 131 LVTVNRYRLGVGLFNLGLE--EAPGNVGLDQVALKRWNNIASFGDDNNVTIEESA 188  
 QY 124 GGASTHWMITQTRGLFHRGIMSGNSMSSASTECQSR--ALTMARVGYGKEENKD 181  
 DB 189 GGASVHYLMISDLKGLFHRKAISSQGSAPFNWALQHDNNKRNAPRLCKLGHV-VDNETE 247  
 QY 182 ILFLKRNAPYDLI-----KEEPOVL 202  
 DB 248 ALKILQAPIDLIDNRIRKPRDKQLI 274

RESULT 14  
 US-08-747-221B-53  
 Sequence 53; Application US/08747221B  
 Patent No. 6063610  
 GENERAL INFORMATION:  
 APPLICANT: Silver, Gary W.  
 APPLICANT: Wisniewski, Nancy  
 TITLE OF INVENTION: No. 6063610el Carboxylesterase Nucleic Acid  
 TITLE OF INVENTION: Molecules, Proteins and Uses Thereof  
 NUMBER OF SEQUENCES: 66  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Carol Talkington Verser, Ph.D.  
 STREET: 1825 Sharp Point Drive  
 CITY: Fort Collins  
 STATE: Colorado  
 COUNTRY: USA  
 ZIP: 80525  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: Windows 95  
 SOFTWARE: WordPerfect for Windows, Version 7.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/747,221B  
 FILING DATE: No. 6063610ember 12, 1996  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Verser, Carol Talkington  
 REGISTRATION NUMBER: 37,459

REFERENCE/DOCKET NUMBER: FC-1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 970/493-7272  
 TELEFAX: 970/484-9505  
 INFORMATION FOR SEQ ID NO: 53:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 530 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-747-221B-53

Query Match 39.2%; Score 428; DB 3; Length 530;  
 Best Local Similarity 46.0%; Pred. No. 1.3e-45;  
 Matches 91; Conservative 29; Mismatches 74; Indels 4; Gaps 3;  
 QY 3 DFISKPTGSEDCLYLVNTDLPDKRPVWFIHGGGFTFGEANRWYGPDYFMKRPV 62  
 DB 69 NFELKRIEGDEDCLVLYVYVKTSDKLPVFWYHGGGFTGSGNLEFGSPDYLVYDV 128  
 QY 63 LVTVQVRLGVGLFSLKSENLNPGNAGLKDQVALRFRKSNIAIFGADVNTIVGES 122  
 DB 129 LVTVNRYRLGVGLFNLGLE--GAPGNVGLDQVALKRWNNIEKFGDDNNVTIEGVS 186  
 QY 123 GGASTHWMITQTRGLFHRGIMSGNSMSSA-STECQSRALTMARVGYGKEENKD 181  
 DB 187 GGASVHYLLISHTTGTGLYKRAIASSGALNPWAFQRRHPKRSLOLAEILGHV-TNNTQD 245  
 QY 182 ILFLKRNAPYDLIKEEP 199  
 DB 246 ALFLQKAPVDSLKKMP 263

RESULT 15  
 US-09-005-051-53  
 Sequence 53; Application US/09005051  
 Patent No. 6291222  
 GENERAL INFORMATION:  
 APPLICANT: Silver, Gary W.  
 APPLICANT: Wisniewski, Nancy  
 TITLE OF INVENTION: No. 6291222el Carboxylesterase Nucleic Acid  
 TITLE OF INVENTION: Molecules, Proteins and Uses Thereof  
 NUMBER OF SEQUENCES: 66  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Carol Talkington Verser, Ph.D.  
 STREET: 1825 Sharp Point Drive  
 CITY: Fort Collins  
 STATE: Colorado  
 COUNTRY: USA  
 ZIP: 80525  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: Windows 95  
 SOFTWARE: WordPerfect for Windows, Version 7.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/005,051  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/747,221  
 FILING DATE: No. 6291222ember 12, 1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Verser, Carol Talkington  
 REGISTRATION NUMBER: 37,459  
 REFERENCE/DOCKET NUMBER: FC-1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 970/493-7272  
 TELEFAX: 970/484-9505  
 INFORMATION FOR SEQ ID NO: 53:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 530 amino acids







Query March	33.4%	Score 365.5;	DB 9;	Length 574;
Best Local Similarity	39.7%;	Pred. No. 2.5e-31;		
Matches 79;	Conservative 42;	Mismatches 63;	Indels 15;	Gaps

QY	12	SEDCLYINVT-NDLPDKRPVVFHGGGFGEAN----	FNMYGPDYFMKRPVLYT	66
Db	91	SEDCLYINVTPTKNTKPSKLPVYMWIHGGCFMGSHSLPLSYGSELAEGVNIYVS		150
QY	67	VQRLVGLGLSLKSDNLNVGNGLDQWALRWFKSNIAIFGSDVNTVYFESAGA		126
Db	151	INRLPLGLTSGDKLPFGSNGGLDDQRLATKWODNIAAFGGPNSVTTFESGAA		210
QY	127	STHYMITE-----QTRGLPHRCIMMSGMS-----CSSASTECOSRALTMKRGYKGE		177
Db	211	SVALLSLNSGNDNPPSSGGLPHRAISQGSALSPWALIOSESNAKRAEIALLLGC-NET		269

Page 2

10

NUMBER OF SEQ ID NOS: 31  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 23  
 LENGTH: 574  
 TYPE: PRF  
 ORGANISM: Rattus sp.  
 US-09-748-739A-23

Query Match  
 Best Local Similarity 31.8%; Score 347.5; DB 10; Length 574;  
 Matches 81; Conservative 38; Mismatches 69; Indels 7; Gaps 5;

QY 12 SEDCLYLVNTDNDLPDKRPVWFHGGGTFEGEANNRMWGPDPYFMK-KPVVLVTVOYR 70  
 DB 89 SEDCLYLVNTDNDLPDKRPVWFHGGGTFEGEANNRMWGPDPYFMK-KPVVLVTVOYR 147  
 QY 71 LGVLGFLSKSENLNVPGNAGLKDQVMAIRFKSNIAIFGSDVNTIVFESAGASTHY 130  
 DB 148 VGALGFLALPG-NPEVAPGNMGLFDQALQWQKNIAAFGNGKSVTLFESAGASVSL 206  
 QY 131 MMITQOTGLFHRGIMSGNSMCSA--STECOSRALTMARKRVYKGEENEKDIIEFLM 187  
 DB 207 HLCSQSYPLFTFRALIESGSSNAPVAVKHPPEARNTLTLAKFTGC-SKENDTEITICLR 265  
 QY 188 KANPYDLIKEEPOVL 202  
 DB 266 SKDPOEITLNEKVL 280

RESULT 6  
 US-09-748-739A-22  
 Sequence 22, Application US/09748739A  
 Patent No. US20020119489A1  
 GENERAL INFORMATION:  
 APPLICANT: Lockridge, Oksana  
 APPLICANT: Watkins, Jeffrey D.  
 TITLE OF INVENTION: Butyrylcholinesterase Variants and  
 FILE REFERENCE: P-IX 4143  
 CURRENT APPLICATION NUMBER: US/09/748,739A  
 NUMBER OF SEQ ID NOS: 31  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 22  
 LENGTH: 574  
 TYPE: PRF  
 ORGANISM: Felis catus  
 US-09-748-739A-22

Query Match  
 Best Local Similarity 31.4%; Score 343.5; DB 10; Length 574;  
 Matches 78; Conservative 46; Mismatches 69; Indels 7; Gaps 5;

QY 12 SEDCLYLVNTDNDLPDKRPVWFHGGGTFEGEANNRMWGPDPYFMK-KPVVLVTVOYR 70  
 DB 89 SEDCLYLVNTDNDLPDKRPVWFHGGGTFEGEANNRMWGPDPYFMK-KPVVLVTVOYR 147  
 QY 71 LGVLGFLSKSENLNVPGNAGLKDQVMAIRFKSNIAIFGSDVNTIVFESAGASTHY 130  
 DB 148 VGALGFLALPG-NPEVAPGNMGLFDQALQWQKNIAAFGNGKSVTLFESAGASVSL 206  
 QY 131 MMITQOTGLFHRGIMSGNSMCSA--STECOSRALTMARKRVYKGEENEKDIIEFLM 187  
 DB 207 HLCSQSYPLFTFRALIESGSSNAPVAVKHPPEARNTLTLAKFTGC-SKENDTEITICLR 265  
 QY 188 KANPYDLIKEEPOVL 202  
 DB 266 NKDPOEITLNEKVL 285

RESULT 7  
 US-09-748-739A-4  
 Sequence 4, Application US/09748739A

Patent No. US20020119489A1  
 GENERAL INFORMATION:  
 APPLICANT: Lockridge, Oksana  
 APPLICANT: Watkins, Jeffrey D.  
 TITLE OF INVENTION: Butyrylcholinesterase Variants and  
 FILE REFERENCE: P-IX 4143  
 CURRENT APPLICATION NUMBER: US/09/748,739A  
 NUMBER OF SEQ ID NOS: 31  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 4  
 LENGTH: 574  
 TYPE: PRF  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Human Butyrylcholinesterase variant  
 US-09-748-739A-4

Query Match  
 Best Local Similarity 30.7%; Score 336; DB 10; Length 574;  
 Matches 79; Conservative 41; Mismatches 70; Indels 10; Gaps 6;

QY 12 SEDCLYLVNTDNDLPDKRPVWFHGGGTFEGEANNRMWGPDPYFMK-KPVVLVTVOYR 70  
 DB 89 SEDCLYLVNTDNDLPDKRPVWFHGGGTFEGEANNRMWGPDPYFMK-KPVVLVTVOYR 147  
 QY 71 LGVLGFLSKSENLNVPGNAGLKDQVMAIRFKSNIAIFGSDVNTIVFESAGASTHY 130  
 DB 148 VGALGFLALPG-NPEVAPGNMGLFDQALQWQKNIAAFGNGKSVTLFESAGASVSL 206  
 QY 131 MMITQOTGLFHRGIMSGNSMCSA--STECOSRALTMARKRVYKGEENEKDIIEFLM 187  
 DB 207 HLCSQSYPLFTFRALIESGSSNAPVAVKHPPEARNTLTLAKFTGC-SKENDTEITICLR 265  
 QY 188 KANPYDLIKEEPOVL 204  
 DB 266 NKDPOEITLNEKVL 285

RESULT 8  
 US-09-748-739A-17  
 Sequence 17, Application US/09748739A  
 Patent No. US20020119489A1  
 GENERAL INFORMATION:  
 APPLICANT: Lockridge, Oksana  
 APPLICANT: Watkins, Jeffrey D.  
 TITLE OF INVENTION: Butyrylcholinesterase Variants and  
 FILE REFERENCE: P-IX 4143  
 CURRENT APPLICATION NUMBER: US/09/748,739A  
 NUMBER OF SEQ ID NOS: 31  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 17  
 LENGTH: 574  
 TYPE: PRF  
 ORGANISM: Homo sapiens  
 US-09-748-739A-17

Query Match  
 Best Local Similarity 30.7%; Score 336; DB 10; Length 574;  
 Matches 79; Conservative 41; Mismatches 70; Indels 10; Gaps 6;

QY 12 SEDCLYLVNTDNDLPDKRPVWFHGGGTFEGEANNRMWGPDPYFMK-KPVVLVTVOYR 70  
 DB 89 SEDCLYLVNTDNDLPDKRPVWFHGGGTFEGEANNRMWGPDPYFMK-KPVVLVTVOYR 147  
 QY 71 LGVLGFLSKSENLNVPGNAGLKDQVMAIRFKSNIAIFGSDVNTIVFESAGASTHY 130  
 DB 148 VGALGFLALPG-NPEVAPGNMGLFDQALQWQKNIAAFGNGKSVTLFESAGASVSL 206  
 QY 131 MMITQOTGLFHRGIMSGNSMCSA--STECOSRALTMARKRVYKGEENEKDIIEFLM 187

[illegible]

RESULT 9  
US-09-748-739A-18  
; Sequence 18, Application US/09748739A

RESULT 10  
US-09-748-739A-19  
; Sequence 19, Application US/09748739A

Query Match	30.7%	Score 336	DB 10	Length 574
Best Local Similarity	39.5%	Pred. No. 4	1e-28	
Matches 79	Conservative 41	Mismatches 70	Indels 10	Gaps 6

[illegible]

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RESULT 11
US-09-748-739A-20
; Sequence 20, Application US/09748739A
; Patent No. US20020119489A1
; GENERAL INFORMATION:
; APPLICANT: Lockridge, Oksana
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: Butyrylcholinesterase Variants and
; TITLE OF INVENTION: Methods of Use
; FILE REFERENCE: P-IX 4143
; CURRENT APPLICATION NUMBER: US/09/748,739A
; CURRENT FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 574
; TYPE: PKI
; ORGANISM: Homo sapiens
US-09-748-739A-20

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Query Match	30.7%	Score 336;	DB 10;	Length 574;
Similarity	39.5%	Pred. No. 4.1e-28;		
Best Local	41;	Mismatches 70;	Indels 10;	Gaps 6;
Matches 79;	Conservative			

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RESULT 12
US-09-748-739A-2
: Sequence 2, Application US/09748739A
: Patent No. US20020119489A1
: GENERAL INFORMATION:
: APPLICANT: Lockridge, Oksana
: APPLICANT: Watkins, Jeffy D.
: TITLE OF INVENTION: Butyrylcholinesterase Variants and
: TITLE OF INVENTION: Methods of Use
: FILE REFERENCE: P-IX 4143
: CURRENT APPLICATION NUMBER: US/09/748, 739A
: CURRENT FILING DATE: 2000-12-06
: NUMBER OF SEQ ID NOS: 31
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 2

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us-09-776-910-15.rapb

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?   LENGTH: 602
?   TYPE: PRT
?   ORGANISM: Artificial Sequence
?   FEATURE:
?   OTHER INFORMATION: Human Butyrylcholinesterase variant
US-09-748-739v-2

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Query Match	30.7%	Score 336;	DB 10;	Length 602;
Best Local Similarity	39.5%	Pred. No. 4.4e-28;		
Matches	79;	Conservative	41;	Mismatches 70;

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Db 117 SEBCLILNWIPAPKP-KNATVLIMWGGGFGTCSLHAYIDCKFLARERIVVSMYR 175
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 71 LGVIGFLSKSNLWPGNAGLKDQVMAKMFERSNIAIFGGDVDNITYEGESAGASTHY 130
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 176 VGLAGTLALPG-NRPAPGNMGLFDQOLALQWOKNIAAAGGNPKSVTLFEGESAGAASTL 234
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 131 MMITEGTRGLFRGIMSGNMCSSAST--ECSRALMARVYGKGEENKDLIEFLM 187
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Db 235 HLISPGSHSLFTRAILOGSGSNAPMAYVSLYEAKNRTLLAKLTGC-SRENETETICLR 293
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Qy 188 KANPMDLKEEPQVL--TP 204
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 294 NKDPQELLNEAFVVPYGT 313
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RESULT 13
US-09-978-295A-254
? Sequence 254, Application US/09978295A
? Patent No. US2002015606A1
? GENERAL INFORMATION:
? APPLICANT: Ashkenazi, Avi
? APPLICANT: Baker Kevin P.
? APPLICANT: Botstein, David
? APPLICANT: Desnoyers, Luc
? APPLICANT: Eaton, Dan
? APPLICANT: Ferrara, Napoleon
? APPLICANT: Filvaroff, Ellen
? APPLICANT: Fong, Sherman
? APPLICANT: Gao, Wei-Qiang
? APPLICANT: Gerber, Hanspeter
? APPLICANT: Gerritsen, Mary E.
? APPLICANT: Goddard, Audrey
? APPLICANT: Godowski, Paul J.
? APPLICANT: Grimaldi, J. Christopher
? APPLICANT: Gurney, Austin L.
? APPLICANT: Hillan, Kenneth J.
? APPLICANT: Kijavlin, Ivar J.
? APPLICANT: Kuo, Sophia S.
? APPLICANT: Napier, Mary A.
? APPLICANT: Pan, James;
? APPLICANT: Paoni, Nicholas F.
? APPLICANT: Roy, Margaret Ann
? APPLICANT: Shelton, David L.
? APPLICANT: Stewart, Timothy A.
? APPLICANT: Tumas, Daniel
? APPLICANT: Williams, P. Mickey
? APPLICANT: Wood, William I.
? TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
? FILE REFERENCE: P2630P1c11
? CURRENT APPLICATION NUMBER: US/09/978,295A
? PRIOR FILING DATE: 2001-07-30
? PRIOR APPLICATION NUMBER: 09/918585
? PRIOR FILING DATE: 2001-07-30
? PRIOR APPLICATION NUMBER: 60/062250
? PRIOR FILING DATE: 1997-10-17
? PRIOR APPLICATION NUMBER: 60/064249
? PRIOR FILING DATE: 1997-11-03
? PRIOR APPLICATION NUMBER: 60/065311
? PRIOR FILING DATE: 1997-11-13

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1	PRIOR APPLICATION NUMBER: 60/066364
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5	PRIOR APPLICATION NUMBER: 60/077632
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8	PRIOR FILING DATE: 1998-03-11
9	PRIOR APPLICATION NUMBER: 60/077649
10	PRIOR FILING DATE: 1998-03-11
11	PRIOR APPLICATION NUMBER: 60/077791
12	PRIOR FILING DATE: 1998-03-12
13	PRIOR APPLICATION NUMBER: 60/078004
14	PRIOR FILING DATE: 1998-03-13
15	PRIOR APPLICATION NUMBER: 60/078866
16	PRIOR FILING DATE: 1998-03-20
17	PRIOR APPLICATION NUMBER: 60/078936
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19	PRIOR APPLICATION NUMBER: 60/078910
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23	PRIOR APPLICATION NUMBER: 60/079294
24	PRIOR FILING DATE: 1998-03-25
25	PRIOR APPLICATION NUMBER: 60/079656
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37	PRIOR APPLICATION NUMBER: 60/079920
38	PRIOR FILING DATE: 1998-03-30
39	PRIOR APPLICATION NUMBER: 60/079923
40	PRIOR FILING DATE: 1998-03-30
41	PRIOR APPLICATION NUMBER: 60/080105
42	PRIOR FILING DATE: 1998-03-31
43	PRIOR APPLICATION NUMBER: 60/080107
44	PRIOR FILING DATE: 1998-03-31
45	PRIOR APPLICATION NUMBER: 60/080165
46	PRIOR FILING DATE: 1998-03-31
47	PRIOR APPLICATION NUMBER: 60/080194
48	PRIOR FILING DATE: 1998-03-31
49	PRIOR APPLICATION NUMBER: 60/080327
50	PRIOR FILING DATE: 1998-04-01
51	PRIOR APPLICATION NUMBER: 60/080328
52	PRIOR FILING DATE: 1998-04-01
53	PRIOR APPLICATION NUMBER: 60/080333
54	PRIOR FILING DATE: 1998-04-01
55	PRIOR APPLICATION NUMBER: 60/080334
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57	PRIOR APPLICATION NUMBER: 60/081070
58	PRIOR FILING DATE: 1998-04-08
59	PRIOR APPLICATION NUMBER: 60/081049
60	PRIOR FILING DATE: 1998-04-08
61	PRIOR APPLICATION NUMBER: 60/081071
62	PRIOR FILING DATE: 1998-04-08
63	PRIOR APPLICATION NUMBER: 60/081195
64	PRIOR FILING DATE: 1998-04-08
65	PRIOR APPLICATION NUMBER: 60/081203
66	PRIOR FILING DATE: 1998-04-09
67	PRIOR APPLICATION NUMBER: 60/081229
68	PRIOR FILING DATE: 1998-04-09
69	PRIOR APPLICATION NUMBER: 60/081955
70	PRIOR FILING DATE: 1998-04-15
71	PRIOR APPLICATION NUMBER: 60/081817
72	PRIOR FILING DATE: 1998-04-15
73	PRIOR APPLICATION NUMBER: 60/081819

Mon Apr 14 10:18:14 2003

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PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081952  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081838  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/082568  
PRIOR FILING DATE: 1998-04-21  
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PRIOR FILING DATE: 1998-04-21  
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PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082804  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082700  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082797  
PRIOR FILING DATE: 1998-04-22  
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PRIOR FILING DATE: 1998-04-23  
PRIOR APPLICATION NUMBER: 60/083336  
PRIOR FILING DATE: 1998-04-27  
PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28  
PRIOR APPLICATION NUMBER: 60/083392  
PRIOR FILING DATE: 1998-04-29  
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PRIOR FILING DATE: 1998-05-07  
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PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085323  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085582  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085700  
PRIOR FILING DATE: 1998-05-15

PRIOR APPLICATION NUMBER: 60/085689  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085579  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085580  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085573  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 30.7%; Score 335.5; DB 9; Length 545;  
Best Local Similarity 44.2%; Pred. No. 4.3e-28;  
Matches 80; Conservative 29; Mismatches 63; Indels 9; Gaps 5;

QY 12 SEDCLYNTYNDLNP-DKKRPYVNFHGGGFEGEANKRWGCPDYFMKRPVLYTVQYR 70  
DB 217 SEDCLYNTYVAPARAPDQPLPVMVWFPDGAFLVGAAS-SYEGSDLAAREKTVLFLQHR 275  
QY 71 LGVLFSLKSENLNPNVGNAGLKDQVALRWFKSNITAFGGVDNITTVGESAGASTHY 130  
DB 276 LGIFGFSL--TDSHANGNNGILDQMAALFWOENIAATGCGDGNVTLFGQSGAMNSISG 333  
QY 131 MITEOTRGLFHRGIMMSGMSKCSASTECQSRALTMARVGYKG--EENKXILEFLMK 188  
DB 334 LMSPLASGLFHRALISOSGTALEFLRFT---SNPLKAKVAILLAGCNHNSGTILVNCILR 390  
QY 189 A 189  
DB 391 A 391

RESULT 14  
US-09-978-697-254  
Sequence 254, Application US/09978697  
Patent No. US20020169284A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fond, Sherman  
APPLICANT: Geo, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltzen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavin, Iyar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630PIC27  
CURRENT FILING DATE: 2001-10-16  
CURRENT FILING DATE: 2001-07-30  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250



us-09-776-910-15.rabb

[illegible]

PRIOR FILING DATE: 1998-05-13  
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 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085700  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085689  
 PRIOR FILING DATE: 1998-05-15  
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 PRIOR FILING DATE: 1998-05-15  
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 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085573  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085704  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085697

Query Match 30.7%; Score 335.5; DB 9; Length 545;  
 Best Local Similarity 44.2%; Pred. No. 4.3e-28;  
 Matches 80; Conservative 29; Mismatches 63; Indels 9; Gaps 5;

QY 12 SEDCLYLVNTDINP-DKRRPVVFIHGGFEGEAMRMVYGPDMKRVVLTVOYR 70  
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 DB 217 SEDCLYLVNTDINP-DKRRPVVFIHGGFEGEAMRMVYGPDMKRVVLTVOYR 275  
 QY 71 LGVIGFLSKSENLVPGNAGLKQVVALRMFKSNIALESGDVNITVFGSAGASTHY 130  
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 DB 276 LGIFFLS--IDDSHARNWGLDQMALRWQENIAAFGDPGVNLTFGSAGASTISG 333  
 QY 131 NMITEOTGLFHRGIMSGNSKCSASTECOSRALTMMKRVYKYG--DENKDLIEFLMK 188  
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 DB 334 LKMSPLASGLFHRASQSTALEFLRFT---SNPLKVKKVAHLGACNHNSTQLLVNCLR 390  
 QY 189 A 189  
 DB 391 A 391

RESULT 15  
 US-09-978-192A-254  
 Sequence 254, Application US/09978192A  
 Patent No. US2002017753A1  
 GENERAL INFORMATION:  
 APPLICANT: Ashkenazi, Avi  
 APPLICANT: Baker Kevin P.  
 APPLICANT: Botstein, David  
 APPLICANT: Desnoyers, Luc  
 APPLICANT: Eaton, Dan  
 APPLICANT: Ferrara, Napoleon  
 APPLICANT: Filvaroff, Ellen  
 APPLICANT: Fong, Sherman  
 APPLICANT: Gao, Wei-Qiang  
 APPLICANT: Gerber, Hanspeter  
 APPLICANT: Gerilsen, Mary E.  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Grimaldi, J. Christopher  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Hillan, Kenneth J.  
 APPLICANT: Kijavlin, Ivar J.  
 APPLICANT: Kuo, Sophia S.  
 APPLICANT: Napier, Mary A.  
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 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 FILE REFERENCE: P2630P1C9

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